

GenCore version 5.1.7
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OM nucleic - nucleic search, using bw model

Run on: February 11, 2006, 18:13:38 / Search time 5086.94 Seconds
(without alignments)
10984.434 Million cell updates/sec

Title: US-09-467-368-1
Perfect score: 983
Sequence: 1 TCGGCCCGACGCTCTGCAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:.*
1: gb_da.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_str.*
11: gb_sy.*
12: gb_un.*
13: gb_vl.*
14: gb_hcg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 983 | 100.0 | 983 | 6 AR044575 | AR044575 Sequence |
| 2 | 983 | 100.0 | 983 | 6 AR157660 | AR157660 Sequence |
| 3 | 845.2 | 86.0 | 2460 | 15 TL035436 | U35436 Thermomyces |
| 4 | 585 | 59.5 | 588 | 6 AX244978 | AX244978 Sequence |
| 5 | 262.4 | 26.7 | 89019 | 15 BX842624 | BX842624 Neurospor |
| 6 | 243.6 | 24.8 | 786 | 15 TRU24191 | U24191 Trichoderma |
| 7 | 240.6 | 24.5 | 1039 | 15 HIXY1 | X76047 H.insolens |
| 8 | 239 | 24.3 | 1123 | 6 165436 | 165436 Sequence 3 |
| 9 | 239 | 24.3 | 1123 | 6 BD006885 | BD006885 Aspergill |
| 10 | 232.6 | 23.7 | 841 | 15 AY156910 | AY156910 Trichoder |
| 11 | 228.2 | 23.2 | 672 | 15 AY320048 | AY320048 Trichoder |
| 12 | 214.6 | 21.8 | 2202 | 15 AF246830 | AF246830 Fusarium |
| 13 | 214.6 | 21.8 | 928 | 15 TV1012718 | TV1012718 Trichoder |
| 14 | 213 | 21.7 | 912 | 15 AK110604 | AK110604 Oryza sat |
| 15 | 211.4 | 21.5 | 686 | 15 AY648860 | AY648860 Gibberell |
| 16 | 206.2 | 21.0 | 678 | 15 AY536639 | AY536639 Aspergill |
| 17 | 205 | 20.9 | 1195 | 6 E28868 | E28868 Xylanaase ge |
| 18 | 205 | 20.9 | 1195 | 6 E28869 | E28869 Xylanaase ge |

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| 20 | 204.4 | 20.8 | 843 | 15 AY551187 | AY551187 Aspergill |
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| 22 | 203.4 | 20.7 | 2208 | 15 CEMX82 | D49851 Chaetomium |
| 23 | 203 | 20.7 | 696 | 6 CQ786060 | CQ786060 Sequence |
| 24 | 202.2 | 20.6 | 300800 | 15 SC0939112 | AL939112 Streptomy |
| 25 | 200.8 | 20.4 | 3173 | 15 AB110644 | AB110644 Streptomy |
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| 27 | 199.6 | 20.3 | 1767 | 15 SPXYL1 | X98518 Streptomyce |
| 28 | 199.6 | 20.3 | 851 | 6 AE2443 | AE2443 Sequence 5 |
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| 31 | 199.2 | 20.3 | 1008 | 15 AF194025 | AF194025 Streptomy |
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| 33 | 197.2 | 20.1 | 1375 | 15 AFL508952 | AJ508952 Nonomurae |
| 34 | 197.2 | 20.1 | 1375 | 6 AR274543 | AR274543 Sequence |
| 35 | 197.2 | 20.1 | 1375 | 6 AR369734 | AR369734 Sequence |
| 36 | 197.2 | 20.1 | 1375 | 6 AR41840 | AY575961 Gibberell |
| 37 | 196.8 | 20.0 | 687 | 15 AY575961 | AY575961 Gibberell |
| 38 | 194.8 | 19.8 | 2015 | 15 CEMX1 | D49850 Chaetomium |
| 39 | 194.6 | 19.8 | 695 | 15 CEN01CPS | AL115832 Botrytis |
| 40 | 191.6 | 19.5 | 1020 | 15 TRXN1GNA | X69573 T.reesei xy |
| 41 | 190 | 19.3 | 1015 | 6 AR055687 | AR055687 Sequence |
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| 43 | 190 | 19.3 | 3204 | 1 AY795559 | AY795559 Thermobif |
| 44 | 188.4 | 19.2 | 110000 | 1 CP000088_14 | Continuation (15 o |
| 45 | 188.2 | 19.1 | 514 | 6 E28872 | E28872 Xylanaase ge |

ALIGNMENTS

RESULT 1
LOCUS AR044575
DEFINITION Sequence 1 from patent US 5817500.
ACCESSION AR044575
VERSION AR044575.1 GI:5966040
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 983)
AUTHORS Hansen, P. Kamp., Wagner, P., Mullertz, A. and Knap, I. Helmer.
TITLE Animal Feed Additives
JOURNAL Patent: US 5817500-A 1 06-OCT-1998;
FEATURES
source location/Qualifiers
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ORIGIN

| Query Match | 100.0%; Score 983; DB 6; Length 983; |
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| Matches | 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
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| DB | 121 CGACAGCAACCCCACTCGAGGCTGCGACAGATGTTACTATTCTCGTGGAGT 180 |
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LOCUS ARI57660 983 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6245546.
ACCESSION ARI57660
VERSION ARI57660.1 GI:16218623
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 983)
AUTHORS Hansen, P., Kamp, W., Wagner, P., Mullertz, A. and Knap, I., Helmer.
TITLE Animal feed additives
JOURNAL Patent: US 6245546-A 1 12-JUN-2001;
FEATURES
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/organism="unknown"
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Query Match 100.0%; Score 983; DB 6; Length 983;

Best Local Similarity 100.0%; Pred. No. 7,8e-223;
Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGGCGCGAGCGTTCGCAATCTTGGCAATGATGATGTCGCGCTTTTACCCCGCTTGGCCTTGGC 60
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RESULT 3

TLU35436 2460 bp DNA linear PLN 15-NOV-2001
LOCUS Thermomyces lanuginosus endo-beta-1,4-D-xylanase precursor (xyna)
DEFINITION gene, complete cds.
ACCESSION U35436
VERSION U35436.1 GI:2737877
KEYWORDS Thermomyces lanuginosus
SOURCE Thermomyces lanuginosus
ORGANISM Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
REFERENCE 1 (bases 1 to 2460)
AUTHORS Schlaecher,A., Holzmann,K., Hayn,M., Steiner,W. and Schwab,H.
TITLE Cloning and characterization of the gene for the thermostable
xylanase Xyna from Thermomyces lanuginosus
JOURNAL J. Biotechnol. 49 (1-3), 211-218 (1996)
PUBMED 8879171
REFERENCE 2 (bases 1 to 2460)
AUTHORS Schlaecher,A., Holzmann,K., Hayn,M., Steiner,W. and Schwab,H.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1995) Institute of Biotechnology, SFB
Biocatalysis, TU-Graz, Petergasse 12, Graz 8010, Austria
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Matches 963; Conservative 0; Mismatches 3; Indels 106; Gaps 1;
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AX244978 588 bp DNA linear PAT 28-SEP-2001
LOCUS AX244978
DEFINITION Sequence 9 from Patent WO0166711.
ACCESSION AX244978
VERSION AX244978.1 GI:15859703
KEYWORDS Thermomyces lanuginosus
SOURCE Thermomyces lanuginosus

REFERENCE 1
AUTHORS Sjöbreen, O. and Sorensen, J.P.
TITLE Xylanase variants having altered sensitivity to xylanase inhibitors
JOURNAL Patent: WO 0166711-A 9 13-SEP-2001;
DANISCO A/S (DK)
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ORIGIN
Query Match 59.5%; Score 585; DB 6; Length 588;
Best Local Similarity 100.0%; Pred. No. 3,3e-128;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 CAGACAAACCCCAACCTGGAGGGCTGGACGATGTTATTAATTCCTCTGGTGAAGTAC 183
DB 4 CAGACAAACCCCAACCTGGAGGGCTGGACGATGTTATTAATTCCTCTGGTGAAGTAC 63
QY 184 GGTGAGCGCGACGCGACGTAACCACTGGAAAGCGGACACTACGATCAGCTGGGGA 243
DB 64 GGTGAGCGCGACGCGACGTAACCACTGGAAAGCGGACACTACGATCAGCTGGGGA 123
QY 244 GATGCGGGTAACTCTGCTGGTGAAGAGGGCTGGAAACCCGGCTGAAAGCAAGACATC 303
DB 124 GATGCGGGTAACTCTGCTGGTGAAGAGGGCTGGAAACCCGGCTGAAAGCAAGACATC 183
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QY 664 TTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTTGGCTAA 708
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RESULT 5
BX842624/c 89019 bp DNA linear PLN 17-APR-2005
LOCUS Neurospora crassa DNA linkage group I BAC clone B10D6.
DEFINITION BX842624
ACCESSION BX842624.1 GI:38566913
VERSION
KEYWORDS
SOURCE Neurospora crassa
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE 1
AUTHORS Schulte, U., Algn, V., Hohenel, J., Brandt, P., Fartmann, B.,
Holland, R., Nyakatura, G., Mewes, H.W. and Mannhaupt, G.
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 89019)
AUTHORS German Neurospora genome project.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-2003) MIPS, Institut fuer Bioinformatik,
GSP-Forschungszentrum fuer Umwelt und Gesundheit, GmbH
Ingolstaedter Landstrasse 1, D-85764 Neuberg, FRG; E-mail:
G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte,
Institute of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,
E-mail: ulrich-schulte@uni-duesseldorf.de
BAC clone 10D6 (strain OR74A) is available at the Fungal Genetic
Stock Center, <http://www.fgsc.net>
Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
<http://www.mwgda.com>
Information on performance of analysis and a more detailed
annotation of this entry and other sequences can be viewed at:
<http://mips.gsf.de/proj/neurospora>.

FEATURES
source location/Qualifiers
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Query Match 26.7%; Score 262.4; DB 15; Length 89019;
Best Local Similarity 65.3%; Pred. No. 2.1e-51;
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QY 234 CAGCTGGAGAGATGCGCGTAACCTCTCGGTGGAAGAGGCTGGAACCCCGGCTGAAGCG 293
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RESULT 6
TRU24191 786 bp mRNA linear PLN 25-MAR-1997
LOCUS DEFINITION Trichoderma reesei beta-xylanase (XYN2) mRNA, complete cds.
ACCESSION U24191
VERSION U24191.1 GI:780815
KEYWORDS
SOURCE Hypocrea jecorina
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 786)
AUTHORS la Grange,D.C., Preclorius,I.S. and van Zyl,W.H.
TITLE Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in Saccharomyces cerevisiae
JOURNAL Appl. Environ. Microbiol. 62 (3), 1036-1044 (1996)
PUBMED 8975397
REFERENCE 2 (bases 1 to 786)
AUTHORS van Zyl,W.
TITLE Direct Submission
JOURNAL Submitted (06-APR-1995) Willem H. van Zyl, University of Stellenbosch, Microbiology, Victoria street, Stellenbosch, 7600, South Africa

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Matches 406; Conservative 0; Mismatches 249; Indels 3; Gaps 1;
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Db 655 ACAGCGGAACCACTTCAACGCGGTGCTGACGAAGCGCTGACGCT---CGGACGATGG 711
Qy 635 ACTACGAGATGTTGCAACGAGGGCTACTTACAGCAGGCTATGCTGCATCACCGT 692
Db 712 ATTACAGATTTGTTCGCTGAGGAGGTTACTTTAGCTCTGCGCTTGCATCACCGT 769

RESULT 7
HIXYL1 1039 bp mRNA linear PLN 18-APR-2005
LOCUS DEFINITION H. insolens XYL1 mRNA for endoglucanase.
ACCESSION X76047
VERSION X76047.1 GI:505260
KEYWORDS endoxylanase; xyl1 gene.
SOURCE Humicola insolens
ORGANISM Humicola insolens
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Dalboege,H. and Hansen,H.P.H.
TITLE A novel method for efficient expression cloning of fungal enzyme genes
JOURNAL Mol. Gen. Genet. 243 (3), 253-260 (1994)
PUBMED 8190078
REFERENCE 2 (bases 1 to 1039)
AUTHORS Dalboege,H.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1993) H. Dalboege, Manager GeneExpress, Novo Nordisk A/S, Sydhavn, Fruedjervej 3, 2100 Copenhagen OE, DENMARK

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Query Match 24.5%; Score 240.6; DB 15; Length 1039;
Best Local Similarity 64.6%; Pred. No. 2.6e-46;
Matches 392; Conservative 0; Mismatches 209; Indels 6; Gaps 2;

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QY 207 CAACCTGGAAAGCGGACCTTACGAGTACAGTGGGGAATGGCGGTACCTGTGCGGG 266
DB 238 CAACCTCGAGGCGACCGCTTACAGGTACAGATGGGTAAACCGGCACTTGTGCGGG 297
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QY 327 AAAGGCAACGTAACCTTGGGCTTACGGTTGAGACCGGCAACCGGCTGTGAGTATTA 386
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QY 447 CGAGTGCAGAGTACATCTATCGACTCGGCAAGACACTGCGTCAAGCACTAGCAT 506
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DB 712 CTATGTT 718
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RESULT 8
LOCUS 165436 1123 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5667990.
ACCESSION 165436

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VERSION 165436.1 GI:2482006
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1123)
AUTHORS Berka, R. Michael., Yoder, W., Takagi, S. and Boomhathan, K. Chettier.
TITLE Aspergillus expression system
JOURNAL Patent: US 5667990-A 3 16-SEP-1997;
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Query Match 24.3%; Score 239; DB 6; Length 1123;
Best Local Similarity 64.4%; Pred. No. 6.2e-46;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

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DB 257 CTGGCAGCAACGGCTTCTTACTCTGTGTGTGCCACGGCGGAGCGGACGTTCACTA 316
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DB 317 CAACCTCGAGGCGACCGGCTTACAGTCAAGTGGCTGTAAACCGGCAACTTGTGCTGG 376
QY 267 AAAGGCTGGAACCCCGGCTGAAAGCAAGACCACTTCACTTGAAGGTGTTTACAGCC 326
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DB 791 CTATGTT 797
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RESULT 9
LOCUS BD006885 1123 bp DNA linear PAT 31-JAN-2002
DEFINITION Aspergillus expression system.
ACCESSION BD006885
VERSION BD006885.1 GI:18635256
KEYWORDS JP 2001025393-A/2.
SOURCE Humicola insolens
ORGANISM Humicola insolens

REFERENCE 1 (bases 1 to 1123)
AUTHORS Berka, R.M., Yoder, W., Takagi, S. and Boomiazan, C.C.
TITLE Aspergillus expression system
JOURNAL Patent: JP 2001025393-A 2 30-JAN-2001;
NOVO NORDISK BIOTECH INC
COMMENT OS Humicola insolens
PN JP 2001025393-A/2
PD 30-JAN-2001
PR 01-DEC-1993 US 08/161675
PI RANDY M BERKA, WENDY YODER, SHINOBU TAKAGI,
CARAPAN CHEYER BOOMIAZAN
PC C12N15/09, C12N1/15, C12P21/02// (C12N15/09, C12R1:66), (C12N15/09, C12R1:685),
PC (C12N15/09, C12R1:69), (C12N1/15, C12R1:66), (C12P21/02, C12R1:66),
PC (C12N15/00, C12R1:66), (C12N15/00, C12R1:685), (C12N15/00, PC
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FT Key Location/Qualifiers
CDS (126)..(806).
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Best Local Similarity 64.4%; Pred. No. 6.2e-46;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;
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197 GGTTCCTGGGACCACTGACGCGCCCTTCAGGCTGACAGGTCACCCCAAGCGAGG 256
147 CTGGACAGATGGTTATTAATTCTGGTGGAGTACGAGTGGAGCGACGACCTAGAC 206
257 CTGGACACACGCTACTCTTACTCGTGGTGGAGCGACCGGAGGCGAGTTAGTACAC 316
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567 TACCGTCAAGAGGCGCTGCACTTGAAGCGCTGGGCTGCGGCTGTTGATGTAACGG 626
674 CTGGGCAACATGACGAACCACTTGAAGCGGAGGAGCAAGCAAGCAAGCGCT--CGG 730
627 TACCACTTCTACAGATGTTGCAAGGAGGCTTACAGAGGCTTACAGGCTTACAGAT 686
731 CAGACCTACTACAGGCTGTGCGCACGAGGAGCTTACAGAGCAAGTGGAGTTCGACAT 790

QY 687 CACGCT 693
Db 791 CTATGTT 797
RESULT 10
LOCUS AY156910 841 bp mRNA linear PLN 11-DEC-2002
DEFINITION Trichoderma sp. SY xylanase mRNA, complete cds.
ACCESSION AY156910
VERSION AY156910.1 GI:26514829
KEYWORDS
SOURCE
ORGANISM
Trichoderma sp. SY
Trichoderma sp. SY
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma
1 (bases 1 to 841)
REFERENCE
AUTHORS Min, S.Y., Kim, B.G. and Ahn, J.-H.
TITLE Purification, Characterization, and cDNA Cloning of Xylanase from
JOURNAL Fungus Trichoderma Strain SY
REFERENCE 2 (bases 1 to 841)
AUTHORS Min, S.Y., Kim, B.G. and Ahn, J.-H.
TITLE Direct Submission
JOURNAL Submitted (30-SEP-2002) Forest and Environmental Science, Konkuk
University, 1 Hwayang-Dong, Kwangjin-Gu, Seoul 143-701, South Korea
FEATURES
source
1..841
/organism="Trichoderma sp. SY"
/mol_type="mRNA"
/strain="SY"
/db_xref="taxon:215577"
60..722
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/protein_id="P4N78423.1"
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/translation="MVAFTSLAGFAAVAGVLSAPTEVDVQEKQVIGPTGFNNGY
YSVNDHAGVYTNAGGSFVSVMASGAFVGGKGNPSSSTTTFNPSGSYSNDNS
YLSVYGSKNPLIEYIVENRGYTPSTGATKLEGEVLDSDVDIYTORVNPSTIG
TATFTQYVSRVSRSHRSRSGSVNNGHFRAMNLTGLDQDLYQIIAIVSGYFSSGAMIN
VS"
ORIGIN
Query Match 23.7%; Score 232.6; DB 15; Length 841;
Best Local Similarity 60.2%; Pred. No. 2e-44;
Matches 404; Conservative 0; Mismatches 264; Indels 3; Gaps 1;
54 CTTGCGGCTTACCGCGGACTGGGCGCTGGCCCTCCCGGACAGGAATGCCAGGAGCT 113
80 CCGCGCGGCTTTCGCGCTGTCGCGGAGTCTGCTGCGCTCTACTGAAGACGTCAGT 139
114 CGAAAAGGACAGACCAACCCCACTGGAGGCTGGACAGATGTTATTTCTTCTG 173
140 CGAAAAGGCTCAGTCACTTGGCGCCCGGACGCTTCAACACAGGCTACTACTGTA 199
174 GTGAGTGAAGGTTGAGGCGGACGACGACGTAACCAACCTGGAAGGCGGCACTTACGAT 233
200 CTGAAACAGCGGCACTCCGCGCTGATCTTACACCAAGCGGCTGCGGCTGTTACAGGT 259
234 CAGCTGGGAGATGGCGGTAACCTGTCGTGTAAGAAAGGCTGAAACCCCGGCTGAAAGC 293
260 CAACCTGGGCAACCTGCGGCACTTGTGGAGGAGGAGATGAAACCGGCGACGAGAC 319
294 AAGACCATCACTTTGAGGCTTTTACAGGCAACGAGCAACAGTACTCTTGGGCTTA 353
320 CAGAACCATCACTTCTCCGACAGTACAGGCCCAACACACAGCTACTCTCGCTTA 379
354 CGGTTGAGCCGCGCAACCGGCTGTGAGTATTAACCTGCGAGAACTTTGGCACTTATGA 413
380 CGGCTGTCAAGAACCCGCTCATGAGTACTACTATTGTCAAGAACTTTGGCACTTATGA 439

Qy 414 TCCTCTCCGAGTGTACCGATCTAGAACTGTGAGTGACGAGGTATGATTCGACT 473
 Db 440 CCCGTCGACGGGGCCGACCAAGCTGGGAGGTAGCTCGACGGGACGCTTACGACAT 499
 Qy 474 CGGCAAGACCACTCGCTCAACGCACTAGACGCGACCCAAACCTTTCGACCAATA 533
 Db 500 TTACGCGACGAGCGCTCAACGACCGCTCATCTCGGACGCGCACCTTTTACAGTA 559
 Qy 534 CTGCTGCTGCTCCGCGGACGAGCAAGCGGCTACCGTCCAGACGGGCTGCACTTGA 593
 Db 560 CTGGCTGGTGGCGCCGACGACCGCTCCAGCGGCTGGTCAACGTCGCAACACTTTAA 619
 Qy 594 GCGCTGGGCTCGCGCTGTTGAATGTCAACGCTGACACTACTACGATCGTTGCAAC 653
 Db 620 TGCCCTGGGCAATCTCGGCTGACGCT--GGAGACGTGAGACTACGATTTATGGCGT 676
 Qy 654 GAGAGGCTACTTTCAGCAGCGGCTATGCTGCATCAACGTTGCTGACGTTGAGACGT 713
 Db 677 GAGGAGTATTTTCAGCTCTGCGAGCGCGCAACTTAACTGACGTAGTGGCTGATGAGGA 736
 Qy 714 AACCTGTGCT 724
 Db 737 GACATGTAGT 747

RESULT 11

AY320048

LOCUS 672 bp mRNA linear PLN 14-JUN-2003

DEFINITION Trichoderma viride strain YNUCC0183 endo-1,4-beta-xylanase mRNA,

complete cds.

ACCESSION AY320048

VERSION AY320048.1 GI:32481056

KEYWORDS

SOURCE

ORGANISM

Trichoderma viride

Trichoderma viride

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreales; Hypocreales; mitosporic Hypocreales;

Trichoderma; Trichoderma viride species complex.

REFERENCE 1 (bases 1 to 672)

Li, W.P., Zhang, Q., Liao, C.L., Zhou, J.G., Yang, Y.H., Liu, W.J. and

Yang, Z.W.

Cloning and characterization of endo-1,4-beta-xylanase from

Trichoderma viride YNUCC0183

Unpublished

2 (bases 1 to 672)

Li, W.P., Zhang, Q., Liao, C.L., Zhou, J.G., Yang, Y.H., Liu, W.J. and

Yang, Z.W.

Direct Submission

Submitted (10-JUN-2003) Key Laboratory of Industrial Microbiology &

Fermentation Technology of Yunnan, School of Life Science, Yunnan

University, 2 North Road, Green Lake, Kunming, Yunnan 650091, China

Location/Qualifiers

1..672

/organism="Trichoderma viride"

/mol_type="mRNA"

/strain="YNUCC0183"

/db_xref="taxon:5547"

1..672

/EC_number="3.2.1.8"

/product="endo-1,4-beta-xylanase"

/protein_id="AAP83925.1"

/db_xref="GI:32481057"

/translation="MVSEPTLLAGFVAATGVALSPTENEVVDVEKQITGPGFNN

GYYSYNDGSGVTVYTNAGAGSFSVNNANGNFGKGMPPSSSRVINFSGSNP

GNSYLSYVGSKNPLIERYIVENFGTSTGTTGLGSDGSDVYDIYRTORVNS

IIGTATFYQVSVNRNRRSSGVTVAHFNMRNLGLTLGLDVIILAVEGYFSSGNA

NINNS"

ORIGIN

Query Match 23.2%; Score 228.2; DB 15; Length 672;
 Best Local Similarity 60.6%; Pred. No. 2.2e-43;
 Matches 393; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

Qy 45 CCCGTTGCCCTTGGGCTTACCGGAGACTGGGCGCTGGCTTCCCGGAGGAAATGC 104
 Db 21 CTGCGCGGCTTCTCGCTGTACCGAGATTCTTCGCTCCACTGAAGATGAGGT 80
 Qy 105 CACGAGCTCGAAAAAGCAGACAAACCCCACTCGAGGGCTGAGCAGATGTTATTA 164
 Db 81 CGTGAAGTGAAGAGGCGCAGACGATTTGGCCCGGAGCTAGGCTTAAACAACGCTACTA 140
 Qy 165 CTATTCTGTGTGATGACGCTGAGCGCAGGCCAGTACCAACTGGAAGCGGAC 224
 Db 141 CTACTCTACTGGAACCATGGCCATTCGCGGTGACATACCAACGATGTGCGGCTC 200
 Qy 225 CTAGAGATCAGCTGGGAGATGGCGGTTAACCCTGCGGTGGAAGAGGCTGGAACCCCG 284
 Db 201 ATTCAGGCTCACTGGGCAACTCGGCAACTTGTGAGAGCAAGAGATGAACCCCG 260
 Qy 285 CTTGAAGCAAGACCAATCCACTTTGAGGGTGTATACAGCCAAACGGCAACACTACT 344
 Db 261 CAGAGCTCCAGGGTCAATCACTTCTGAGAGCTAACCCCAACGGCAATACTACT 320
 Qy 345 TGCGGTCTAGGTTGAGAACCGGCAACCGCTGCTGAGTATTACATCGTCGAACCTTGG 404
 Db 321 CTAGTCTATGGCTGTGTCAAGAAACCTCATCATGAGTACTACATCGTTGAACTTTGG 380
 Qy 405 CACCTATGATCCTTCCCTCGGCTGCTACGATCTAGAACTGTGAGTGCAGCGGTAGCAT 464
 Db 381 AACCTACCAACCACTGACCGGCAACCAAGCTGGGAGAGTACTCTGACGCAAGGT 440
 Qy 465 CTATGACTCGGCAAGACCACTCGCTCAACGCACTAGCATGACGAGCAACCAACTT 524
 Db 441 CTAGCATCTACCGGCAACGAGCAAGTCAACACACTTTCATCTCGGAACCGGCACTT 500
 Qy 525 GACCAATATCTGTGCTGCTCGGCAAGCAAGCGCAACGCGTACCGTCCAGCGGCTG 584
 Db 501 TTACCACTATCTGCTGTGCTCGGCAACCAACCGCTCCAGCGGCTGCTGAGTGGCAA 560
 Qy 585 CCACTTTCAGCGCTCGGCTGCGGCTGCTGTTGAATGTCAACGCTTACCACTACTACGAT 644
 Db 561 CCATCTCAACCGCGGCAACCTGCGCTTGA--CCCTGGAAACTTTGACTACACAGAT 617
 Qy 645 CGTTGCAACGAGGCTACTTACAGACGCGCTATGCTGCATCAACCGTT 693
 Db 618 CATTCGCGTGAAGGCTACTTATGCTCTGTTAAGCCCAACTTAACGTT 666

RESULT 12

AF246830

LOCUS 2202 bp DNA linear PLN 20-FEB-2002

DEFINITION Fusarium oxysporum f. sp. lycopersici xylanase 5 protein (xyl5)

gene, complete cds.

ACCESSION AF246830

VERSION AF246830.1 GI:13491872

KEYWORDS

SOURCE

ORGANISM

Fusarium oxysporum f. sp. lycopersici

Fusarium oxysporum f. sp. lycopersici

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreales; Hypocreales; mitosporic Hypocreales; Fusarium;

Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 2202)

Gomez-Gomez, B., Isabel, M., Roncero, G., Di Pietro, A. and Hera, C.

Molecular characterization of a novel endo-beta-1,4-xylanase gene

from the vascular wilt fungus Fusarium oxysporum

Curr. Genet. 40 (4), 268-275 (2001)

Hera, C., Gomez-Gomez, B. and Roncero, M.

Direct Submission

Submitted (17-MAR-2000) Departamento de Genetica, Universidad de

Cordoba, Avda. San Alberto Magno s/n, Cordoba 14071, Spain

Location/Qualifiers

1..2202

/organism="Fusarium oxysporum f. sp. lycopersici"

gene
mRNA
CDS
ORIGIN

/mol_type="genomic DNA"
/db_xref="taxon:59765"
/note="forma_specialis: lycopersici"
<686..>1667
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/gene="xy15"
/codon_start=1
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GFYSSMDGADATYTNKGSGYSMEKDGANTVGGKMGPGKARTSYEGEYKPNQ
NSYLSVGMTRNPLVEYTVESFGYNSGATKTKGTAEAGSYDIPEITRNAPSI
DGTOTPOQYMSVRQKHSTGSDVDGHLHDANERKMKLGTIDYQILATBEGFSSGSH
MTVBGASGGAGSTGGDASQGGSDVQGGDASQGGSDGNGNSFQDPS
SENPOQDEIDTGANPEQ"

Query Match 21.8%; Score 214.6; DB 15; Length 2202;
Best Local Similarity 64.7%; Pred. No. 4,1e-40;
Matches 377; Conservative 0; Mismatches 159; Indels 47; Gaps 2;

QY 162 TTAATAATCTGTGTGAGTGAAGTGAAGCGGAGCCAGTACCAACTGGAAGCGG 221
DB 870 TGACTTTATATAGTGAATGATGGCGGATCCGATCCACTTACCAACGGTGAAGGAG 929
QY 222 CACCTACGAGATCACTGGGAGATGGCGGATCCTCGTGGTGAAGGCGTGAACCC 281
DB 930 TTCTTATCCATGAGTGAAGATGGCGGAGCAGTCTCGTGGTGAAGGCGTCTCC 989
QY 282 CGGCGTGAAC-----GCAAG 297
DB 990 TGGAAAGGCGCGTTATGATACACATTAAGCTTACATGCGCTCTGCTATATCTGTATGA 1049
QY 298 GCCATCCACTTTGAGGGTGTATACCAAGCCAAACGCAACAGTACCTTGGGTCTACCGGT 357
DB 1050 ACGATCTGTAGAGGAGAGATGACAAAGCCCAACAGTACCTCTGTGTACGGGT 1109
QY 358 TGAAGCCGCAACCGCGTGTGATATTAATCTGTGGAACCTTGGACCTATGATCCT 417
DB 1110 TGGACCCCAAAACCTCTGTGATATTAATCTGTGAGTCCCTGTGATATTAACAACCC 1169
QY 418 TCCTCGGAGTACCGATCTAGGAATGTGAGTGCAGCGGATGATCTATGACTCGGC 477
DB 1170 TCCAGCGTGTCTACCAAGAGGACCGTTGAGCGGATGGCAGACCTTACGACATCTTC 1229
QY 478 AAGACACTCGCGTCAACGCACTTAGCATTCAGCGGACCCAAACCTTGCACCAATATCG 537
DB 1230 GAGACCACTCGGACCAACGCGCCCTTCAATCGAGGATCTAGACCTTCAAGAGTACG 1289
QY 538 TCGGTCCGCGAGGACAAAGGACCAAGCGGTACCGTTCAGAGGCGGTCCACTTCAAGCC 597
DB 1290 TCTGTTCGCGAGCACACGCTCTACTGCGACCGTTCAGACATGAGTCTTCAATTCATC 1349
QY 598 TGGGCTCGCGGTGTTGAATGTCAACGCTGACCACTACTACAGATGTTGCAACGGAG 657
DB 1350 TGGGAGAGGCGCGGATGAAGCT---CGTACTCAACGACTTCAAGATCTCGCTACTAG 1406
QY 658 GGTACTTCAAGAGCGGCTATGCTGCACTCAACGTTGCTGAG 700
DB 1407 GGTACTTCAAGAGCGGATGCTCCACATGACCGTCTGAGG 1449

RESULT 13
LOCUS TV1012718 928 bp mRNA linear PLN 15-APR-2005
DEFINITION Trichoderma viride mRNA for endo-1,4-beta-xylanase.
ACCESSION AJ012718
VERSION AJ012718.1 GI:6434132

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCES
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

endo-1,4-beta-xylanase.
Trichoderma viride
Trichoderma viride
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma; Trichoderma viride species complex.
1 Furman-Matraso, N., Cohen, E. and Avni, A.
Mutations in the Active Site of the Ethylene Inducing Xylanase
Elicitor Inhibits the b-1,4-Endoxylanase Activity But Not the
Elicitation Activity
Unpublished
2 (bases 1 to 928)
Avni, A.
Direct Submission
Submitted (10-NOV-1998) Avni A., Plant Sciences, Tel-Aviv
University, Tel-Aviv University, Tel-Aviv, 69978, ISRAEL
Location/Qualifiers
1..928
/organism="Trichoderma viride"
/mol_type="mRNA"
/db_xref="taxon:5547"
63..734
/EC_number="3.2.1.8"
/codon_start=1
/product="endo-1,4-beta-xylanase"
/protein_id="CAB60757.1"
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/db_xref="InterPro:IPR001137"
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162..731
/product="endo-1,4-beta-xylanase"
/EC_number="3.2.1.8"

ORIGIN

Query Match 21.8%; Score 214.4; DB 15; Length 928;
Best Local Similarity 56.8%; Pred. No. 4.4e-40;
Matches 454; Conservative 0; Mismatches 341; Indels 5; Gaps 3;

QY 45 CCCGTTGCCCTTCCGCGCTTAGCGCGAGTGGGCGCTTCCGCGAGGGAATGC 104
DB 83 CTTGCGAGGCTTCCGCTGTATCCGAGTTCTGTCCGCTCCACTGAGACGTTGAGGT 142
QY 105 CACGAGCTCGAAAGGACAGACCAACCCCACTCGAGGCGTGGCAGATGTTATTA 164
DB 143 CGTGAAGTGAAGAGCGCCAGAGATGGCGCCGCGACTGGCTTCAACAACGCGTACTA 202
QY 165 CTATTTCTGTGTGAGTACCGTGTGAGCGGCAACGATCAACAACGTTGGAAGCGGAC 224
DB 203 CTACTCTCACTGGAACGATGGCAATTCGCGGTGACATACCAACGTTGGGCGCTC 262
QY 225 CTACGAGTCACTGGGAGATGGCGGTAACTCGTGGTGAAGAGGCTGAAACCCCGG 284
DB 263 ATTACAGGTCAACTGGGCAACTGGGCAACTTGTGTGAGAGCAAGGATGGAACCCCTG 322
QY 285 CCGTAACGCAAGACCAATCCACTTGAAGGTGTTTACAGGCCAAACGGCAACAGTACT 344
DB 323 CAGAGCTCCGAGATCACTTCTCTGAGAGCTACCAACCCCAACGGCAACAGTACT 382
QY 345 TCGGCTTACGCTTGAACCGGCAACCGCGTGTGAGATTAATCGTTCGAGAACTTTGG 404
DB 383 CTCACTATGAGCTGTGTCAGAGAACCCCTCATGAGTACTACATGTTGAGAACTTTGG 442
QY 405 CACCTATGATCTTCTCGGTGCTACGATCTAGGAACCTGACGATCGACGAGTATGAT 464
DB 443 AACCTAACCACTGACTGAGCAACCAACGAGCTGGGTGAGGTGAGTCTGACGAGCGT 502

| | | | |
|------------|----------|---|-----|
| Qy | 465 | CTATGACTCGGCAAGACCACTCGGTGACGCACTTAGATCGACGGCAACCAACCTT | 524 |
| Db | 503 | CTAGACGATCTAACCGCAGCAGCGAGGTCAACAGCTTCCATCATTCGGAAGGCCACTT | 562 |
| Qy | 525 | CGACCAATATCTGTCGTGGTCCGCGCAGACAGCGCACCGCGTACCGTTCAGACGGGTG | 584 |
| Db | 563 | TTACCAAGTACTGCTGTGCTCCGCGCACCA-CGCTCCGCGCGTCTCGGTCAAGGTTGCGAA | 621 |
| Qy | 585 | CCACTTCGACGCGTGGGCTGGCTGTTGAATGTCAAGGTTGACCACTACTACCGAT | 644 |
| Db | 622 | CCACTTTCACGCGTGGGCGCAACCTGGGCTTGA--CTTGGGAACCTTGAATACGAGAT | 679 |
| Qy | 645 | CGTTTGAACGAGGCGTACTTTCAGACGCGGTATCTTCGATCAACCTTGTCTGACGTG | 703 |
| Db | 680 | CATTGCGGTGAGGGGCTACTTATGCTCTGTGTAAGCCCACTTAACGTCACCTAAAGGC | 739 |
| Qy | 704 | -GCTTAAGCTTAACCTGCTGTGTATCTTCGACGACCAAGCCAAAGATGTCTGACATGT | 762 |
| Db | 740 | TGGTGGGTGGCGCATGAGAGAGATCATCTATTGAGCAACGACTATATGTGATTTAT | 799 |
| Qy | 763 | GCGCGTTGAAGGTATTCATATGACATATCTGTCTGCGCTTCGAGTATTAATTGGAGGA | 822 |
| Db | 800 | GCGGTACGATGTATTAACAAGCAGACAGATAGCCTTAACACCAATGTAACTTGAATAG | 859 |
| Qy | 823 | CTGTGAGAACTTGTGCGCA | 842 |
| Db | 860 | CAGTACGACTTGTGCGCA | 879 |
| RESULT 14 | | | |
| AK110604 | | | |
| LOCUS | | | |
| DEFINITION | AK110604 | 912 bp mRNA linear PLN 24-JUN-2003 | |
| ACCESSION | | Oryza sativa (japonica cultivar-group) cDNA clone:002-168-G08, full | |
| VERSION | | inbert sequence. | |
| KEYWORDS | | AK110604.1 GI:32995813 | |
| SOURCE | | FLI CDNA; oligo capping. | |
| ORGANISM | | Oryza sativa (japonica cultivar-group) | |
| REFERENCE | | Oryza sativa (japonica cultivar-group) | |
| AUTHORS | | Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | |
| | | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; | |
| | | Erihartoideae; Oryzaceae; Oryza. | |
| | | 1 | |
| | | The Rice Full-length cDNA Consortium, National Institute of | |
| | | Agrobiological Sciences Rice Full-length cDNA Project Team; | |
| | | Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., | |
| | | Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., | |
| | | Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., | |
| | | Ohtsuki,K., Shishiki,T., Foundation of Advancement of International | |
| | | Science Genome Sequencing & Analysis Group; Ootomo,Y., Murakami,K., | |
| | | Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., | |
| | | Kurotsuki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., | |
| | | Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nishikura,J., | |
| | | Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., | |
| | | Kusunegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; | |
| | | Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., | |
| | | Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., | |
| | | Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Oato,N., Oca,Y., | |
| | | Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., | |
| | | Yoshino,M. and Hayashizaki,Y. | |
| TITLE | | Collection, mapping, and annotation of over 28,000 cDNA clones from | |
| JOURNAL | | japonica rice | |
| PUBMED | | Science 301 (5631), 376-379 (2003) | |
| REFERENCE | | 12869764 | |
| AUTHORS | | 2 (bases 1 to 912) | |
| | | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., | |
| | | Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., | |
| | | Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hizumoto,K., Hirooka,T., | |
| | | Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., | |
| | | Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., | |
| | | Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., | |
| | | Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., | |

TITLE JOURNAL COMMENT

Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusunegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nishikura,J., Nishii,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Oato,N., Oca,Y., Ootomo,Y., Ryu,R., Satoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami,Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyota,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

Direct Submission

Submitted (27-ANG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28k full-length cDNA clones from japonica rice.

URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurotsuki,T., Kusunegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nishikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hizumoto,K., Hirooka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohtsuki,N., Ooka,Y., Satoh,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyota,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

Location/Qualifiers

1. 912

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="002-168-G08"

FEATURES source ORIGIN

Query Match 21.7%; Score 213; DB 15; Length 912;

Best Local Similarity 62.8%; Pred. No. 9,4e-40;

Matches 365; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

| | | | |
|----|-----|--|-----|
| Qy | 112 | CTTGAAAGGAGGACAGACCAACCCCACTCGGAGGCTCGGACGATGTTACTATTC | 171 |
| Db | 159 | CTTGAGAGGCGGACGTCACCGCACTCGGTGGAACTCAACAGGCTACTTTACTCG | 218 |
| Qy | 172 | TGGTGAAGTACCGTGAAGCGCAGCGACCTACACCACTGGAAGCGGCACCTACGAG | 231 |
| Db | 219 | TGGTGAAGTACCGTGAAGCGCAGCGCTCTGCTATTAACCATGGCCAGGCTCAATACCT | 278 |
| Qy | 232 | ATGACGTGGGAGATGCGGTAACTTCTGCTGTGAAGAGGCTGGAACCCCGGCTGGAAC | 291 |
| Db | 279 | GTCAGTGGCGCAACTGGCACTTCTGCTGTGGGAAGGATGGAACCCAGG---AACG | 335 |

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:07:17 ; Search time 615.413 Seconds
(without alignments)
10645.530 Million cell updates/sec

Title: US-09-467-368-1
Perfect score: 983
Sequence: 1 TCGGCCGACGCTTGCAAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :
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2: geneseqn1980s:*
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14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 983 | 100.0 | 983 | 2 AAT40742 | Aat40742 Xylanase |
| 2 | 983 | 100.0 | 983 | 2 AAT43010 | Aat43010 Endo-1,4- |
| 3 | 585 | 59.5 | 588 | 5 AAS13813 | Aas13813 DNA encod |
| 4 | 374 | 38.0 | 678 | 4 AAD11927 | Aad11927 Thermomyc |
| 5 | 239 | 24.3 | 1123 | 2 AAO74098 | Aao74098 Humicola |
| 6 | 239 | 24.3 | 1123 | 2 AAO94952 | Aao94952 Humicola |
| 7 | 224.6 | 22.8 | 666 | 10 ABO80362 | Abg80362 A. fumiga |
| 8 | 223 | 22.7 | 705 | 10 ABO80364 | Abg80364 A. fumiga |
| 9 | 205 | 20.9 | 1195 | 2 AAZ28864 | Aaz28864 Streptomy |
| 10 | 205 | 20.9 | 1195 | 2 AAZ28865 | Aaz28865 Streptomy |
| 11 | 203.4 | 20.7 | 576 | 10 ADK70798 | Adk70798 Streptomy |
| 12 | 203 | 20.6 | 696 | 12 ADL23221 | Adl23221 A. niger |
| 13 | 202.2 | 20.3 | 1008 | 12 ADJ35015 | Adj35015 DNA encod |
| 14 | 199.6 | 20.3 | 851 | 2 AAT63044 | Aat63044 Aspergill |
| 15 | 197.2 | 20.1 | 1375 | 2 AAX90405 | Aax90405 Actinomad |
| 16 | 197.2 | 20.1 | 1375 | 2 AAT64930 | Aat64930 Actinomad |
| 17 | 194.2 | 19.8 | 822 | 2 AAV29598 | Aav29598 DNA seque |
| 18 | 190.6 | 19.4 | 739 | 10 ABO80363 | Abg80363 A. fumiga |
| 19 | 190 | 19.3 | 1015 | 2 AAG54775 | Aag54775 T. reesei |

| | | | | | |
|----|-------|------|------|-------------|--------------------|
| 20 | 190 | 19.3 | 1015 | 2 AAV81332 | AAV81332 T. reesei |
| 21 | 187.8 | 19.1 | 1273 | 2 AAG90388 | Aag90388 Xylanase |
| 22 | 186.2 | 18.9 | 1059 | 2 ADJ35009 | Adj35009 DNA encod |
| 23 | 185 | 18.8 | 1047 | 12 ADJ34949 | Adj34949 DNA encod |
| 24 | 183.4 | 18.7 | 1057 | 2 AAO03405 | Aao03405 Streptomy |
| 25 | 181.8 | 18.5 | 1281 | 2 AAT71585 | Aat71585 Chaetomiu |
| 26 | 181.2 | 18.4 | 712 | 10 ABO80361 | Abg80361 A. fumiga |
| 27 | 171.8 | 17.5 | 572 | 2 AAO43458 | Aao43458 Sequence |
| 28 | 170 | 17.3 | 1074 | 12 ADJ34983 | Adj34983 DNA encod |
| 29 | 170 | 17.3 | 1137 | 12 ADJ35039 | Adj35039 DNA encod |
| 30 | 168.4 | 17.1 | 675 | 2 AAO36563 | Aao36563 Endo-xyla |
| 31 | 165.8 | 16.9 | 1041 | 12 ADJ34953 | Adj34953 DNA encod |
| 32 | 165.6 | 16.8 | 1044 | 12 ADJ35005 | Adj35005 DNA encod |
| 33 | 165.4 | 16.8 | 942 | 10 ABO80366 | Abg80366 A. fumiga |
| 34 | 165.4 | 16.8 | 1299 | 12 ADJ34961 | Adj34961 DNA encod |
| 35 | 165.2 | 16.8 | 927 | 2 AAO74638 | Aao74638 Aspergill |
| 36 | 164 | 16.7 | 516 | 2 AAO28828 | Aao28828 Recombina |
| 37 | 161.6 | 16.4 | 1083 | 12 ADJ35001 | Adj35001 DNA encod |
| 38 | 160.8 | 16.4 | 1044 | 12 ADJ34979 | Adj34979 DNA encod |
| 39 | 160.8 | 16.4 | 1083 | 12 ADJ34967 | Adj34967 DNA encod |
| 40 | 159 | 16.2 | 1581 | 2 AAO69150 | Aao69150 Aspergill |
| 41 | 156.2 | 15.9 | 1047 | 12 ADJ35037 | Adj35037 DNA encod |
| 42 | 153.6 | 15.6 | 2439 | 12 ADL23220 | Adl23220 A. niger |
| 43 | 150.8 | 15.3 | 1065 | 12 ADJ34999 | Adj34999 DNA encod |
| 44 | 150.6 | 15.3 | 1071 | 12 ADJ35017 | Adj35017 DNA encod |
| 45 | 150.2 | 15.3 | 1041 | 12 ADJ34943 | Adj34943 DNA encod |

ALIGNMENTS

| | |
|-------------------------------------|--|
| RESULT 1 | |
| AAAT40742 | |
| ID AAT40742 standard; cDNA; 983 BP. | |
| XX | AAAT40742; |
| AC | |
| XX | |
| DT | 21-MAY-1997 (first entry) |
| XX | |
| DE | Xylanase coding sequence. |
| XX | |
| KW | Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoaecius; |
| KW | Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia; |
| KW | Byssotrichum; Paecilomyces; animal feed additive; in-vivo breakdown; |
| KW | plant cell wall; growth rate; feed conversion; ss. |
| OS | Thermomyces lanuginosus. |
| XX | |
| FN | Key |
| FT | CDS |
| FT | Location/Qualifiers |
| FT | 31..708 |
| FT | /*tag= a |
| FT | /product= "xylanase" |
| XX | |
| PN | WO9623062-A1. |
| XX | |
| PD | 01-AUG-1996. |
| XX | |
| PF | 26-JAN-1996; 96WO-DX000046. |
| XX | |
| PR | 26-JAN-1995; 95DK-00000094. |
| XX | |
| PA | (NOVO) NOVO-NORDISK AS. |
| XX | |
| PI | Hansen PK, Wagner P, Muelleritz A, Knap IH, |
| XX | |
| DR | WPI; 1996-454790/45. |
| DR | P-PSDB; AAW01112. |
| XX | |
| PT | Fungal xylanase preps. for use as animal feed additives - and DNA |
| PT | construct for producing recombinant Thermomyces xylanase. |
| XX | |
| PS | Claim 5; Page 45-46; 69pp; English. |

CC This sequence represents the coding sequence for the xylanase from
 CC Thermomyces lanuginosus strain DSM 4109. The encoded xylanase, and
 CC xylanases derived from Humicola, Thermascus, Chaetomium, Mucor,
 CC Talaromyces, Maltibranchia, Myceliophthora, Thielavia, Byssoschlamus or
 CC Paecilomyces strains can be used in the monocomponent xylanase
 CC preparations of the invention. The xylanase preparations and the
 CC recombinant Thermomyces xylanase are useful as animal feed additives,
 CC which promote in-vivo breakdown of plant cell wall material and thus
 CC improve digestibility, growth rate and/or feed conversion
 CC
 XX Sequence 983 BP, 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 983; DB 2; Length 983;
 Best Local Similarity 100.0%; Pred. No. 5.1e-255;

Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TCGGCCGACGCTTTGCAATCTTGCAATGATGGCTTACCCCGTTGCCCTTGGC 60
QY 61 GCCTTAAGCCGACCTGGGGCCCTTCCCGCAGGGAATGCAAGAGCTGAAAAG 120
DB 61 GCCTTAAGCCGACCTGGGGCCCTTCCCGCAGGGAATGCAAGAGCTGAAAAG 120
QY 121 CGACGACAAACCCCAACTCGGAGGCTGACGAGTGTATTAATTCTCTGGTGAAGT 180
DB 121 CGACGACAAACCCCAACTCGGAGGCTGACGAGTGTATTAATTCTCTGGTGAAGT 180
QY 181 GACGCTGAGAGCGAGCCACGTACCAACCTGGAAGGCGCACCTACGAGATCAGCTGG 240
DB 181 GACGCTGAGAGCGAGCCACGTACCAACCTGGAAGGCGCACCTACGAGATCAGCTGG 240
QY 241 GGAATGCGCGGTAACTCTGCTGAGTGAAGGAGCTGGAACCCCGGCTGAACGCAAGAGCC 300
DB 241 GGAATGCGCGGTAACTCTGCTGAGTGAAGGAGCTGGAACCCCGGCTGAACGCAAGAGCC 300
QY 301 ATCCACTTTGAGGGTGTATTACAGCCAAACGGCAACAGCTTACGGGTCTACGGTTGG 360
DB 301 ATCCACTTTGAGGGTGTATTACAGCCAAACGGCAACAGCTTACGGGTCTACGGTTGG 360
QY 361 ACCGCGCAACCCGCTGGTGTGAGTATTTACATGCTCGAAGAACTTTGGCACTTATGATCTTCC 420
DB 361 ACCGCGCAACCCGCTGGTGTGAGTATTTACATGCTCGAAGAACTTTGGCACTTATGATCTTCC 420
QY 421 TCCGGTGTACCGATCTTGAAGACTGTGAGTGCAGCGGTAGACATCTATCGATCGGCAAG 480
DB 421 TCCGGTGTACCGATCTTGAAGACTGTGAGTGCAGCGGTAGACATCTATCGATCGGCAAG 480
QY 481 ACCACTCGCTCAACGCACTAGCATCGACGCGCAACCCAACTTCGACCAATACTGTGTG 540
DB 481 ACCACTCGCTCAACGCACTAGCATCGACGCGCAACCCAACTTCGACCAATACTGTGTG 540
QY 541 GTCCGCCAGGACAAAGCGGCTACCGTCCAGAGGGGCTGCCACTTTGAGCGCTGG 600
DB 541 GTCCGCCAGGACAAAGCGGCTACCGTCCAGAGGGGCTGCCACTTTGAGCGCTGG 600
QY 601 GCTGCGCGTGTGTTGAATGTCAACGAGTCAACCTACTCAAGATGTTGCAACGAGAGGC 660
DB 601 GCTGCGCGTGTGTTGAATGTCAACGAGTCAACCTACTCAAGATGTTGCAACGAGAGGC 660
QY 661 TACTTCAGACAGCGGCTATGCTCGCATCAACCGTGTGCTGAGTGGGCTGAAGAGTAACTGG 720
DB 661 TACTTCAGACAGCGGCTATGCTCGCATCAACCGTGTGCTGAGTGGGCTGAAGAGTAACTGG 720
QY 721 TGTGTGATTCGCGAGGCAACAGCCAAAGATGTCTCAATGTGCGCGTGTGAAGGTATTC 780
DB 721 TGTGTGATTCGCGAGGCAACAGCCAAAGATGTCTCAATGTGCGCGTGTGAAGGTATTC 780
QY 781 ATTCAGCATATCTGTGCTGCTTGGAGAGTACTTTGAGAGCACTGTGAGAACTTTGTC 840
DB 781 ATTCAGCATATCTGTGCTGCTTGGAGAGTACTTTGAGAGCACTGTGAGAACTTTGTC 840
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DB 841 GAGCTGCGCAGGATCAGTATGTTGCTTGGCGGTGTTTGTCTCCCTATTCCTGTAAGAAA 900
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DB 901 TTGTTATTTGCTTGTGTCTAGTGTACATGACGAGCAATTGAGGCTCAGCTTGGAA 960
QY 961 AAAAAAAAAAAAAAAAAAAAAA 983
DB 961 AAAAAAAAAAAAAAAAAAAAAA 983

```

RESULT 2

AAT43010
 ID AAT43010 standard; cDNA; 983 BP.

AC AAT43010;

DE 16-OCT-2003 (revised)

DT 22-FEB-1997 (first entry)

DE Endo-1,4-beta-D-xylanase gene.

XX Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;

KM Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;

XX flour; baking; dough; ss.

OS Thermomyces lanuginosus; (strain DSM 4109).

XX Key

FT 5'UTR Location/Qualifiers

FT 1..30

FT /*tag= a

FT 31..708

FT /*tag= b

FT /product= "Endo-1,4-beta-D-xylanase"

FT /note= "EC-3.2.1.8"

FT 709..983

FT /*tag= c

FT 3'UTR

XX W09632472-A1.

XX 17-OCT-1996.

XX 11-APR-1996; 96MO-DK000171.

XX 11-APR-1995; 95DK-00000435.

XX (NOVO) NOVO-NORDISK AS.

XX Jorgensen OB, SI JU, Jakobsen TS;

XX WPI: 1996-477123/47.

XX P-PSDB: MAM05187.

XX Claim 7; Page 30-31; 41pp; English.

XX The sequence encodes an endo-1,4-beta-D-xylanase from Thermomyces

XX lanuginosus (Humicola lanuginosa), which may be used as a bread-

XX improving additive. The enzyme may be expressed recombinantly from a

Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 983; DB 2; Length 983;

Best Local Similarity 100.0%; Pred. No. 5,1e-25; Mismatches 0; Indels 0; Gaps 0;

Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCGGCCCGACGCTCTTGGCAATCCTTGCAGTGTGCTGCTTACCCCGCTTGGCCG 60
 1 TCGGCCCGACGCTCTTGGCAATCCTTGCAGTGTGCTGCTTACCCCGCTTGGCCG 60
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 61 GCCTTAGCCGCGACTGGGGCCCTTGGCCCGGAGGAAATGCCAGGAGCTGAAAAG 120
 121 CGACAGCAACCCCAACTGGAGGGCTGGACAGATGTTTACTATTCCTGGTGAAGT 180
 121 CGACAGCAACCCCAACTGGAGGGCTGGACAGATGTTTACTATTCCTGGTGAAGT 180
 181 GACCGTGAAGCGCAGGCGACGTAACCAACCTGGAGGCGGACCTACGAGATGAGCTG 240
 181 GACCGTGAAGCGCAGGCGACGTAACCAACCTGGAGGCGGACCTACGAGATGAGCTG 240
 241 GGAATGCGCGGTAACTCTGCTGGTGGAAAAGGCTGGAAACCCCGGCTTGAACGCAAGACC 300
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 361 ACCGCGCAACCCGCTGCTGCTGATATTAATCACTGCGAAGCTTGGCACTTATGATCTTCC 420
 361 ACCGCGCAACCCGCTGCTGCTGATATTAATCACTGCGAAGCTTGGCACTTATGATCTTCC 420
 421 TCGCGTGCATCCGATCTTAGAAGAACTGTGCGACGCGTACATCTATGCACTCGGCAAG 480
 421 TCGCGTGCATCCGATCTTAGAAGAACTGTGCGACGCGTACATCTATGCACTCGGCAAG 480
 481 ACCAATGGCGCTCAACGCACTTAGATGACAGGCAACCCCAACCTTGCACCAATATCTGGTGG 540
 481 ACCAATGGCGCTCAACGCACTTAGATGACAGGCAACCCCAACCTTGCACCAATATCTGGTGG 540
 541 GTCCGCGAGCAGCAAGCGCAGCAGGCTGACCTGCAAGAGGCGCTGCCACTTGCAGCGCTGG 600
 541 GTCCGCGAGCAGCAAGCGCAGCAGGCTGACCTGCAAGAGGCGCTGCCACTTGCAGCGCTGG 600
 601 GCTGCGCGCTGTTGAATGTCAACGCTGACCACTACTACAGATCGTTGCAACGGAAGGCG 660
 601 GCTGCGCGCTGTTGAATGTCAACGCTGACCACTACTACAGATCGTTGCAACGGAAGGCG 660
 661 TACTTTCAGCAGCGGCTATGCTGCGATCACCGTGTGCTGAGCTGGGCTAAGAGTAACTGG 720
 661 TACTTTCAGCAGCGGCTATGCTGCGATCACCGTGTGCTGAGCTGGGCTAAGAGTAACTGG 720
 721 TGGTGATCTGCGCGAGGCAACGCAAGAAATGTGCTGAGATGTGCGGTTGAAGGATTTCA 780
 721 TGGTGATCTGCGCGAGGCAACGCAAGAAATGTGCTGAGATGTGCGGTTGAAGGATTTCA 780
 781 ATCAGCATATCTGTCTGCGCTTGGCAGATGATCTTGGAGAGCTGTGGAAGAACTTTGTGC 840
 781 ATCAGCATATCTGTCTGCGCTTGGCAGATGATCTTGGAGAGCTGTGGAAGAACTTTGTGC 840
 841 GAGCGTGGCGAGATCAAGTATGCTTGGCGGTGTTTGTGCTCCCTATCTCTGTGAAAAA 900
 841 GAGCGTGGCGAGATCAAGTATGCTTGGCGGTGTTTGTGCTCCCTATCTCTGTGAAAAA 900
 901 TTGTTATTTGCTTCTGCTGCTAGTGAACAATAGCCGAGAAATGAGAGCCCTACGCTTGGAAA 960
 901 TTGTTATTTGCTTCTGCTGCTAGTGAACAATAGCCGAGAAATGAGAGCCCTACGCTTGGAAA 960
 961 AAAAAAAAAAAAAAAAAAAAAA 983
 961 AAAAAAAAAAAAAAAAAAAAAA 983

RESULT 3

AAS13813
 ID AAS13813 standard; DNA, 588 BP.

AAS13813;

18-DEC-2001 (first entry)

DNA encoding Thermomyces lanuginosus xylanase A.

Xylanase A; plant cell wall; baking; cereal; starch production; wood; wood pulp bleaching; hemicellulose; arabinoxylan; foodstuff; bread; ds.

Thermomyces lanuginosus.

MO20016711-A1.

13-SEP-2001.

08-MAR-2001; 2001WO-1B000426.

08-MAR-2000; 2000GB-00005585.

27-JUN-2000; 2000GB-00015751.

(DANI-) DANISCO AS.

Sibbesen O, Sorensen JF;

WPI; 2001-596834/67.

Novel variant xylanase polypeptide or its fragment useful for degrading or modifying plant cell wall, comprises amino acid modifications such that the polypeptide has altered sensitivity to xylanase inhibitor.

Disclosure; Page 64; 70pp; English.

The invention relates to a variant xylanase polypeptide (I) or its fragment having xylanase activity, comprising one or more amino acid modifications such that (I) or its fragment has an altered sensitivity to a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or its coding sequence (II) is useful for degrading or modifying plant cell wall or for processing a plant material by contacting the plant cell wall or plant material with (I) or (II). (I) is useful for modifying plant materials, and in baking, processing cereals, starch production, processing wood and enhancing the bleaching of wood pulp. (I) is useful for altering the viscosity derived from the presence of hemicellulose or arabinoxylan in a solution or system comprising plant cell wall material. (I) is useful for preparing a foodstuff such as bread, pretzels, tortillas, cakes, cookies, biscuits or crackers. The present sequence represents the coding sequence of Thermomyces lanuginosus xylanase A as described in the method of the invention

Sequence 588 BP; 131 A; 178 C; 168 G; 111 T; 0 U; 0 Other;

Query Match 59.5%; Score 585; DB 5; Length 588;

Best Local Similarity 100.0%; Pred. No. 1.4e-147; Mismatches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

124 CAGACAAACCCCAACTGGAGGGCTGGACAGATGTTTACTTCTGGTGAAGTAC 183
 124 CAGACAAACCCCAACTGGAGGGCTGGACAGATGTTTACTTCTGGTGAAGTAC 183
 4 CAGACAAACCCCAACTGGAGGGCTGGACAGATGTTTACTTCTGGTGAAGTAC 63
 184 GGTGAGCGCAGGCGCAGTACCAACCACTGAAAGCGGCACTACGATCACTGGGGA 243
 184 GGTGAGCGCAGGCGCAGTACCAACCACTGAAAGCGGCACTACGATCACTGGGGA 243
 64 GGTGAGCGCAGGCGCAGTACCAACCACTGAAAGCGGCACTACGATCACTGGGGA 123
 64 GGTGAGCGCAGGCGCAGTACCAACCACTGAAAGCGGCACTACGATCACTGGGGA 123
 244 GATGCGCGTAACTCTGCTGGTGGAAAAGGCTGGAACCCCGGCTGGAACGCAAGCCATC 303
 244 GATGCGCGTAACTCTGCTGGTGGAAAAGGCTGGAACCCCGGCTGGAACGCAAGCCATC 303
 124 GATGCGCGTAACTCTGCTGGTGGAAAAGGCTGGAACCCCGGCTGGAACGCAAGCCATC 183
 124 GATGCGCGTAACTCTGCTGGTGGAAAAGGCTGGAACCCCGGCTGGAACGCAAGCCATC 183
 304 CACTTGAGGGGTGTTTACAGCCAAACGCAACGATCACTTGGGCTACGCTTGAACC 363
 304 CACTTGAGGGGTGTTTACAGCCAAACGCAACGATCACTTGGGCTACGCTTGAACC 363

DB 184 CACTTGAGGGGTGTTTACGACCAACGGCAACGCTACCTGGGGTCTACGGTTGACC 243
QY 364 CGCAACCCCGTGGTGCAGATATTACATGCTGCAGAACTTTGGACCTATGATCTTCTCC 423
DB 244 CGCAACCCCGTGGTGCAGATATTACATGCTGCAGAACTTTGGACCTATGATCTTCTCC 303
QY 424 GGTGCTACCGATCTAGGAACTGTGAGTGCACGGTAGCATCTATCGACTCGGCAAGACC 483
DB 304 GGTGCTACCGATCTAGGAACTGTGAGTGCACGGTAGCATCTATCGACTCGGCAAGACC 363
QY 484 ACTGCGCTCAACGCACTAGCATGACGCGCAACCCAACTTTGACCAATATGCTGCTC 543
DB 364 ACTGCGCTCAACGCACTAGCATGACGCGCAACCCAACTTTGACCAATATGCTGCTC 423
QY 544 CGCCAGCAAGCCGCAACGAGGGTACCGTGCAGACGGGCTGCCACTTTCAGAGCTTGAGCT 603
DB 424 CGCCAGCAAGCCGCAACGAGGGTACCGTGCAGACGGGCTGCCACTTTCAGAGCTTGAGCT 483
QY 604 CGGCGTGGTTGAATGTCACAGGTGACCACTACTACAGATCGTTGCACAGAGGGCTAC 663
DB 484 CGGCGTGGTTGAATGTCACAGGTGACCACTACTACAGATCGTTGCACAGAGGGCTAC 543
QY 664 TTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAA 708
DB 544 TTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAA 588

RESULT 4

AAD17927
ID AAD17927 standard; DNA; 678 BP.

AC AAD17927;
DT 10-DEC-2001 (first entry)

DE Thermomyces lanuginosus codon optimised xylanase gene.

XX Xylanase; Pichia cell; heterologous nucleotide; codon optimisation; de.

OS Thermomyces lanuginosus.

XX Synthetic.

PN MO20016693-A1.

XX 13-SEP-2001.

PF 09-MAR-2001; 2001WO-DK000154.

PR 10-MAR-2000; 2000DK-00000392.

PR 15-MAR-2000; 2000DK-00000419.

XX (NOVO) NOVOZYMES AS.

PI Takagi S, Terui Y, Teutsuni N, Taira R;

DR WPI; 2001-582273/65.

PT Novel Pichia cell useful for producing polypeptide of interest, comprises
a copy of heterologous nucleotide sequence encoding polypeptide of
interest.

XX Claim 14; Page 38-39; 61pp; English.

CC The invention relates to a Pichia cell comprising at least one copy of
heterologous nucleotide sequence encoding a polypeptide of interest,
where the codon usage of the sequence has been adjusted to match the
preferred codon usage of P. methanolic. The invention also relates to a
method for producing high yields of heterologous codon optimised
polypeptide in a Pichia cell. The Pichia cell is useful for producing a
polypeptide of interest, where the polypeptide is encoded by a nucleotide
sequence heterologous to P. methanolic. The present sequence is
Thermomyces lanuginosus codon optimised xylanase gene which is the

CC heterologous DNA used in the invention

XX Sequence 678 BP; 180 A; 89 C; 152 G; 257 T; 0 U; 0 Other;

SQ Query Match 38.0%; Score 374; DB 4; Length 678;

Best Local Similarity 72.0%; Pred. No. 1.5e-30; Mismatches 190; Indels 0; Gaps 0;

Matches 488; Conservative 0;

QY 31 ATGATCGGCTTTTACCCCGGTTGCGCTTGCAGGCTTACCGGAGGCTTGCCTTC 90
DB 1 ATGATCGGCTTTTACCCCGGTTGCGCTTGCAGGCTTACCGGAGGCTTGCCTTC 60
QY 91 CGGCAAGGGAATGCCAGAGCTGAAAGCAAGCAACCCCAACTCGAGGGCTCG 150
DB 61 CGAGAGGTAATCTACTGAAATTAAGAAAAGCAAACTCAATTCGAAAGGTTGG 120
QY 151 CAGATGTTTATTAATTTCTGTTGAGAGTGAAGGTGAGAGGCAAGCTACCAAC 210
DB 121 CATGATGGTTATTAATTTCTGTTGAGAGTGAAGGTGAGAGGCTACCTTATTAAT 180
QY 211 CTGGAAGGCGGCACTACAGATCAGCTGGGAGATGCGGTAACTCGTGGTGAAG 270
DB 181 TTGAAGGTGTAACCTATGAAATTTCTTGGGGTGAATGTTAGTTGGTGAAG 240
QY 271 GGTGGAACCCCGGCTGAAAGCAAGAGCCATCACTTGAAGGTTTAAACGCAAC 330
DB 241 GGTGGAATCAGGTTTAAATGCAAGAGCTATTCATTTGAAGGTTTAAACCAAT 300
QY 331 GGCACAGCTACCTTGGGTTCTACGGTTGAGACCCGCAACCCGCTGCTGAGTATTAATC 390
DB 301 GGTAAATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
QY 391 GTCGAGAACTTTGGACCTATGATCTTCTCGGTTGCTACCGTACCTGAGAACTGTCGAG 450
DB 361 GTTGAATAATTTGGTACTTATGATCCATCTTCTGCTGCTACTGATTTAGTACTGTA 420
QY 451 TGGACGCTGAGCTATGATCTGAGCAAGCACTGCGTCAACGCACTAGCATGAC 510
DB 421 TGGATGCTTCTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
QY 511 GGCACCCAACTTTGACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570
DB 481 GGTACTCAAACTTTCGATCAATATTTGCTGTTAGAAAGATMAAACTTCTGTAAT 540
QY 571 GTCAGAGCGGCTGCGCACTTGCAGCGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCT 630
DB 541 GTTCAATCTGTTGCTATTTGATGCTTGGGCTGAGCTGTTGAATGTTAATGTTGAT 600
QY 631 CACTACTACAGATGTTGCAACGAGGGCTACTTTCAGACGCGCTATGCTGCATCAC 690
DB 601 CATTAATATCAAAATGTTGCAACTGAAGGTTATTTCTTCTGTTATGCTAAGATTACT 660
QY 691 GTTCTGACGTGGGCTAA 708
DB 661 GTTCTGATGTTGGTTAA 678

RESULT 5

AAQ74098
ID AAQ74098 standard; DNA; 1123 BP.

XX AAQ74098;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 14-NOV-1995 (first entry)

DE Humicola xylanase gene.

XX Xylanase; vector; pAXX40-1-1; Aspergillus foetidus; ss.

OS Humicola insolens.

FN Key Location/Qualifiers
FT CDS 126..809
/*tag= a
XX M09515390-A1.
XX
XX 08-JUN-1995.
XX PD
XX 29-NOV-1994; 94WO-US013612.
XX PR 01-DEC-1993; 93US-00160591.
XX (NOVO) NOVO NORDISK BIOTECH INC.
XX Berka RM, Yoder W, Takagi S, Boomlnathan K;
XX WPI; 1995-215270/28.
XX P-PSDB; AAR75421.
XX
XX Aspergillus foetidus cells expressing heterologous enzyme - partic.
XX fungal lipase or xylanase, provide high yields without significant prodn.
XX of protease or mycotoxin.
XX
XX Disclousure; Page 35-36; 47pp; English.
XX
XX A DNA fragment (AA074098) encoding H. insolens xylanase (AAR75421) was
XX isolated from pYBS (DSM 6995) and inserted into pHD414 (contg. the TAKA
XX promoter and AMG terminator) to form pAXX40-1-1-1. This plasmid and
XX pJAL77 (impairing hygromycin B resistance) were used to transform
XX protoplasts of A. foetidus N0953. The xylanase yield was 0.12 g/l.
XX (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
XX correct OS field.)
XX
XX Sequence 1123 BP; 249 A; 342 C; 293 G; 239 T; 0 U; 0 Other;

Query Match 24.3%; Score 239; DB 2; Length 1123;
Best Local Similarity 64.4%; Pred. No. 5,4e-54;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

QY 87 CTTCCCGGACGAGAAATGCGACGAGCTCGAAAAGCGACAGAACCCCAACTCGAGGG 146
DB 197 CGTTCCTCGGACCAACTCGAGCGCCCTTCAGGCTTCGACAGGTGACCCCAACGCGAGGG 256
QY 147 CTGGCAAGATGTTATTCTATTCTCTGCTGAGAGTGAAGTGAAGCGAGCGCAAGTACAC 206
DB 257 CTGGCAACAGCGCTACTTCTACTCGTGTGTCGACGCGGAGCGCCAGTTCACTAC 316
QY 207 CAACCTGGAAAGCGGCACTACGAGATCAGCTGGGGAGATGCGGGTAACTCTGTCGGTGG 266
DB 317 CAACCTCGAAGGCGAGCGCTACAGGTACAGATGGCGTAAACCGGCAACTTCGTCGGTGG 376
QY 267 AAAGGGCTGGAACCCCGGCTGAAAGCAAGAACCATCTTTGAGGGTGTTTACCAACC 326
DB 377 TAAAGGTTGGAACCCGGG---AACCGGCGGACGATCAATACGCGCGCTACTTCAACC 433
QY 327 AAAGGGAACAGCTACTTGGGTCTACGTTGATGATCCCGCAACCCGCTGTCGATATA 386
DB 434 CCAAGGCAACGCGCTACTGCGCTGCTAGGCTGAGCCGCAACCCGCTGTCGATATA 493
QY 387 CATGCTCGAAGAACTTTGGCACTATGATCTTCTCCGGGTCTACCGATCTAGGAATGT 446
DB 494 TGTGATGAGTCTGATACGCACTACATTCGCGAGCGAGGCTCAGTACAAAGGCACTT 553
QY 447 CGAGTGGAGGATGATCTATGCACTCGGCAAGCACTGCGCTCAAGCGCACTAGCAT 506
DB 554 CTATACGACGCGCATCAGTATGACATCTTTGTGAGCACCGCTTAAACGAGCCGACAT 613
QY 507 CGAAGGCAACCAACTTTCGACCAATATGATGCTCGGCAAGCAAGGCAAGCGG 566
DB 614 CGAGGCAACCCGAGCTTTCAGAGTACTGTCTATTCGCAAGAAAGCGCTGTCGAGG 673
QY 567 TACCGTCCAGACGGGCTGCTCACTTCAGAGCTGCGGCTGCGCTGTTGAATGTCACGG 626

DB 674 CTGCGTCAACATGACGAACCACTTCAACGCGTGGCAGAGACCGAAATGCCGT---CGG 730
QY 627 TGACCACTACTACCAAGATCGTTGCAACGAGAGGGCTACTTCAGCAGCGGCTATGCTCGAT 686
DB 731 CCAGCACTACTACCAAGGCTGTCGACCGAGGCTTACAGAGAGTGGCGATCGACAT 790
QY 687 CACCGTT 693
DB 791 CTATGTT 797

RESULT 6

AA094952
ID AA094952 standard; DNA; 1123 BP.

XX AC AA094952;

XX AC 25-MAR-2003 (revised)

XX DT 02-DEC-1995 (first entry)

XX DB Humicola insolens xylanase.

XX XN Xylanase; DSM 6995; ss.

XX OS Humicola insolens.

XX FH Key Location/Qualifiers

XX FT CDS 126..806
/*tag= a

XX M09515391-A2.

XX PD 08-JUN-1995.

XX PP 29-NOV-1994; 94WO-US013613.

XX PR 01-DEC-1993; 93US-00161675.

XX PA (NOVO) NOVO NORDISK BIOTECH INC.

XX PI Berka RM, Yoder W, Takagi S, Boomlnathan K;

XX WPI; 1995-215271/28.

XX P-PSDB; AAR78231.

XX DR

XX PT Aspergillus japonicus-type cells expressing heterologous protein - esp.

XX PT fungal enzyme, provide high yields without significant prodn. of protease

XX PT or mycotoxin.

XX PS Example; Page 39-40; 50pp; English.

XX CC A strain of B. coli contg. the approx. 1,100 bp xylanase HindIII/ XbaI

XX CC cDNA fragment in pYBS is deposited in DSM as DSM 6995. The xylanase cDNA

XX CC fragment is isolated from one of the clones. The sequence of the xylanase

XX CC gene and protein are given in AA094952 and AAR78231 and the gene is

XX CC deposited as DSM 6995. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 1123 BP; 249 A; 342 C; 293 G; 239 T; 0 U; 0 Other;

Query Match 24.3%; Score 239; DB 2; Length 1123;
Best Local Similarity 64.4%; Pred. No. 5,4e-54;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

QY 87 CTTCCCGGACGAGAAATGCGACGAGCTCGAAAAGCGACAGAACCCCAACTCGAGGG 146
DB 197 CGTTCCTCGGACCAACTCGAGCGCCCTTCAGGCTTCGACAGTGAACCCCAACGCGAGGG 256
QY 147 CTGGCAAGATGTTATTCTATTCTCTGCTGAGAGTGAAGTGAAGCGAGCGCAAGTACAC 206
DB 257 CTGGCAACAGCGCTACTTCTACTCGTGTGTCGACGCGGAGCGCCAGTTCACTAC 316
QY 207 CAACCTGGAAGGCGGCACTACGAGATCACTGGGAGATGCGGGTAACTCTGTCGGTGG 266

Db 317 CAACTCGAGGCGAGCCGCTAACAGAGTCAGATGGCGTAACACCGCAACTTCGTGGTGG 376
 Qy 267 AAAGGCTGGAACCCCGGCTGAAGCAAGAGCCATCTTTGAGGATGTTTACCAACC 326
 Db 377 TAAAGGTTGAAACCCGG--AACCGCGCGACATCACTACGCGCGCTACTTCAACC 433
 Qy 327 AAACGGCAACGACTACCTTGGGCTCTACGCTTGAACCCGCAACCCGCTGTGAGTATTA 386
 Db 434 CCAAGGCAACGCTACCTGGCGCTACGAGCTGAACCCGCAACCCGCTCGTCAAGTACTA 493
 Qy 387 CATGCTGGAACCTTTGGACACTTATGATCTTCTCCGAGTCTACCATCTAGAACACTGT 446
 Db 494 TGTATCGAGTCGATCGGCACTGATCAATCCGCGACCGAGCTAGTACAAAGGACATTT 553
 Qy 447 CGAGTGGCAAGGATGATCTATTCAGCTCGGCAAGCACTGCGCTCAACGCACTTACAT 506
 Db 554 CTAATACGACCGGCGATGATGATGATCTTTGTGAGCAACCGCTTACAAACGAGCCAGAT 613
 Qy 507 CGACGGCAACCAACCTTGAACCAATCTGCTCGGCTCGGCAAGCAACGCGACACGCG 566
 Db 614 CGACGGCAACCGGACGTTCCAGCACTGATCTGCTTATCGGCAAGCAACGCTGTGAGAG 673
 Qy 567 TACCGTCAAGCGGCTGCTGCTTGAAGCCTTGGGCTGCGCTGTTGATGTCMAAG 626
 Db 674 CTGCTCAACATGACGAACCACTTCAACGCGTGGACAGACGGAATGCGCT--CGG 730
 Qy 627 TGACCACTACTACCGATGCTTGAACGAGAGGCTACTTCAAGCGGCTATGCTCGCAT 686
 Db 731 CCAAGCACTACTACCGATGCTTGAAGCCTTCAACGCGTGGACAGACGGAATGCGCAT 790
 Qy 687 CACCGTT 693
 Db 791 CTATGTT 797
 RESULT 7
 ABQ80362
 ID ABQ80362 standard; cDNA; 666 BP.
 AC ABQ80362;
 DT 11-AUG-2003 (first entry)
 DE
 XX A. fumigatus AfXYL1 cDNA.
 KW Gene; enzyme; tannase; cellulase; glucose oxidase; glucosylase; phytase;
 KW beta-galactosidase; invertase; lipase; alpha-amylase; lactase;
 KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
 KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
 KW glyceride; starch; maltodextrin; oxidated phenolic compound;
 KW polygalacturonic acid chain; xylan; xylol-oligomer; food; feed; beverage;
 KW textile; tea liquor; cleaning ability; ss.
 OS Aspergillus fumigatus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..666
 FT /tag= a
 FT /product= "Xylanase 1"
 FT
 XX MO2003012071-A2.
 PD 13-FEB-2003.
 XX
 PE 05-AUG-2002; 2002MO-US024842.
 XX
 PR 03-AUG-2001; 2001US-0309870P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Jiang B, Storms R, Roemer T, Bussey H;
 XX
 DR WPI; 2003-332729/31.

DR P-PSDB; ABB80185.
 XX
 PT Novel isolated Aspergillus fumigatus polypeptide, useful in various
 PT industries such as those involved in the making of food and feed,
 XX beverages, textiles and detergents.
 XX
 PS Claim 2; Page 163-64; 169pp; English.
 XX
 CC The sequences given in ABQ80319-66 encode enzymatic proteins derived from
 CC A. fumigatus. The resulting proteins display the catalytic activity of an
 CC enzyme such as tannase, cellulase, glucose oxidase, glucosylase,
 CC phytase, beta-galactosidase, invertase, lipase, alpha-amylase, lactase,
 CC polygalacturonase or xylanase. Compositions comprising the tannase are
 CC useful for modulating the amount of compounds that comprise a gallate
 CC ester linkage in a composition. Compositions comprising cellulase are
 CC useful for modulating the amount of cellulose in a composition.
 CC Compositions comprising glucose oxidase are useful for modulating the
 CC amount of glucose or oxygen in a composition. Compositions comprising
 CC phytase are useful for modulating the amount of myo-inositol phosphates
 CC in a composition. Compositions comprising beta-galactosidase are useful
 CC for modulating the amount of lactose in a composition. Compositions
 CC comprising sucrose or invertase are useful for modulating the amount of
 CC sucrose in a composition. Compositions comprising lipase are useful for
 CC modulating the amount of glyceride in a composition. Compositions
 CC comprising alpha-amylase are useful for modulating the amount of
 CC starches or maltodextrins in a composition. Compositions comprising
 CC lactase are useful for modulating the amount of oxidated phenolic
 CC compounds in a composition. Compositions comprising polygalacturonase
 CC are useful for modulating the amount of high or low molecular weight
 CC polygalacturonic acid chains in a composition. Compositions comprising
 CC xylanases are useful for modulating the amount of xylan or xylol-oligomers
 CC in a composition. The A. fumigatus proteins and corresponding DNA's are
 CC useful in various industries such as those involved in the making of food
 CC and feed, beverages, textiles and detergents. The DNA's are useful to
 CC express recombinant enzymes for characterization, modification or
 CC industrial uses; to compare with the nucleotide sequence of A. fumigatus
 CC to identify duplicated genes of paralogs having the same or similar
 CC biochemical activity and/or function, to compare with nucleic acid
 CC sequence of other related or distant fungal organisms to identify
 CC potential orthologous enzyme genes, for selecting and making oligomers
 CC for attachment to a nucleic acid array for examination of expression
 CC patterns, and to raise anti-protein antibodies. The polypeptide having
 CC tannase activity increases the yield of tea liquor from tea leaves,
 CC improves the colour, flavour and health benefits of tea products,
 CC particularly an instant tea product. The polypeptide having cellulase
 CC activity enhances cleaning ability of detergent compositions
 XX
 SQ Sequence 666 BP; 142 A; 199 C; 192 G; 133 T; 0 U; 0 Other;
 Query Match 22.8%; Score 224.6; DB 10; Length 666;
 Best Local Similarity 61.5%; Pred. No. 3.4e-50;
 Matches 413; Conservative 0; Mismatches 249; Indels 9; Gaps 3;
 Qy 31 ATGTGGGCTTTACCCCGCTTGGCGCTTACCGCGAGATGGGGCCCTGCTTC 90
 Db 1 ATGTCTCATCTCTTCTCTGCTGCTGCTTCCACCGCTTGGGCTGCTGCTTACA 60
 Qy 91 CCGG---CAGGGAATGACAGAGCTCGAAAGAGAGAGCAACCCCACTCGAGGGC 147
 Db 61 CCGGCTCGAGCAATGCTTGAAGCTAGCCAGCGGAGCTCACAGTCTCAAGACTGGC 120
 Qy 148 TGGCAGATGGTTTATTAATCTTCTGATGAGTACGCGTGAAGCGACAGCTTACCC 207
 Db 121 ACGAATAACGGCTACTACTCTTCTGACCGACGCGGCGGCGAGGTACCTACAC 180
 Qy 208 AACCTGGAAGCGGACCTACAGATCACTGGGGAATGGCGGTAACTCTGCTGATGA 267
 Db 181 AACGCAATGGCGGCGAGTACAGTGAAGCAACCTGCGGCACTTTGTGCTGGG 240
 Qy 268 AAGGCTGGAACCCCGGCTGAACGCAAGAGCCATCTTGAAGGCTTTACAGAGCA 327
 Db 241 AAGGCTGGAACCCCGGCTGAACGCAAGAGCCATCTTGAAGGCTTTACAGAGCA 297

Qy 328 AACGGCAAGCTACCTTCCGGTCTACGATGGAGCCCGCAACCCGCTGATCGATATTAC 387
Db 298 AGCGGAACGGCTACCTCTCCGCTGACCGCTGAGCAACGACGCTCGCTGGAAATTAC 357
Qy 388 ATTCGCAAGAACTTTGGCACTTATATCTTCTCCGCTGCTACCGATCTAGAACTGTC 447
Db 358 ATTCGCAAGAACTTTGGCACTTATATCTTCTCCGCTGCTACCGATCTAGAACTGTC 417
Qy 448 GAGTCGACGGGTAGCATATGATCGATCGGCAAGACCATCGGCTCAAGCACTTAGCATC 507
Db 418 GAGGACGACGGGGCCACGTCACACCTCTACAGAGACGAGCGGACGAATGCGCTCCATC 477
Qy 508 GACGCAACCAAACTTTCGACCAATATCTGCTGCTCCGCAAGCAAGCAAGCAAGCTG 567
Db 478 CAGGCAAGGGCTACTTTGACAGATCTGCTGCTCGGCTTCCGACCTGGAGAGTGA 537
Qy 568 ACCGTCAGAGCGGCTGCCACTTTCGACCGCTGCGCTCCGCTGTTGAATGTCACGCT 627
Db 538 ACTGTGACGAGCAAGAACCACTTGTATGCTGTGAGAAATGCGGCTCTCAATT--GGGG 594
Qy 628 GACCACTACTACCAATGCTTTCGACGAGGCTACTTTCAGACGCGCTATGCTCGCATC 687
Db 595 AACTGTGACTATATGATTTGTGCGAGGAGGCTACCAAGAGCAAGCGGCTCTGCTACTATC 654
Qy 688 ACCGTTGCTGA 698
Db 655 ACTGTTTCTTA 665

RESULT 8
AB080364
ID AB080364 standard; cDNA; 705 BP.

AC AB080364;
XX 11-AUG-2003 (first entry)
DT 11-AUG-2003 (first entry)
XX A. fumigatus AfXYL2 cDNA.
DE A. fumigatus AfXYL2 cDNA.

XX Gene, enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
XX beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
XX polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
XX glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
XX glyceride; starch; maltodextrin; oxidated phenolic compound;
XX polygalacturonic acid chain; xylan; xylol-oligomer; food; feed; beverage;
XX textile; tea liquor; cleaning ability; ss.

XX Aspergillus fumigatus.

XX Key Location/Qualifiers
XX CDS 1..705
XX FT /tag= a
XX FT /product= "Xylanase 2"

XX MO2003012071-A2.

XX 13-FEB-2003.

XX 05-AUG-2002; 2002MO-US024842.

XX 03-AUG-2001; 2001US-0309870P.

XX (BLIT-) ELITRA PHARM INC.

XX Jiang B, Storms R, Roemer T, Bussey H;

XX WPI, 2003-332729/31.

XX P-PSDB; ABB80186.

XX Novel isolated Aspergillus fumigatus polypeptide, useful in various
XX industries such as those involved in the making of food and feed,
XX beverages, textiles and detergents.

PS Claim 2; Page 165-66; 169pp; English.

XX The sequences given in AB080319-66 encode enzymatic proteins derived from
CC A. fumigatus. The resulting proteins display the catalytic activity of an
CC enzyme such as tannase, cellulase, glucose oxidase, glucoamylase, laccase,
CC phytase, beta-galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylase are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC laccase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xylol-oligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A. fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers
CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC tannase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions
CC
XX

Sequence 705 BP; 151 A; 227 C; 183 G; 144 T; 0 U; 0 Other;

Query Match 22.7%; Score 223; DB 10; Length 705;

Best Local Similarity 60.5%; Pred. No. 9,4e-50; Mismatches 250; Indels 18; Gaps 2;

Matches 411; Conservative 0; Mismatches 250; Indels 18; Gaps 2;

Qy 29 TGATGTCGCTTAAACCCCGCTTGCCTTGAAGCGGCACTGAGGCTCTGACCT 88
Db 23 TGCTGGGGGTGCTCCGCATTTGAGCTGTGGTGGCCCCGTGAAACCGAGACCACTGCT 82
Qy 89 TCCCGCAGAGGATGCCACGAGCTCGAAGGACGACACACCCCACTCGAGGGCT 148
Db 83 TCATGAGACTGCTCTTATGAGTTCCGTGACCGCGCGGACCCCAAGCTCCACCGCT 142
Qy 149 GGCACATGTTATTAATTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 208
Db 143 GGAACAAACGCTACTACTCTTCTGACTGATGCGGCGGCGGAGCTGACCTACCA 202
Qy 209 AACTGGAAGCGGCACTTACGATCAGCTGAGGAGATGAGCGGTAACTGTCGTCGTCGTC 268
Db 203 ATGGCGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 262
Qy 269 AGGCTGGAACCC-----CGGCTGAAACGAGACCATCACTTGAAG 313
Db 263 AGGCTGGAACCCCTGGAAGCGCTAGTACCGAGCTTAACTAGAACCACTACACGAG 322
Qy 314 GTGTTTACGCGCAAGGCAAGCTACCTTGGCGTCGTCGTCGTCGTCGTCGTCGTCGTC 373
Db 323 GCAAGCTTCAACCCGAGGCGGCAATGCTACCTGCTGTCGTCGTCGTCGTCGTCGTCGTC 382
Qy 374 TGATGAGTATTAATCATGTCGAGAACTTGGCACTTGAATCCCTTCCGTCGTCGTCGTC 433

```

Db      383 TGATTGAGTACTAGCTTTGTTGAGTGTGATGATACATACACCCCGGAGCGGCGTACT 442
Oy      434 ATTAGGAACTGTGAGTGCAGCGGTAGCATCTATTCGACTCGGCAAGACCACTCGCGTCA 493
Db      443 TCAGGGGCACTGTCAACACCGTGCATCTACACATCTACAGCGCGCTTGCATACA 502
Oy      494 ACGCACTAGCATGACGCGACCCCAACCTTCGACCAATCTGTGCTCGGCGCAGACA 553
Db      503 ATGCTCCCTCCATCGAAGGACCAAGACCTTCACCCAGTACTGGTCTGTGCGCACCTCCA 562
Oy      554 AGCGCACCAAGGCGTACCTCCAGACGGGCTGCACTTCGAGCGCTGGGCTGCGCTGTT 613
Db      563 AGCGTACCGGCGGACCTGTCAACATGCGCAACCTTCAGCGTGAAGACTGGGCA 622
Oy      614 TGAATGTCAAGCGTGAACCACTACTACGAGATGTTGCAACGAGGCGTACTTCAGCAGCG 673
Db      623 TGA---CTGGGAAGTCAACACTACAGATTGTGCGCACTGAGGGTTTACAGAGCAGCG 679
Oy      674 GCTATGCTCGCATCACCGT 692
Db      680 GATCGCTTCATCATCTGT 698

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RESULT 9

AAZ28864 ID AAZ28864 standard; DNA; 1195 BP.

XX AC AAZ28864;

XX DT 27-AUG-2003 (revised)

XX DT 01-FEB-2000 (first entry)

XX DE Streptomyces olivaceoviridis xylanase (XynG) gene.

XX KM xylanase; plasmid; expression; E.coli; xylO-oligosaccharide; xylan; pulp-bleaching; ds.

XX OS Streptomyces olivaceoviridis.

XX FH Key Location/Qualifiers

FT CDS 298..993

FT FT /*tag= a

FT FT /gene= "XynG"

FT FT /product= "xylanase"

FT FT sig_peptide 298..417

FT FT /*tag= b

FT FT mat_peptide 418..990

FT FT /*tag= c

FT FT /note= "mature peptide is claimed"

XX JPI1266873-A.

XX PD 05-OCT-1999.

XX PF 20-MAR-1998; 98JP-00090702.

XX PR 20-MAR-1998; 98JP-00090702.

XX PA (NORO) NORINSUISANSHO SHOKUHIN SOGO.

XX PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.

XX DR WPI; 1999-613780/53.

XX DR P-PsDB; AAY44183.

XX PT A xylanase gene, contiguous with a vector and a transformant - used for pulp-bleaching.

XX PS Claim 1; Page 5-6; 10pp; Japanese.

CC This sequence corresponds to a degenerate sequence encoding a xylanase precursor from Streptomyces olivaceoviridis. The sequence can be inserted into the plasmid pQ860 to generate plasmid pERM P-16713 for expression in e.g. E.coli. The xylanase is useful for the preparation of xylO-

CC oligosaccharide from xylan and for pulp-bleaching. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 1195 BP; 230 A; 457 C; 333 G; 174 T; 0 U; 1 Other;

SO Query Match 20.9%; Score 205; DB 2; Length 1195;

Best Local Similarity 62.9%; Pred. No. 8.5e-45;

Matches 354; Conservative 0; Mismatches 200; Indels 9; Gaps 2;

```

Oy      130 ACCCCCACTCGAGGCGTGGACGATGTTATTACTTCTGTTGAGTGAAGTGA 189
Db      430 ACCACCAACAGACCGGACACCAACAGGTTCTACTACTCTTCTGACCGAGCGGC 489
Oy      190 GCGCAGGCAACGTACACCAACCTGGAAGCGGCACTTACAGATCACTGGGAGATGCC 249
Db      490 GGTTCGCTCTGATGACCTTGAACTCGGCGGCACTACAGACCTCGTGAACGAACTGC 549
Oy      250 GGTAACTCTGCTCGGTGGAAGGGTGGAAACCCGCGCTGAAACGCAAGCATCACTTT 309
Db      550 GGGAACTTGTGTGCGCGGCAAGGGCTGAGCAACGCGGAGCGC--AGGAAGTCACTAC 606
Oy      310 GAGGCTGTTTACAGCCAAACGGCAAGCTTACCTGCGTCTACGCTTGAACCGGCAC 369
Db      607 TCGGACAGCTTCTACCCGTCGCGGCAAGGCTTACTGCGCTGTACGGGTGGAACCTCGAAC 666
Oy      370 CCGCTGTGTGAGTATTTACATGTCGAGAACTTTGGCACTTATGATCCTTCTCGGTGCT 429
Db      667 CCGCTGTGTGAGTATTTACATGTCGAGAACTTTGGCACTTATGATCCTTCTCGGTGCT 429
Oy      430 ACCGATCTAGGAAGTGTGAGTGTGAGAGGTGAGATGATCTATGATCTGCGGCAAGCACTGCC 489
Db      721 ACGTACAAAGGCAAGTGTGAGAGGTGAGAGGTGAGAGGTGAGAGGTGAGAGGTGAGAGGTGAG 780
Oy      490 GTCAAGCAACCTAGCATCGACGCGACCAACCTTTCAGCAACATAGTGTGCGTCCGCGAG 549
Db      781 TACAAGCGCCCTCTCGTGAAGGCAACCAAGCTTCAACAGTACTGAGAGGTGCGGAG 840
Oy      610 GGTTCGATGTCAACGCTGACACTTACATCAAGTGTGCAAGGAGGCTTACTTCC 669
Db      901 GGCATGTCAACTGGCACTTACGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Oy      670 AGCGCTATGCTGCATCACCGT 692
Db      961 AGCGCTCTTCAACTCACCGT 983

```

RESULT 10

AAZ28865 ID AAZ28865 standard; DNA; 1195 BP.

XX AC AAZ28865;

XX DT 27-AUG-2003 (revised)

XX DT 01-FEB-2000 (first entry)

XX DE Streptomyces olivaceoviridis xylanase (XynG) gene.

XX KM xylanase; plasmid; expression; E.coli; xylO-oligosaccharide; xylan; pulp-bleaching; ds.

XX OS Streptomyces olivaceoviridis.

XX FH Key Location/Qualifiers

FT CDS 298..993

FT FT /*tag= a

FT FT /gene= "XynG"

FT FT sig_peptide 298..417

FT FT /*tag= b

FT mat_peptide 418. .990
 FT /*tag= c
 FT /note= "mature peptide is claimed"
 XX
 XX JP11266873-A.
 XX
 XX 05-OCT-1999.
 XX
 XX 20-MAR-1998; 98JP-00090702.
 XX
 XX 20-MAR-1998; 98JP-00090702.
 XX
 XX (NORO) NORINSUISANSHO SHOKUIN SOGO.
 XX (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIUTSU.
 XX
 XX WPI, 1999-613780/53.
 XX P-PSDB; AA144183.
 XX
 XX A xylanase gene, contiguous with a vector and a transformant - used for
 XX pulp-bleaching.
 XX
 XX Claim 4; Page 6-7; 10pp; Japanese.
 XX
 XX This sequence corresponds to the complete sequence encoding a xylanase
 XX precursor from Streptomyces olivaceoviridis. The sequence can be inserted
 XX into the plasmid p0560 to generate plasmid pERM-P-16713 for expression in
 XX e.g. E.coli. The xylanase is useful for the preparation of xylol-
 XX oligosaccharide from xylan and for pulp-bleaching. (Updated on 27-AUG-
 XX 2003 to correct OS field.)
 XX
 XX Sequence 1195 BP; 230 A; 457 C; 333 G; 175 T; 0 U; 0 Other;
 SQ

Query Match 20.9%; Score 205; DB 2; Length 1195;
 Best Local Similarity 62.9%; Pred. No. 8,5e-45;
 Matches 354; Conservative 0; Mismatches 200; Indels 9; Gaps 2;

QY 130 ACCCCCACTCGAGAGGCTGACAGATGATTATTAATTCCTTGGTGAAGTACGGTGA 189
 DB 430 ACCACCAACGACGCGGACCAACACGCGTTCTACTCTTGTGACCGACGCGGCG 489
 QY 190 GCGGAGGCGACGTACCAACCTGGAGCGGCGACCTTACGAGTACGCTGGGAGATGCG 249
 DB 490 GATTGCGTCTGATGACCTGAACTCGGCGGCACTACAGACCTCGTGACGAACTGC 549
 QY 250 GGTAACTCTGCTGGTGAAGAGGCTGGAACCCCGGCTGAAAGCGAAGCCATCTT 309
 DB 550 GGGAACTTCTGCTGCGCGGAAAGGCTGGAAGCAACGCGGACGCG--AGGAACTGCACTAC 606
 QY 310 GAGGAGTGTTCACGACCAAGCGCAACGCTACCTTGGGCTTACGTTGACCGCGAAC 369
 DB 607 TCGGAGAGCTTTCACCTCCGCGCAACGCTACCTGCGGCTGTACGGGTGACCTCGAAC 666
 QY 370 CCGCTGCTGAGTATTATCATGCTGCAAGAACTTTGGACCTTATGATCTTCTCCGGTCT 429
 DB 667 CCGCTGCTGAGTATTATCATGCTGCAAGAACTTTGGACCTTATGATCTTCTCCGGTCT 429
 QY 430 ACCGATCTAGGAACCTGTGAGTGGACGCTGACATCTTACGCTGGGCAAGCACTTGC 489
 DB 721 ACGTACAAAGGCGACGCTACCAACGCGCGGCAAGTACGCTTACCAAGCAAGCGG 780
 QY 490 GTCAAGCAGACCTAGATGACGCGGACCAACCTTGCACCAATACTGCTGGTCCGCGAG 549
 DB 781 TACAAAGCCTCTCGTGGAGGACCAAGACCTTCAACCACTTGAAGGCTCCGGAG 840
 QY 550 GACAAAGCAGACGCGGCTACGCTGCAAGCGGCTGCACTTGCAGCTGGGCTTGCCT 609
 DB 841 TCAAGCGGAGCGGCGGACCATCACACCGGCAACCACTTGCAGGCTGGGCGCGTAC 900
 QY 610 GGTGTAATGTCAAGGCTGACCACTACTACCAAGTCTTGGCAAGGAGGCTACTTCCG 669
 DB 901 GGCATGCAACTGGGAGGCTTACGCTACTACATGATCATGGCCACCGAGGCTTACCAAGC 960
 QY 670 AGCGGCTATGCTCGCATACCGT 692

DB 961 AGCGGCTCTCCCACTCACCGT 983

RESULT 11
 ADK70798
 ID ADK70798 standard; DNA; 576 BP.
 XX
 XX ADK70798;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX Streptomyces olivaceoviridis xylan enzyme encoding DNA SEQ ID NO:1.
 XX
 XX Streptomyces olivaceoviridis; xylan enzyme; enzyme; feed additive;
 XX animal feed; gene; ds.
 XX
 XX Streptomyces olivaceoviridis.
 XX
 XX Key Location/Qualifiers
 FT CDS 1..576
 FT /*tag= a
 FT /product= "xylan enzyme"
 FT
 FT CNI405304-A.
 XX
 XX 26-MAR-2003.
 XX
 XX 14-SEP-2001; 2001CN-00142163.
 XX
 XX 14-SEP-2001; 2001CN-00142163.
 XX
 XX (FODDER-) FODDER INST CHINESE ACADEMIC SCI.
 XX
 XX Yao B, Fan Y, Zhang H;
 XX
 XX WPI; 2003-514374/49.
 XX
 XX P-PSDB; ADK70799.
 XX
 XX Heat-resisting, antiprotease acidic-neutral xylanase and its gene.
 XX
 XX Claim 3; SEQ ID NO 1; 21pp; Chinese.
 XX
 XX The present sequence encodes the Streptomyces olivaceoviridis xylan
 XX enzyme. The xylan enzyme has good heat stability, high activity under
 XX acidic and neutral pH. The xylan enzyme can be used as a feed additive
 XX and can be widely used in animal feed.
 XX
 XX Sequence 576 BP; 125 A; 207 C; 165 G; 79 T; 0 U; 0 Other;
 SQ

Query Match 20.7%; Score 203.4; DB 10; Length 576;
 Best Local Similarity 62.7%; Pred. No. 1.7e-44;
 Matches 353; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

QY 130 ACCCCCACTCGAGAGGCTGACAGATGATTATTAATTCCTTGGTGAAGTACGGTGA 189
 DB 13 ACCACCAACGACGCGGACCAACACGCGTTCTACTCTTGTGACCGACGCGGCG 72
 QY 190 GCGGAGGCGACGTACCAACCTGGAAGCGGCACTTACGAGTACGCTGGGAGATGCG 249
 DB 73 GATTGCGTCTGATGACCTGAACTCGGCGGCACTACGACCTGTGACGAACTGC 132
 QY 250 GGTAACTCTGCTGGTGAAGAGGCTGGAACCCCGGCTGAAAGCGAAGCATCTT 309
 DB 133 GGGAACTTCTGCTGCGCGGCAAGGCTGGAAGCAACGCGGAGCGC--AGGAACTGCACTAC 189
 QY 310 GAGGAGTGTTCACGACCAAGCGCAACGCTTACCTGCGGCTTACGCTGGGCTTGCCT 369
 DB 190 TCGGAGAGCTTTCACCTCCGCGCAACGCTGACCTTGTGACCGGCTGACCTCGAAC 249
 QY 370 CCGCTGCTGAGTATTATCATGCTGCAAGAACTTTGGCACTTATGATCTTCTCCGGTCT 429
 DB 250 CCGCTGCTGAGTATTATCATGCTGCAAGAACTTTGGCACTTATGATCTTCTCCGGTCT 429

CC method involves the direct screening of a cDNA library prepd. in bacteria
 CC (e.g. E. coli) transformed with DNA from a eukaryotic organism (e.g. A.
 CC niger) that produces the protein. Screening for xylanase-producing clones
 CC can be performed on agar plates containing oat spelt xylan and RBB-xylan.
 CC The method was utilised in the identification of cDNA clones (AA173042-
 CC 46) coding for A. niger cellulase, xylanase and arabinoxylan degrading
 CC enzymes (AAW14595-99). (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 851 BP; 201 A; 244 C; 224 G; 182 T; 0 U; 0 Other;

Query Match 20.1%; Score 199.6; DB 2; Length 851;
 Best Local Similarity 61.3%; Pred. No. 2.1e-43;

Matches 357; Conservative 0; Mismatches 219; Indels 6; Gaps 2;

128 CAACCCCACTCGAGGAGCTGGACGATGTTATTAATTCCTGTGGAGTACGAGT 187
 142 CGACCCCGAGCTCCAGCCGCGAGAACAGCGCTTCTACTACTCTTTGTGACCGACG 201
 188 GAGCGCAGGCCACGTACACCACTGGAMGGCGCACTTACGAGATCAGCTGGGAGATG 247
 202 GTGAGACGTGACCTACCAACGAGATGCTGGAGCTTACACTGTGAGTGTCCACAG 261
 248 GCGGTAACTCTGTGTGTGAGAAAGGCTGTGAACCCCGCTTGAACGACGACCTCACT 307
 262 TGGGCAACTTGTGTGTGAGAAAGGCTGTGAACCCCG--AAAGTCCGACGACATCACT 318
 308 TTGAGGAGTTTACAGCCAAACGCAACAGCTTACGCTTACGCTTGAACCCGCA 367
 319 ACAGCGGACCTTACACCTTACCGGACGCAACGCTTACCTCGTCTATAGCTGACACTG 378
 368 ACCGCTGTGTGAGTATTATTCGTGTGAGAACTTTGGACCTATGATCTTCTCCGATG 427
 379 ACCCTGTATGAGTACTATACGTCGTGTGAGTCTTACGCGGACATCAACCCCGGAGTGA 438
 428 CTACGATCTTGAAGTCTCGAGTCCGACGAGTGTGAGTATCTACGACTCGGCAAGCACTC 487
 439 GCACGTAAAGGGGACCTGTACCTCGACGAGTCCGTTACGATATCTACAGGCTACCC 498
 488 GCGTCAACGACCTAGATTCAGACGCGCAACCTTGAACCAATCTGTGCTGCGCC 547
 499 GTACCAATGCTGCTTCCATTTCAGGAGACCGCTACCTTACCTACGATCTGTGCTGCGCC 558
 548 AGAAGACGACGACGACGCGTACCTGTCCAGACGGGCTGACCTTGCAGCGCTGCGCG 607
 559 AGAACAAAGAGTGTGGCGGAAACGTTTACCACTCCCAACCACTTCAATGCTTGGGCTAAGC 618
 608 CTGCTTTGAATGTCACGCTGACCTACTACTTACCAATGCTTGGCAACGAGGCTTACTCA 667
 619 TGGGAAATGAA--CCTGGGTACTCTCAACATCTACAGATGTGGCTTACCGAGGGTTAACAGA 675
 668 GCAGCGGCTATGCTGCTGATCAACCGTTGCTGAGCTGGGCTAAG 709
 676 GCAGTGATCTTCTGCTCATCACTGTTCGGTAAAGCGGTGAAAG 717

RESULT 15
 AAX90405
 ID AAX90405 standard; DNA; 1375 BP.

XX AAX90405;

XX 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-SEP-1999 (first entry)

XX Actinomadura sp. DSM43186 35 kDa xylanase encoding DNA.

XX Actinomadura sp. DSM43186; xylanase; Actinomadura flexuosa; lignin;
 KW thermostable; biobleaching; wood pulp; bleaching; hemicellulase;
 KW paper processing; hemicellulose; ss.

XX Nonomuraea flexuosa.

XX

FR Key Location/Qualifiers
 FT CDS 303..1337
 FT /*tag= a
 FT /product= "xylanase"
 XX
 XX US5935836-A.
 XX
 XX 10-AUG-1999.
 XX
 XX 06-JUN-1995; 95US-00468812.
 XX
 XX 29-JUL-1994; 94US-00282001.
 PR 31-OCT-1994; 94US-00332412.
 XX
 PA (ROHG) ROEHM ENZYME FINLAND OY.
 PI Fingerstrom R, Lantto R, Paloheimo M, Suominen P, Vehmaanperae J;
 PI Maenylae A;
 XX WPI: 1996-141347/38.
 DR P-PSDB; AAY24480.
 XX
 PT Actinomadura xylan sequences and method of use.
 PS Disclosure; Fig 13; 54pp; English.
 XX
 CC The present invention describes a culture medium obtained from the
 CC culture of a recombinant host cell that is not Actinomadura flexuosa and
 CC has been transformed with a vector encoding a protein having xylanase
 CC activity, where the protein comprises an amino acid sequence from a
 CC xylanolytic fragment of the amino acid sequence in AAY24480 or AAY24481.
 CC Also described is an enzyme preparation derived from the culture medium.
 CC The enzyme composition can be used in a method for biobleaching,
 CC modifying plant biomass properties, especially the reduction of lignin
 CC content in pulp and paper processing. The xylanases are hemicellulases
 CC which partially degrade the hemicellulose and enhance the extractability
 CC of lignins by conventional chemical bleaching of wood pulp. It can be
 CC used alone or as a supplement to other treatments that reduce lignin
 CC content of wood pulp, increase its drainability or decrease its water
 CC retention. The culture medium can be used directly without the need to
 CC purify the enzymes. Actinomadura flexuosa xylanases have a pH optimum and
 CC thermostability desirable for the biobleaching of wood pulp reducing the
 CC need to acidify the pulp prior to xylanase treatment. The xylanases
 CC partially degrade the hemicellulose in wood pulp which enhances the
 CC extractability of lignins by conventional bleaching chemicals and results
 CC in a lower consumption of bleaching chemicals reducing the formation of
 CC environmentally undesired organic compounds. The present sequence encodes
 CC Actinomadura sp. DSM43186 35 kDa xylanase. N.B. This sequence is indexed
 CC from US5935836 which is a treat as basic specification for F19503639.
 CC (Updated on 25-MAR-2003 to correct DR field.) (Updated on 16-OCT-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 1375 BP; 265 A; 517 C; 400 G; 193 T; 0 U; 0 Other;

Query Match 20.1%; Score 197.2; DB 2; Length 1375;
 Best Local Similarity 58.6%; Pred. No. 1.1e-42;
 Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;

35 TCGGCTTACCCCGCTTGGCTTACGCGGAGCTGGGCGCTGCTCCCGG 94
 349 TCGGCTTCCGCGCATGTGACCAAGTCTTCCGCTGCGCATTCGCGATGCGG 408
 95 CAGGGAATGCGACGAGCTCGAAAGGACAGACCAACCCCACTCGAGGCTGCGACG 154
 409 TGCCTCCCGGACGCGCCACGACACACATCACTCCGAACCAACCGGCTACGACA 468
 155 ATGCTTATTAATCTTCTGTGTGAGTACGCGGTGAGCGGACCACTACCAACTCGG 214
 469 ACGGCTACTTCTACTCGTTCGACGACGCGCCGGGACCGTCTCATGACCTTCCACT 528
 215 AAGCGGCACTTACGAGATGCTGGGAGATGCGCGGTAACTCTGTGTGAGAAAGGCT 274
 529 CGGCGGCACTTACGACCTCGTGTGCGAACAACCGGGAATCTGTGCGCGCAAGGCT 588

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Oy 275 GGAACCCCGGCTGTAACGCAAGACCATCTTGAGGGTGTTTACGACCAACGGCA 334
Db 589 GGTCCACCGG---GGGACGGGGGACCGTACCTTACACGCCCTCTTCAACCGTGGGTA 645
Oy 335 ACAAGCTACCTTGGGCTTACGGGTGGAACCCGCAACCGCTGGTGCAGTATTACATCGTCG 394
Db 646 ACGGCTACCTCAACGCTTACGGCTGGACAGGAAACCGCTCGTGAATACTACATCGTCG 705
Oy 395 AGAATTGGGCACTTATGATCCTTCTCGGTGCTAACCGATCTAGGAACGTGAGTGG 454
Db 706 AGAGCTGGGGCACTTACCGGCCACCC-----GGCCTTACAAAGGGCACCGTCAACACCG 759
Oy 455 ACGGTAGCATCTATGCACTCGGCAAGACCACTCGGTCACGCACTTAGCATTCAGGCA 514
Db 760 ACGGGGGAAAGTACGACATCTTACGAGACCTGGCGGTACACGCGCTTCATTCAGGGCA 819
Oy 515 CCCAAACCTTGCACCAATACTGGTCGATCCGCGAGGACAGGCAACGCGTACCGTCC 574
Db 820 CCCGACCTTCAAGCAGTTCTGGAGCGTCCGGCAGCAGAGGGAGCAGCGGCACATCA 879
Oy 575 AGACGGGCTGCACTTGCACGCTGGGCTCGGCTGTGTTGATGTCAACGGTACCACT 634
Db 880 CCATCGGCAACCACTTGCACGCTGGGCGCGCGCATGMA---CCTGGGCAAGCCACG 936
Oy 635 ACTACCAATCGTTGCAACGAGGCTTTCAGCAGGGGCTATGCTGCAATCACCGTTG 694
Db 937 ACTACCAATCATGCGAGCCGAGGCTTACAGAGCAGCGTACCTCAACCGTTCATCA 996
Oy 695 CTGACGTGGGCTAAGACGTAACTTGGTG 722
Db 997 GCGAGGCTGGCAACCCGCGCAACCCGGG 1024

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Search completed: February 11, 2006, 18:30:52
 Job time : 619.413 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:13:54 ; Search time 4979.03 Seconds
(without alignments)
9237.078 Million cell updates/sec

Title: US-09-467-368-1
Perfect score: 983
Sequence: 1 TCGGCCCCGAGCTTGCAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_est4:
5: gb_est5:
6: gb_est6:
7: gb_est7:
8: gb_est8:
9: gb_est9:
10: gb_est10:
11: gb_est11:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 291.2 | 29.6 | 860 | 8 | DR637934 EST102855 |
| 2 | 291.2 | 29.6 | 883 | 8 | DR643290 EST103391 |
| 3 | 240.2 | 24.4 | 882 | 8 | DR037502 49478.2 L |
| 4 | 233.4 | 23.7 | 675 | 8 | DN588726 49478.1 L |
| 5 | 229 | 23.3 | 744 | 7 | CR867983 tric013xe |
| 6 | 229 | 23.3 | 799 | 6 | CB898036 tric013xe |
| 7 | 222.6 | 22.6 | 772 | 7 | CN133022 OX1_9 D10 |
| 8 | 220.4 | 22.4 | 639 | 8 | DR624928 EST101505 |
| 9 | 220.4 | 22.4 | 749 | 8 | DR623097 EST101322 |
| 10 | 220 | 22.4 | 768 | 7 | CP881056 tric083xj |
| 11 | 220 | 22.4 | 822 | 6 | CB907827 tric083xj |
| 12 | 219.4 | 22.3 | 686 | 8 | DR624738 EST101486 |
| 13 | 219.4 | 22.3 | 719 | 8 | DR631520 EST102164 |
| 14 | 219.4 | 22.3 | 733 | 8 | DR630899 EST102102 |
| 15 | 219.4 | 22.3 | 739 | 8 | DR624376 EST101450 |
| 16 | 219.4 | 22.3 | 741 | 8 | DR625790 EST101591 |
| 17 | 219.4 | 22.3 | 763 | 8 | DR624330 EST101445 |
| 18 | 219.4 | 22.3 | 784 | 8 | DR628641 EST101876 |
| 19 | 219.4 | 22.3 | 801 | 8 | DR631291 EST102141 |
| 20 | 219.4 | 22.3 | 807 | 8 | DR621776 EST101190 |
| 21 | 219.4 | 22.3 | 809 | 8 | DR627394 EST101752 |
| 22 | 219.4 | 22.3 | 842 | 8 | DR630375 EST102040 |

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 23 | 219.4 | 22.3 | 886 | 8 | DR621753 | DR621753 EST101188 |
| 24 | 219.4 | 22.3 | 891 | 8 | DR632055 | DR632055 EST102218 |
| 25 | 219.4 | 22.3 | 916 | 8 | DR622008 | DR622008 EST101213 |
| 26 | 219.2 | 22.3 | 729 | 8 | DR629975 | DR629975 EST102010 |
| 27 | 219.2 | 22.3 | 763 | 8 | DR623625 | DR623625 EST101375 |
| 28 | 219 | 22.3 | 734 | 8 | DR622879 | DR622879 EST101300 |
| 29 | 215.8 | 22.0 | 711 | 8 | DR622908 | DR622908 EST101311 |
| 30 | 215.8 | 22.0 | 770 | 8 | DR622508 | DR622508 EST101263 |
| 31 | 214.6 | 21.8 | 708 | 8 | DR631672 | DR631672 EST102180 |
| 32 | 211.4 | 21.5 | 921 | 6 | CD458837 | CD458837 Fg08_04b1 |
| 33 | 207.2 | 21.1 | 714 | 8 | DR631518 | DR631518 EST102164 |
| 34 | 202.8 | 20.6 | 671 | 8 | DR632323 | DR632323 EST102245 |
| 35 | 202 | 20.5 | 697 | 8 | DR625721 | DR625721 EST101584 |
| 36 | 201.8 | 20.5 | 673 | 8 | DR625705 | DR625705 EST101583 |
| 37 | 199.6 | 20.3 | 746 | 8 | DR701170 | DR701170 Asn_00615 |
| 38 | 199.4 | 20.3 | 655 | 8 | DR625642 | DR625642 EST101527 |
| 39 | 199.4 | 20.3 | 677 | 8 | DR629147 | DR629147 EST101927 |
| 40 | 199.4 | 20.3 | 738 | 6 | CD464145 | CD464145 ETH1_48_B |
| 41 | 198.6 | 20.2 | 871 | 8 | DR037503 | DR037503 49478.3 L |
| 42 | 196.4 | 20.0 | 746 | 6 | CB901964 | CB901964 tric028xi |
| 43 | 196.4 | 20.0 | 746 | 7 | CP871731 | CP871731 tric028xi |
| 44 | 196.2 | 20.0 | 680 | 8 | DR707969 | DR707969 Asn_08783 |
| 45 | 191.4 | 19.5 | 682 | 8 | DR702584 | DR702584 Asn_02201 |

ALIGNMENTS

RESULT 1
LOCUS DR637934 860 bp mRNA linear EST 11-JUL-2005
DEFINITION EST1028559 Fwv Gibberella moniliformis cDNA clone FwvB275, mRNA
ACCESSION DR637934
VERSION DR637934.1 GI:70712768
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Bakaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 860)
Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Uterback,T., Smith,S., Feldblum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
JOURNAL USDA/ARS/NCAR
COMMENT Contact: Brown, D.W.
USDA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncar.usda.gov
TIGR sequence name: FwvB275TH
Seq primer: AAT TAA CCC TCA AAG CG.
Location/Qualifiers
1. 860
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/db_xref="FwvB275"
/clone_type="mycelia"
/clone_id="Fwv"
/note="Vector: pBluescript II SK(+); Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fwv was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was

FEATURES

source

Qy 648 TGCAACGGAGGCTACTTACAGACGGGCTATGCTGCATCACCGTTGCTGACGTGG 703
Db 636 CGTACTGAGGGTTACTTACAGACGGGCTATGCTGCATCACCGTTGCTGAGGGGG 691
RESULT 3
LOCUS DR037502 882 bp mRNA linear EST 31-MAY-2005
DEFINITION 49478.2 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
ACCESSION DR037502
VERSION DR037502.1 GI:66839397
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 882)
AUTHORS Flinn, B., Rochwell, C., Sardana, R., Griffiths, R., Laque, M., De Koeijer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruet, G. and Regan, S. Generation of ESTs from late blight-challenged potato tubers Unpublished (2005)
TITLE Contact: Barry Flinn
JOURNAL The Canadian Potato Genome Project - BioAtlantech
COMMENT 921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
FEATURES Email: bflinn@bioatlantech.nb.ca
source Seq primer: T3.
Location/Qualifiers
 1..882
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Shepody"
 /db_xref="taxon:4113"
 /clone="49478"
 /issue_type="Tubers"
 /lab_host="XL10-Gold"
 /clone_lib="Late Blight-Challenged Tubers"
 /note="Vector: pBluescript II SK(+); XR; Site_1: EcoRI; Site_2: XhoI; supplier: Pathogen-challenge series. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with 5 ul of Phytophthora infestans (A2-mating type), through 2 puncture wounds 3 cm apart. The tubers were incubated 1 minute to allow inoculum absorption. The infection area was outlined for future collection reference. Surface slices were sampled from the tubers at 1 day, 5 days, 7 days, 11 days and 14 days post-infection. All samples were pooled and used for RNA isolation and library construction. A normalized library was constructed following a modified protocol of Bonaldo et al. (1996. Genome Research 6: 791-806)."
ORIGIN
 Query Match 24.4%; Score 240.2; DB 8; Length 882;
 Best Local Similarity 60.9%; Pred. No. 1.1e-56;
 Matches 411; Conservative 0; Mismatches 256; Indels 6; Gaps 1;
Qy 31 ATGCTGCGCTTACCCCGCTTGGCGGCTTACCGCGACTGGGGCCCTGCGCTTC 90
Db 25 ATGCTTCCCTTACTACTCTCTCATTTGCTGCGGCTTGGCGCTTCTGCTGAA 84
Qy 91 CCGGCAAGGATGCGACGAGCTCGAAAGACAGACAAACCCCAACTCGAGGGCTGG 150
Db 85 CCCAGACACGCCCTTACCCCGCCACA-----AGAAAGCCACGACCAACTGGCCAG 138
Qy 151 CACGATGGTTATTAATCTTCTGTGTGAGTAGACGCTGAGCGCAGCCACTACACCAAC 210
Db 139 AACGGCGGGTACTACTCTTCTGTGAGTAGACCAAGCCAGGCACTTACACCAAC 198
Qy 211 CTGAAAGCGGCACTTACGAGATCAGCTGGGAGATGCGGTAACTCTGCTGGGAAAG 270
Db 199 AAGGCGGCTGAGAGTACTCCCTGACTGAGAGCGGCAACGGCAACTGCTGGGAAAG 258

Qy 271 GCGTGAACCCCGGCTGAAGACGAAGCCATTCATTTGAGGGTGTTCACGCAAC 330
Db 259 GGATGGAACCCAGGAAGTGCACAGACATGACTCTGGGACTTCAACCCCAATGGT 318
Qy 331 GGCACAGCTTACTTGGCGGTCTACGGTTGACCCCGCAACCGCTGTGAGTATTACATC 390
Db 319 GGCACCGCTTACTTGGCGGTCTACGGTTGACCCCGCAACCGCTGTGAGTATTACATC 378
Qy 391 GTGAGAACTTGGCACTTATGATCTTCCCGGGGTGACCCGATTAAGAACTGTGAG 450
Db 379 GTTGAAGCTTGGCTTATATATGACCCCTCTCCGCTGTGAGCAAGGCAAGGCTAC 438
Qy 451 TGCAGCGGTAGCATCTATTCGAGCTGCGAAGACCACTGCGTCAACGCACTGATGAC 510
Db 439 GTTATGGAGCACTTCAACATCTCTCAAGCTACCGGTACCAACGACCTTCAATGAT 498
Qy 511 GGCACCAACCTTTCGACCAATATCTGTGGTCCGCAAGACCAAGCGACCGGTATCC 570
Db 499 GGCACCTCGACCTTTCGACGATCTGTGCTGTGCGCAAGACCAAGCGACCGGTATCC 558
Qy 571 GTCCAGACGGGCTCCACTTCGACGCTGCGGCTGCGGCTGTTGAATGCAAGGTGAC 630
Db 559 GTTATGTTCGAGCTCACTTTCGCGCTGGAATGTCGAAGGAATGACCTGGGCACTGAG 618
Qy 631 CACTACTACAGATCGTTGCAACGAGGGCTACTTCAGACGCGCTATGCTGCATCAC 690
Db 619 CACAACCTACAGATGTTGCTTCGAGGGTTACCAACAGCAGCGGTTCCGCGAATACAT 678
Qy 691 GTTGTGACCTGGGC 705
Db 679 GTTGTGATCCGGGTGC 693

RESULT 4
LOCUS DN588726 675 bp mRNA linear EST 15-MAR-2005
DEFINITION 49478.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
ACCESSION DN588726
VERSION DN588726.1 GI:61239134
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 675)
AUTHORS Flinn, B., Rochwell, C., Sardana, R., Griffiths, R., Laque, M., De Koeijer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruet, G. and Regan, S. Generation of ESTs from late blight-challenged potato tubers Unpublished (2005)
TITLE Contact: Barry Flinn
JOURNAL The Canadian Potato Genome Project - BioAtlantech
COMMENT 921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
FEATURES Email: bflinn@bioatlantech.nb.ca
source Seq primer: T3.
Location/Qualifiers
 1..675
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Shepody"
 /db_xref="taxon:4113"
 /clone="49478"
 /issue_type="Tubers"
 /lab_host="XL10-Gold"
 /clone_lib="Late Blight-Challenged Tubers"
 /note="Vector: pBluescript II SK(+); XR; Site_1: EcoRI; Site_2: XhoI; supplier: Pathogen-challenge series. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with 5 ul of Phytophthora infestans (A2-mating type), through 2 puncture wounds 3 cm apart. The tubers were incubated 1 minute to allow inoculum absorption. The infection area was outlined for future

Db 693 ATTACAGATGTTGCGGTGGAGGTTACTTACTCTGCGTCTGCTC 741

RESULT 6
LOCUS CB898036 799 bp mRNA linear EST 02-JUL-2003
DEFINITION tricol13xe09 T. reesei mycelial culture, Version 3 april Hypocrea
ACCESSION CB898036
VERSION CB898036.1 GI:30112694
KEYWORDS
SOURCE
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 799)
Foreman, P. K., Brown, D. E., Dankmeyer, L., Dean, R., Diemer, S.,
Dunn-Coleman, N. S., Goedegebuer, F., Houfek, T. D., England, G. J.,
Kelley, A. S., Meerman, H. J., Mitchell, T., Mitchinson, C.,
Olivares, H. A., Teunissen, P. J., Yao, J. and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
12788920
CONTACT: Pamela K. Foreman
Genecor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: pforeman@genecor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
1..799
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="Om6a"
/db_xref="taxon:51453"
/clone="tricol13xe09"
/dev_stage="mycelia"
/clone_1lb="T. reesei mycelial culture, Version 3 april"
/note="Vector: pREP3; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN

Query Match 23.3%; Score 229; DB 6; Length 799;
Best Local Similarity 61.6%; Pred. No. 1.6e-53;
Matches 400; Conservative 0; Mismatches 245; Indels 4; Gaps 2;

QY 35 TCGGCTTACCCCGCTTCCCTTGGGGCTTACCGGACCTGGGCTTCCCGG 94
DB 151 TCACCTCCCTCCGCGCGGTCCGATCTCGGGGCTTGGCCCTCCCGCGG 210
QY 95 CAGGAAATGCCAGAGCTCGAAAAGCAGACAAACCCCACTCGAGGGCTGACG 154
DB 211 AGCTGCAATCCGTGCTGAGAAAGCCGACGATTCAGGCGGACGGGCTTCAACA 270
QY 155 ATGTTATTACTTCTGTTGAGTGAAGCGGTGAGCGCAGGCAAGTACCAACTGG 214
DB 271 ACGGCTACTTACTCTGTAAGTGAAGTGAAGCGGCGGTGACGTAACCAATGGTC 330
QY 215 AAGCGGCACTAGAGATGAGTGGGAGATGGCGGTAACTCGTGGTGGAAAAGGCT 274
DB 331 CCGGCGGAGAGTTCTCGTCAACTGCTCAACTCGGGCACTTTGTGCGCGCAAGGAT 390
QY 275 GGAACCCCGGCTGAACGACAGACATCACTTGAAGGTGTTTACAGGCAAGGCA 334
DB 391 GCGAGCCGCGGACCAAGAACAGTCACTTCTCGGAGAGTCAACCCCAAGGCA 450
QY 335 ACAGCTACTTTCGGTCTACGAGTGAAGCCGCAACCCGCTGCTGAGTATTACATCGTCG 394
DB 451 ACAGCTACTTTCGGTCTACGAGTGAAGCCGCAACCCGCTGATGAGTACATCGTCG 510

QY 395 AGACTTTGACACCTATGATCTTCCGCTGACGATCTAGAACTGTGAGTCG 454
DB 511 AGAATTTGGACACTTACACCCGCTCCAGGCGCCACCAAGCTGGGAGTCACTCCG 570
QY 455 ACGGTAGCATTTATGACTCGGCAAGACACTCGCTGCAAGCACTAGATCGAGCA 514
DB 571 ACGGAGGCTTACGACATTTACCGCAAGCGCGCTCAACAGCCGTCATTCAGGCA 630
QY 515 CCCAACTTGGACCATATCTGTGCTGCTCCCGCAGACAGCGCAACGCGTACCGTCC 574
DB 631 CCGGCACTTTTACAGTACGATCGCTCCCGCCGCAACACCGCTCGAGCGGCTCCGCA 690
QY 575 AGACGGGCTGCACCTTGCAGCGCTGAGGCTCGCGCTGTTGATGATCAAGTACCACT 634
DB 691 ACAGCGGCAACCACTTACACCGCTGAGGCTCAGCAAGGCTTACGCT--CGGACGATGG 747
QY 635 ACTACCAAGATGTTG-CAACGAGGCTACTTTCAGACGCGGCTATGCTC 682
DB 748 ATTACAGATGTTTCCGCTGAGGAGGTTACTTTAGCTGCTGCTC 796

RESULT 7
LOCUS CN133022 772 bp mRNA linear EST 01-APR-2004
DEFINITION OX1 9 D10.G1 A002 Oxidatively-stressed leaves and roots Sorghum
ACCESSION CN133022
VERSION CN133022.1 GI:45963542
KEYWORDS
SOURCE
ORGANISM Sorghum bicolor (sorghum)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 772)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R. R., Liang, C.,
Sun, F., Sullivan, R., Lim, S., Baerman, A. and Pratt, L. H.
An EST database from Sorghum: oxidatively stressed leaves and roots
Unpublished (2003)
Other ESTs: OX1_9_D10.b1 A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTTAAAGCTGCG).
Location/Qualifiers
1..772
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cullivar="BTx623"
/db_xref="taxon:4558"
/clone="OX1_9_D10_A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/note="Organ: Leaf and Root; Vector: pMT188-Fl3; Site 1:
XhoI; Site 2: XhoI; The library was prepared from polyA+
RNA from oxidatively stressed, hydroponically grown
Sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003% and leaves
were misted with 10 uM methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all

tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pMB18-FL3 vector (5-prime DraIII site is CACTGATG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 22.4%; Score 222.6; DB 7; Length 772;
Best Local Similarity 63.5%; Pred. No. 1.1e-51;
Matches 374; Conservative 0; Mismatches 209; Indels 6; Gaps 2;

Qy 104 CCACGAGCTCGAAAAGCAGACACCCCACTCGAGGCTGGACATGTTATT 163
Db 132 CCTGGTCTTGAAGCCCGCAGGCTACTGGTAATCTGAGAGGTTACCATATGATACT 191
Qy 164 ACTATTCCTGGAGAGTGAAGGCGGAGGCGACAGTACCAACCACTGGAGGCGCA 223
Db 192 TCTACTCTTGGTGGTCTATGCGGGTCTATGCCAATTCAGTGGGTAGGGAATC 251
Qy 224 CCTACGAGATCAGCTGGGAGAGTGGCGTTAACTCTGCTGGTGAAGGGCTGGAACCCCG 283
Db 252 ACTACAGCTTGAATGGCGCAACCTGGTTACTTTGGTGGAAAGGTTGGAACCCCG 311
Qy 284 GCCTGAACGAAAGCCATCCACTTTGAGGGTTTACAGCCAAACCGCAACAGCTACC 343
Db 312 G---TACTGGCCGAACCATCAATATGCGGGTCTTTCAGCCCTCAGGTTAACGGCTACC 368
Qy 344 TTGGGGTATAGGTTGAGCCCGCAACCGCGTGGTGAATTTAATCGTGGAGAACTTGG 403
Db 369 TCTGGGTCTACGGCTGAGCTGAGCCCTCTGCTTGAATCTCACTCATCAAGAACTACG 428
Qy 404 GCACCTATGATCTCTCTCCGGTGTCTACCGATCTAGAACTGTGATGTCAGCGTAGCA 463
Db 429 GCACTTAAACCCCTGCTCTGTGTCGACGACAAAGGACCGTCTAACAACGACGGCACA 488
Qy 464 TCTATCAGCTGGGCAAGACCACTGCGTCAACAGCACTAGCATGACGGCACCCAACT 523
Db 489 CCTACGATCTTACAGACCAACCCGCTCAACCAACCCCTATCAACGCGCAACAGACT 548
Qy 524 TCGACCAATATCTGGTGGTCCGCGCAGGACAGCGGATACCGGTCCAGACGGGCT 583
Db 549 TCAACCAATATCTGGGCTTCCGCGCAGGACAGGAGGAGCGGCGCTCAACATGACGA 608
Qy 584 GCACTTTCAGCGCTGGGCTCGCGCTGGTTGTAATGTCAACGCTGACCACTACTACAGA 643
Db 609 CTATCTTCAATGCTTGGGCTAAGCGTGTATGAGACT---TGGAAACCACTACTACAGA 665
Qy 644 TCGTTGCAACGAGGGCTACTTACAGACGGGCTATGCTCGCATCACCGT 692
Db 666 TCTGGCTACCGAGGATACAGACAGTGAATCTTCTATCTATGT 714

RESULT 8
DB624928 639 bp mRNA linear EST 11-JUL-2005
LOCUS EST1015056 Fv1 Gibberella moniliformis cDNA clone FVIB05, mRNA

DEFINITION
Sequence.
ACCESSION
DB624928
VERSION
DB624928.1 GI:70699610

KEYWORDS
SOURCE
ORGANISM
Gibberella moniliformis
Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocistaceae; Nectriaceae; Gibberella.

REFERENCE
1 (bases 1 to 639)
Brown, D.W., Cheung, F., Proctor, R.H., Butcho, A.E., Zheng, L., Lee, Y.,
Kender, D.F., Town, C.D., and Whitelaw, C.A.

TITLE
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster

JOURNAL
Contact: Brown, D.W.
COMMENT
USDA/ARS/NCAUR

FEATURES

source
USDA
1815 N. University St., Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIB05TH
Seq primer: AAT TAA CCC TCA AAG GG.
Location/Qualifiers
1..639
/organism="Gibberella moniliformis"
/mol_type="mRNA"
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/clone="FVIB05"
/tissue_type="mycelia"
/clone_id="Fv1"
/note="Vector: Bluescript II SK(+); Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the Bluescript II SK(+) XR
vector (cDNA Synthesis Kit, Stratagene)."

ORIGIN

Query Match 22.4%; Score 220.4; DB 8; Length 639;
Best Local Similarity 63.2%; Pred. No. 4.3e-51;
Matches 373; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Qy 104 CCACGAGCTCGAAAAGCAGACACCCCACTCGAGGCTGGACATGTTATT 163
Db 24 CCTCTGCTTGAAGCCCGCAGGCTCACTGGAGGTTACCAACCGATACT 83
Qy 164 ACTATTCCTGGAGAGTGAAGGCGGAGGCGACAGTACCAACCTGGAGGCGCA 223
Db 84 TCTACTCTTGGTGGTCTATGCGGGTCTATGCCAATTCAGTGGGTAGGGAATC 143
Qy 224 CCTACGAGATCAGCTGGGAGAGTGGCGTTAACTCTGCTGGTGAAGGGCTGGAACCCCG 283
Db 144 ACTACAGCTTGAATGGCGCAACCTGGTTACTTTGGTGGAAAGGTTGGAACCCCG 203
Qy 284 GCCTGAACGAAAGCCATCCACTTTGAGGGTTTACAGCCAAACCGCAACAGCTACC 343
Db 204 G---TACTGGCCGAACCATCAATATGCGGGTCTTTCAGCCCTCAGGTTAACGGCTATC 260
Qy 344 TTGGGGTATAGGTTGAGCCCGCAACCGCGTGGTGAATTTAATCGTGGAGAACTTGG 403
Db 261 TCTGGGTCTACGGCTGAGCTGAGCCCTCTGCTTGAATCTCACTCATCAAGAACTACG 320
Qy 404 GCACTTATGATCTTCTCTCCGGTGTCTACCGATCTAGAACTGTGAGTGCAGCGTAGCA 463
Db 321 GCACTTAAATCCCGGCTGCTGCTGGCAGCAAGAGGACCGTCTAACAACGCGCACA 380
Qy 464 TCTATCAGCTGGGAGAGCACTGGCGTCAACGCACTAGCATGACGGCACCCAACT 523
Db 381 CCTATGATCTGTATCACAGCAACCCGCTTCAACCAAGCCCTTATGACGCGCAACGACT 440
Qy 524 TCGACCAATATCTGGTGGTCCGCGCAGGACAGCGGATACCGGTCCAGACGGGCT 583
Db 441 TCAACCAATATCTGGGCTTCCGCGCAGGACAGGAGGAGCGGCTGTCAACATGACGA 500
Qy 584 GCACTTTCAGCGCTGGGCTCGCGCTGGTTGTAATGTCAACGCTGACCACTACTACAGA 643
Db 501 CTATCTTCAATGCTTGGGCTAATGCTGACATGAGACT---TGGAAACCACTACTACAGA 557
Qy 644 TCGTTGCAACGAGGGCTACTTACAGACGGGCTATGCTCGCATCACCGTT 693

Db 558 TTCTAGTACCGAGGATACGAGCAGATCTTCTTCATCTATGTT 607

RESULT 9
DR623097 749 bp mRNA linear EST 11-JUL-2005
LOCUS EST1013225 Fv1 Gdbberella moniliformis cDNA clone FV1AM2, mRNA
DEFINITION
ACCESSION DR623097
VERSION DR623097.1 GI:70697745
KEYWORDS
SOURCE
ORGANISM
Gdbberella moniliformis
Gdbberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreales; Nectriaceae; Gdbberella.
REFERENCE
AUTHORS
1 (bases 1 to 749)
Brown, D.W., Cheung, P., Proctor, R.H., Butcho, A.E., Zheng, L., Lee, Y.,
Utecherback, T., Smith, S., Feldblyum, T., Glenn, A.B., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
JOURNAL
COMMENT
USDA/ARS/NCAR
Contact: Brown, D.W.
USDA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncar.usda.gov
TIGR sequence name: FV1AM22TH
Seq primer: AAT TAA CCC TCA AAG GG.
Location/Qualifiers
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/db_xref="taxon:117187"
/clone="FV1AM22"
/isue_type="mycelia"
/clone_1lb="FV1"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad, CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (CDNA Synthesis Kit, Stratagene)."

ORIGIN

Query Match 22.4%; Score 220.4; DB 8; Length 749;
Best Local Similarity 63.2%; Pred. No. 4.5e-51;
Matches 373; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

104 CCACGAGCTCGAAGAGGAGCAACCCCACTCGAGGGGCTGCGAGATGTTATT 163
Db 114 CCTGTGCTCTTGAAGCCCGCCAGGTCACTGAGGGTTACCAACAGGATCT 173
Gy 164 ACTATTCTGTGAGTGAAGCGTGAAGCGCAAGCCACCACTGGAAGCGGCA 223
Db 174 TCTACTTGTGATGCTGATGCTGATGCTGCTAATCACTGATGCTGAGGAGTC 233
Gy 224 CTTAGAGATCAAGCTGGGAGATGCGGTAACCTGCTGCTGGAAGAGGCTGGAACCCG 283
Db 234 ACTACGAGTGTATTGGCGCAACACTGTGTAATTGTTGGAAGGTTGGAACCTGT 293

Gy 284 GCCTGAAGCAAGAGCCATTCACCTTGAAGGTGTTTACAGCAAAACGGCAACGCTACC 343
Db 284 G---TACGGCGCAACTATCAACTATGCGGTTCTTTACGCCCTCAGGTTAACGGCTATC 350
Gy 344 TTGGGCTTACGCTTGAAGCCCGCAACCCGCTGCTGAGTATTACATCGTCGAACCTTTG 403
Db 351 TCTGCTTACGCTGAGCCCGCAGCCCTCTGCTGAGTACTACGTCATCAAGAACTACG 410
Gy 404 GCACCTTGAATCTTCCCTCGGCTGCTACCGATCTTAGAACTGTGAGTGCAGCGTACGA 463
Db 411 GCACCTTGAATCTTCCCTCGGCTGCTACCGATCTTAGAACTGTGAGTGCAGCGTACGA 470
Gy 464 TCTATGACTGCGGAAGCAACTGCGCTCAACGCACTGAGATGAGCGGCAACCAACT 523
Db 471 CTTATGATCTTACAGCAACCGCTACCAACGAGCCCTTATGAGCGGCAACGAGCT 530
Gy 524 TGAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 583
Db 531 TCAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
Gy 584 GCACCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643
Db 591 CTATCTTCAATGCTTGGGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
Gy 644 TCGTTGCAACGAGGAGGCTACTTCAAGAGCGGCTATGCTGCTGCTGCTGCTGCTGCT 693
Db 648 TTCTAGTACCGAGGATACGAGCAGTGGATCTTCTTCATCTATGTT 697

RESULT 10
CF881056 768 bp mRNA linear EST 31-OCT-2003
LOCUS trico83xj11.b1 T.reesei mycelial culture, Version 6 October 2003
DEFINITION
ACCESSION CF881056
VERSION CF881056.1 GI:38135738
KEYWORDS
SOURCE
ORGANISM
Hypocrea jecorina (anamorph: Trichoderma reesei)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreales; Hypocreales; Hypocreales.
REFERENCE
AUTHORS
1 (bases 1 to 768)
Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,
Teunissen, P.J.M., van Solingen, P., Danneberg, L., Mitchell, T.K.,
Ward, M. and Dean, R.A.
Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei
JOURNAL
PUBMED
14757250
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: UT-P1 primer.
Location/Qualifiers
1..768
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QMe6"
/db_xref="taxon:51453"
/clone="trico83xj11"
/dev stage="mycelia"
/clone_1lb="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: pREP3Y, Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN

frozen in liquid nitrogen, ground to a powder, and then added to Trizol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml Trizol. The cDNA was directionally ligated into the pBluescript II SK(+) XR vector (cDNA Synthesis Kit, Stratagene)."

ORIGIN

Query Match 22.3%; Score 219.4; DB 8; Length 719;
Best Local Similarity 63.2%; Pred. No. 8.6e-51;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

104 CCACGAGCTCGAAAGCGACAGACACCCCACTCGAGAGGCTGGCAGATGTTATT 163
108 CCTCTGCTTGGAGCCCGCCAGGTCAACCGGTACTGAGGGTTACACACGAGTACT 167
164 ACTATTCCTGGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 223
168 TCTACTCTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 227
224 CTTACGAGATCAGCTGGGAGATGCGGTAACTCTGCTGATGAAAGGCTGAAACCCG 283
228 ACTACAGGTGATGATGAGGAGCACTGGTAACTTTGTTGGTGAAGGTTGAAACCTG 287
284 GCTGAAACGAAAGCCATCTTCACTTTGAGGTTTACAGCCAAAGCGCAACGTTACC 343
288 G---TACTGGCCGAATCACTATGCGGCTTCTTCAAGCCCTCAGGCTAACGCTATC 344
344 TTGGGCTCTAGGTTGAGCCGCAACCCGCTGATGATATACATGCTGAGAACTTTG 403
345 TCTGCGTCTAGGCTGAGCCGCAACCCCTCTGCTGATGATCTATGATGATGATGAT 404
404 GCACCTATGATCTTCTCCGCTGCTACCGATCTAGAACTGTGAGTGCAGCGGTAGCA 463
405 GCATTTCAATCCGGGCTCTGCTGCGCAAGCAAGGGGACCGTCAACAGACGCGGCA 464
464 TCTATCGACTCGGCAAGCACTGCGTCAACGCACTAGATGAGGAGCCCAACT 523
465 CCTATGATCTGTACAGACCAACCGCTAACCAAGCCCTCTATGACGCGCCAAAGACT 524
524 TCGACCAATATCTGCGCTCGCGCAAGCAAGCGGAGGATGATGATGATGATGATGAT 583
525 TCAACCAATATCTGCGCTCGCGCAAGCAAGCGGAGGATGATGATGATGATGATGAT 584
584 GCACTTTCGACGCTGCGCTCGCGCTGCTGATGATGATGATGATGATGATGATGAT 643
585 CTATCTTCAATGCTTGGGCTAATGCTGCGATGAGACT---TGAAACCACTACTATGAGA 641
644 TCGTTGCAACGAGGAGGCTACTTACAGACGCGCTATGCTGCATCAACCT 692
642 TTCTAGTACCAAGGAGATACAGACAGTGTATCTTTCATCATATGT 690

RESULT 14
DR630899 733 bp mRNA linear EST 11-JUN-2005
LOCUS EST1021027 Fv1 Gibberella moniliformis cDNA clone FVIDX40, mRNA

DEFINITION sequence.
ACCESSION DR630899
VERSION DR630899.1 GI:70705629

KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 733)
AUTHORS Brown, D.W., Cheung, F., Proctor, R.H., Butcher, A.E., Zheng, L., Lee, Y.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.

TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster

JOURNAL unpublished (2005)
COMMENT Contact: Brown, D.W.
USDA/ARS/NCAR

USDA
1815 N. University St. Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncar.usda.gov
TIGR sequence name: FVIDX40TH
Seq primer: MAT TMA CCC TCA AAG GG.
Location/Qualifiers

FEATURES

source

1. 733
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIDX40"
/issue_type="mycelia"
/note="Vector: pBluescript II SK(+) XR; Site 1: SecRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit, Stratagene)."

ORIGIN

Query Match 22.3%; Score 219.4; DB 8; Length 733;
Best Local Similarity 63.2%; Pred. No. 8.6e-51;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

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147 CCTCTGCTTGGAGCCCGCCAGGTCAACCGGTACTGAGGGTTACACACGAGTACT 206
164 ACTATTCCTGGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 223
207 TCTACTCTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 266
224 CTTACGAGATCAGCTGGGAGATGCGGTAACTCTGCTGATGAAAGGCTGAAACCCG 283
267 ACTACAGGTGATGATGAGGAGCACTGGTAACTTTGTTGGTGAAGGTTGAAACCTG 326
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524 TCGACCAATATCTGCGCTCGCGCAAGCAAGGCGGATGATGATGATGATGATGATGAT 583
564 TCAACCAATATCTGCGCTCGCGCAAGCAAGGCGGATGATGATGATGATGATGATGAT 623
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624 CTATCTTCAATGCTTGGGCTAATGCTGCGATGAGACT---TGAAACCACTACTATGAGA 680
644 TCGTTGCAACGAGGAGGCTACTTACAGACGCGCTATGCTGCATCAACCT 692

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:19:44 ; Search time 215.809 Seconds
(without alignments)
8096.696 Million cell updates/sec

Title: US-09-467-368-1
Perfect score: 983
Sequence: 1 TCGGCCCCGAGCTTGCAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
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8: /cgn2_6/ptodata/1/ina/RG COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 983 | 100.0 | 983 | 2 | US-09-115-660-1 |
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| 4 | 197.2 | 20.1 | 1375 | 2 | US-08-468-812-1 |
| 5 | 197.2 | 20.1 | 1375 | 3 | US-08-590-563-1 |
| 6 | 197.2 | 20.1 | 1375 | 3 | US-09-770-621-1 |
| 7 | 197.2 | 20.1 | 1375 | 3 | US-09-235-832-1 |
| 8 | 194.2 | 19.8 | 822 | 3 | US-09-254-733-8 |
| 9 | 190 | 19.3 | 1015 | 2 | US-08-121-436A-1 |
| 10 | 181.8 | 18.5 | 1281 | 3 | US-08-768-373-1 |
| 11 | 181.8 | 18.5 | 1281 | 3 | US-08-849-242A-1 |
| 12 | 168.4 | 17.1 | 675 | 2 | US-07-744-570B-1 |
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| 15 | 165.2 | 16.8 | 927 | 3 | US-08-116-622-5 |
| 16 | 165.2 | 16.8 | 927 | 3 | US-09-219-277-5 |
| 17 | 165.2 | 16.8 | 927 | 3 | US-09-599-661-5 |
| 18 | 162.4 | 16.5 | 489 | 2 | US-08-119-169A-7 |
| 19 | 159 | 16.2 | 2219 | 2 | US-08-230-979A-7 |
| 20 | 144.8 | 14.7 | 573 | 2 | US-08-709-912-18 |
| 21 | 144.8 | 14.7 | 573 | 2 | US-09-047-370-18 |
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| 24 | 129.6 | 13.2 | 2055 | 3 | US-09-367-891A-1 |

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| 25 | 124 | 12.6 | 2898 | 3 | US-09-462-246-1 | Sequence 1, Appli |
| 26 | 119.2 | 12.1 | 557 | 3 | US-09-230-590-1 | Sequence 1, Appli |
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| 28 | 119 | 12.1 | 744 | 3 | US-09-189-060B-11 | Sequence 11, Appli |
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| 32 | 103.6 | 10.5 | 2054 | 3 | US-09-613-811-5 | Sequence 5, Appli |
| 33 | 101.4 | 10.3 | 2967 | 3 | US-09-367-891A-4 | Sequence 4, Appli |
| 34 | 98.2 | 10.0 | 685 | 3 | US-07-955-766A-7 | Sequence 7, Appli |
| 35 | 98.2 | 10.0 | 2059 | 2 | US-08-244-686-1 | Sequence 1, Appli |
| 36 | 97.6 | 9.9 | 954 | 2 | US-08-315-695-15 | Sequence 15, Appli |
| 37 | 97.6 | 9.9 | 1945 | 3 | US-09-595-344-1 | Sequence 1, Appli |
| 38 | 96.2 | 9.8 | 234 | 3 | US-09-189-060B-46 | Sequence 46, Appli |
| 39 | 95.8 | 9.7 | 847 | 3 | US-09-260-283-1 | Sequence 1, Appli |
| 40 | 94 | 9.6 | 2055 | 2 | US-07-842-349-1 | Sequence 1, Appli |
| 41 | 84.6 | 8.6 | 941 | 2 | US-08-121-436A-3 | Sequence 3, Appli |
| 42 | 83 | 8.4 | 2364 | 3 | US-09-330-234-23 | Sequence 23, Appli |
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| 44 | 82.6 | 8.4 | 642 | 2 | US-08-104-445-2 | Sequence 2, Appli |
| 45 | 82.6 | 8.4 | 1413 | 2 | US-08-104-445-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-08-886-765-1
Sequence 1, Application US/08886765
Patent No. 5817500
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knapp, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5817500 No. 5817500disk of No. 5817500th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Thermomyces lanuginosus
STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705

US-08-886-765-1

Query Match 100.0%; Score 983; DB 2; Length 983;
 Best Local Similarity 100.0%; Pred. No. 3.6e-269;
 Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 961 AAAAAAAAAAAAAAAAAAAAAA 983

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RESULT 2

US-09-115-660-1

Sequence 1, Application US/09115660
 Patent No. 6245546

GENERAL INFORMATION:

APPLICANT: Hansen, Peter Kamp

APPLICANT: Wagner, Peter

APPLICANT: Mulert, Anette

APPLICANT: Knap, Inge Helmer

TITLE OF INVENTION: Animal Feed Additives

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6245546 No. 6245546disk of No. 6245546th America, Inc.

STREET: 405 Lexington Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10174

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS Version 2.0

SOFTWARE: FastSeq for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/115,660

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/886,765

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4324, 204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 983 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Thermomyces lanuginosus

STRAIN: DSM 4109

FEATURE:

NAME/KEY: CDS

LOCATION: 31..705

US-09-115-660-1

Query Match 100.0%; Score 983; DB 3; Length 983;
 Best Local Similarity 100.0%; Pred. No. 3.6e-269;
 Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 781 ATCCAGCATCTGCTGCGCTTGGAGTATCTTGGAGACCTGTGAGAACTTTGGC 840
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DB 841 GAGCTGCGCAAGATCAGTATGCTTGGGTTTGTCTCCCTATCTCTGTAAGAAAA 900
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DB 961 AAAAAAAAAAAAAAAAAAAAAA 983

RESULT 3

US-08-458-023B-3

Sequence 3, Application US/08458023B
Patent No. 5667990
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boomlinathan, Karuppan C.
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5667990 No. 5667990disk of No. 5667990th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086,010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Humicola insolens
INDIVIDUAL ISOLATE: DSM 6995
FEATURE:
NAME/KEY: CDS
LOCATION: 126..806
US-08-458-023B-3

Query Match 24.3%; Score 239; DB 2; Length 1123;
Best Local Similarity 64.4%; Pred. No. 1.1e-57;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

QY 87 CTTCCCGGCGGGAATGCGGAGCTGAAAGGCAAGCAACCCCAACCTGGAGG 146
DB 197 CTTCCCGGCGGGAATGCGGAGCTGAAAGGCAAGCAACCCCAACCTGGAGG 256
QY 147 CTGCAAGATGTTTACTTACTTCTGTTGAGTGAAGGCGAGGCAAGTACAC 206
DB 257 CTGCAAGATGTTTACTTACTTCTGTTGAGTGAAGGCGAGGCAAGTACAC 316
QY 207 CAACCTGGAAGCGGCACTTACGATGAGTGGGAGAGTGGCTTAACTGTCGTTG 266
DB 317 CAACCTGGAAGCGGCACTTACGATGAGTGGGAGAGTGGCTTAACTGTCGTTG 376
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DB 434 AAACGGCAACGATACCTTGGGTCTACGTTGAGACCCGCTGGTGTGATTTA 493
QY 494 TGTATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAG 553
DB 447 TGTATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAG 506
QY 554 CTATACGAGCGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 613
DB 507 CGAAGGCAACCAACCTTTCAGCAATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566
QY 614 CGAAGGCAACCAACCTTTCAGCAATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
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QY 674 CTGCTCAACATGAGAACCACTTTCAGCAATCTGTTGCTGCTGCTGCTGCTGCTGCTGCT 730

Qy 627 TGACCACTACTACGATCGTTGGCAAGGAGGCTACTTTCAGACGCGCTATGCTCCGAT 686
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Qy 687 CACCGTT 693
Db 791 CTATGTT 797

RESULT 4

US-08-468-812-1
Sequence 1, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmaaper, Jari
APPLICANT: M nely, Arja
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-08-468-812-1

Query Match 20.1% Score 197.2; DB 2; Length 1375;
Best Local Similarity 58.6% Pred. No. 9.1e-46;
Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;
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Db 349 TCGGCTTACCCCGGCTTACCGATGCTTCCCTTGGCACTCGCATGCGGCTGCGC 408
Qy 95 CAGGAAATGCGAGAGCTGAAAGGAGACAGCAACCCCAACTCGAGAGGCTGCGACG 154
Db 409 TCGTCCCGGAGAGGCGCCAGCCGACACCACTACCAAGACAGACCGGGATGACA 468
Qy 155 ATGGTTATTAATTCCTGTTGAGTACGTTGAGAGGAGCGGACGCTACCAACTGG 214
Db 469 ACGGCTACTTCTACTGTTCTGACCGAGCGGCCGGGACCGTTCATGACCTCCACT 528
Qy 215 AAGCGGCACTTACGAGATACGCTGGGGAATGGCGTTACTCTGTTGGAAGGAGCT 274
Db 529 CGGCGGCACTTACGAGATACGCTGGGGAATGGCGTTACTCTGTTGGAAGGAGCT 588
Qy 275 GGAACCCCGGCTGAAAGCAAGAGCCATCCACTTTGAGGCTGTTTACGACCAAGGCA 334
Db 589 GGTCCACCG--GGAGCGCGAGCGGTGACTTACCAAGCGCTCTTCAACCCGTCGGTA 645
Qy 335 ACAGCTACTTGGGCTTACGAGTGGACCGCAACCGCTGTTGAGATTATTCATGCTG 394
Db 646 ACGGCTACTTCAAGCTTACGAGTGGACCGCAACCGCTGTTGAGATTATTCATGCTG 705
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Db 706 AGAGCTGGGCACTTACCGGCCAC--GGCACTTACAAAGGCACTGTCACACG 759
Qy 455 ACGGTACATCTATGACCTGGGCAAGACCACTGCGTCAAGCACTGATCGACGCA 514
Db 760 ACGGAGGAAAGTACGATCTTACGAGACTGGCGGTACCAAGCGCTCATTCAGAGCA 819
Qy 515 CCCAACTTTCAGCAATTAATGTTGCTGCGCGCAGAGCAAGGAGCAAGCGGTAACGTC 574
Db 820 CCGGACTTTCAGCAATTAATGTTGCTGCGCGCAGAGCAAGGAGCAAGCGGTAACGTC 879
Qy 575 AGAGGCTGCACTTGAAGCTTGGGCTGCGCTGCTGTTGAATGTCAACGTTACCACT 634
Db 880 CCATCGCAACCACTTGAAGCTTGGGCTGCGCTGCTGTTGAATGTCAACGTTACCACT 936
Qy 635 ACTACGATGTTGCAAGGAGGCTACTTACGACGCGCTATGCTGATCAACGTTG 694
Db 937 ACTACGATGTTGCAAGGAGGCTACTTACGACGCGCTATGCTGATCAACGTTG 996
Qy 695 CTGACGTGGGTTAAGCTAATCTGTTG 722
Db 997 GCGAGGGTGGCAACCGGCAACCGGG 1024

RESULT 5

US-08-590-563-1
Sequence 1, Application US/08590563
Patent No. 6300114
GENERAL INFORMATION:
APPLICANT: Vehmaaper, Jari
APPLICANT: M nely, Arja
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-08-590-563-1

Query Match 20.1%; Score 197.2; DB 3; Length 1375;
Best Local Similarity 58.6%; Pred. No. 9,1e-46;
Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;

Qy 35 TCGGCTTAAACCCCGTGGCTGCGGCTTAAAGCCGCACTGGGGCCCTGCTCCCGG 94
Db 349 TCGGCTCCGGCGCATCGTCAACAGTGCCTTCCGCTGGCACTGCCGCGTGGC 408
Qy 95 CAGGAAATGCCACCGAGCTCCGAAAAGCAGACACACCCCACTCGAGGGCTGGACG 154
Db 409 TGTGCCCCGGACCGCCACCGCCGACACACCATCAACCGAACGACCGGGTACGCA 468
Qy 155 ATGGTTATTATCTATCTGTGTGAGTGAAGTGAAGCGCAGGCGCACTGAACCACTGG 214
Db 469 ACGGCTATTCTATCTGCTGTGACCGACCGCCCGGACCGTCTCCATGACCTCCACT 528
Qy 215 AAGGCGGACCTACGATCAAGCTGGGGAGATGGCGGTAACTCGTGGTGAAGGGCT 274
Db 529 CGGGGGGACGTACGACCTGTGGCGGAAACCGGGAACTTGTGCGCGGCAAGGGCT 588
Qy 275 GGAACCCCGGCTGAACGAAAGCATTCACCTTTGAGGGTGTTCACAGCCAAACGCA 334
Db 589 GGTCCACCGG---GGACGGGGGACCGTGAACCTTCAACCTCTCCGCGGTA 645
Qy 335 ACAGCTACCTTGGGCTTACGAGTGGAGCCGCAACCGCTGATGAGTATTAATCTGCG 394
Db 646 ACGGCTACTCAGCGTCTACGGCTGACAGAACCCGCTGTGAAGTACTACATGTCG 705
Qy 395 AGAATTGGACCTATGATCTTCTCCGCTGCTACCGATCTAGGAACCTGCAAGTCG 454
Db 706 AGAGCTGGGGACCTACCGGCCAC-----GGACCTAACAGGACCGTCAACACG 759
Qy 455 ACGGTAGCATATGTGACTCGGCAAGACCACTCGGTCAAGGCACTAGCATGACGCA 514
Db 760 ACGGGGAACTGACATCTACGAGACTGGCGGTAAAGCGCGCTGCTCATCAAGGCA 819
Qy 515 CCNAACCTTGACCAATATCTGTGCTCGCGCAGGACCAAGGACCAAGCGTACCGTCC 574

Db 820 CCCGACCTTCACAGATTCTGAGCGTCCGGCAGAGAACGACGACCGGACATCA 879
Qy 575 AGACGGCTGCTACTTGAAGCCCTGGGCTCGCGCTGTGTAATGTAACGATCACT 634
Db 880 CCATCGGCAACCACTTGGACCGCTGGGCGCCGCGCGCATGA---CCTGGGACCGCA 936
Qy 635 ACTACGATGCTTGAACGAGGAGGCTTACGACGAGGCTATGCTGCATCAACCGTTG 694
Db 937 ACTACGATGATGACGACGAGGCTTACGAGACGAGCGGTAGCTCAACGCTTCATCA 996
Qy 695 CTGACGTGGGCTAAGACGTAACTGTG 722
Db 997 GCGAGGGGTGCAACCCGCGCAACCCGGG 1024

RESULT 6
US-09-770-621-1
Sequence 1, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M nely, Arja
APPLICANT: Vehmanper, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. 6506593 Relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 303..1334
US-09-770-621-1

Query Match 20.1%; Score 197.2; DB 3; Length 1375;
Best Local Similarity 58.6%; Pred. No. 9.1e-46;
Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;

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QY 35 TCGGCTTTACCCCGGTTGCGGCTTACGCGGCACTGGGAGCCCTTCCCGG 94
DB 349 TCGGCTTCCGCGCATCTCAACAGTCTTCCGCTTGGCACTGCGCATCGCGTGGC 408
QY 95 CAGGAAATGCCAGGAGCTCGAAAAGCAGACAAACCCCACTCGAGGGCTGGACG 154
DB 409 TGTGCCCCGGGACCGCCGACCGCAGACACCATCACCAGAACAGACGGGTACGCA 468
QY 155 ATGTTATTACTTATCTCTGTGTGAGTACGCGTGAAGCGCAGCCAGTACCACTGG 214
DB 469 ACGGCTACTTCTACTCTGTTCTGTGACCGACGCGCCGGGACCGTCTCCATGACCTTCACT 528
QY 215 AAGGCGGACCTACGAGATCAAGTGGGGAGATGGCGGTACCTGCGGTGAAAAGGCT 274
DB 529 CGGGGGGACGCTACGACCTCTGTGGCGAAACCGGGAACTTGTCTCGCGGCAAGGCT 588
QY 275 GGAACCCCGGCTTGAACGCAAGAGCCATCACTTTGAGGGTGTTCACAGCCAAACGCA 334
DB 589 GGTTCACCGG---GGAGCGGGGACCGTACCTTCAACGCTCTTCAACCGTGGGTA 645
QY 335 ACAGTTACTTGGGCTTACGCTTACGCTTGAACCCGCAACCCGCTGTGAGTATTCATCTG 394
DB 646 ACGGCTACTTCACTGCTTACGCTGAGACAGAAACCCGCTGTCAGTACTACATCTGTCG 705
QY 395 AGAATTGGGACCTATGATCTTCTCGGCTTACCGATCTAGGAATGGAATCTGAGTGG 454
DB 706 AGAGTGGGGACCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGG 759
QY 455 ACGGTAGCATCTATGATCTGCGGCAAGACCACTCGGCTTCAACGCACTTACGCACTGCA 514
DB 760 ACGGGGAAACGTAAGCATCTTACGAGACCTGGCGGTACACGCGCGTCACTGAGGCA 819
QY 515 CCCAACTTGAACCAATATCTGTGCTGCTGCGGCAAGACGCGGCAACGCGGTACCGTCC 574
DB 820 CCGGACCTTCCAGAGTCTGAGGCTGCGGCAAGACGCGGCAAGGCGGCAACGCACTCA 879
QY 575 AGAGCGGCTGCACTTGAACGCTGCGGCTGCGGCTGCTTGAATGCAACGCTGACACT 634
DB 880 CCATCGGCAACCACTTCAACGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 936
QY 635 ACTACGATCTGTTGCAACGAGGCTTCTTCAAGAGGCTGCTGCTGCTGCTGCTGCTG 694
DB 937 ACTACGATCTGTTGCAACGAGGCTTCTTCAAGAGGCTGCTGCTGCTGCTGCTGCTG 996
QY 695 CTGACGTGGCTTGAAGCTTACCTGCTG 722
DB 997 GCGAGGCTGCGCAACCCCGGCAACCCGCG 1024
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RESULT 7
US-09-235-832-1
Sequence 1, Application US/09235832
Patent No. 6667170
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmanper, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palomeimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Laitinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.T.C.

```
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,832
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. 6667170 Relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-09-235-832-1
Query Match 20.1%; Score 197.2; DB 3; Length 1375;
Best Local Similarity 58.6%; Pred. No. 9.1e-46;
Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;
QY 35 TCGGCTTTACCCCGGTTGCGGCTTACGCGGCACTGGGAGCCCTTCCCGG 94
DB 349 TCGGCTTCCGCGCATCTCAACAGTCTTCCGCTTGGCACTGCGCATCGCGTGGC 408
QY 95 CAGGAAATGCCAGGAGCTCGAAAAGCAGACAAACCCCACTCGAGGGCTGGACG 154
DB 409 TGTGCCCCGGGACCGCCGACCGCAGACACCATCACCAGAACAGACGGGTACGCA 468
QY 155 ATGTTATTACTTATCTCTGTGTGAGTACGCGTGAAGCGCAGCCAGTACCACTGG 214
DB 469 ACGGCTACTTCTACTCTGTTCTGTGACCGACGCGCCGGGACCGTCTCCATGACCTTCACT 528
QY 215 AAGGCGGACCTACGAGATCAAGTGGGGAGATGGCGGTACCTGCGGTGAAAAGGCT 274
DB 529 CGGGGGGACGCTACGACCTCTGTGGCGAAACCGGGAACTTGTCTCGCGGCAAGGCT 588
QY 275 GGAACCCCGGCTTGAACGCAAGAGCCATCACTTTGAGGGTGTTCACAGCCAAACGCA 334
DB 589 GGTTCACCGG---GGAGCGGGGACCGTACCTTCAACGCTCTTCAACCGTGGGTA 645
QY 335 ACAGTTACTTGGGCTTACGCTTACGCTTGAACCCGCAACCCGCTGTGAGTATTCATCTG 394
DB 646 ACGGCTACTTCACTGCTTACGCTGAGACAGAAACCCGCTGTCAGTACTACATCTGTCG 705
QY 395 AGAATTGGGACCTATGATCTTCTCGGCTTACCGATCTAGGAATGGAATCTGAGTGG 454
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Db 706 AGAGCTGGGGGCACTACCGGCCCCACC-----GGCACCCTACAAAGGCAACCGTCAACACCG 759
Qy 455 AGCGTAGCATCTATGAGCTCGGCAAGACCACTCGCGTCAACGACCTAGCATGACGCGCA 514
Db 760 ACGGGGGAACGTAACACATCTACGAGACCTGGCGGTACAAACCGCGCTTCATCGAGGGCA 819
Qy 515 CCCAAACCTTGCAGCAATATCTGTCGTCGCCAGAGCAAGGCGCAACGCGGTACCGTCC 574
Db 820 CCCGACCTTCCAGAGCTTCTGAGCGCTCCGCGACAGAGCGAGCGAGCGGACCATCA 879
Qy 575 AGACGGGCTGCCACTTTCGACGCTCGGCTCGGCTGTTGAATGTCAACGTTGACCACT 634
Db 880 CCATCGGCAACCACTTTCGACGCTCGGCGCGCGCGGATGAA---CCGCGGCAACGCG 936
Qy 635 ACTACCAATCGTTTCGAACGAGGCGCTACTTACGACGCGGTATCTGCGATCACCGTTG 694
Db 937 ACTACCAATCATGCGGAGCGCGGCTTACGAGAGCGGTAGCTTCAACCGTCTCCATCA 996
Qy 695 CTGACGTGGGCTAGACGCTATCTGTTG 722
Db 997 GCGAGGCTGGCAACCCCGCAACCCGCG 1024

RESULT 8

US-09-254-733-8
; Sequence 8, Application US/09254733
; Patent No. 6275596

GENERAL INFORMATION:

APPLICANT: WATANABE, MANABU

APPLICANT: MORIYA, TATSUKI

APPLICANT: AOYAGI, KAORU

APPLICANT: SUMIDA, NAOMI

APPLICANT: MURAKAMI, TAKESHI

TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING

TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING

TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH

FILE REFERENCE: 99-0266*/LC(WMC)/00144

CURRENT APPLICATION NUMBER: US/09/254,733

CURRENT FILING DATE: 1999-05-07

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 822

TYPE: DNA

ORGANISM: TRICHODERMA VIRIDE MC300-1

FEATURE:

NAME/KEY: sig_peptide

LOCATION: (14)..(112)

FEATURE:

NAME/KEY: CDS

LOCATION: (14)..(112)

FEATURE:

NAME/KEY: mat_peptide

LOCATION: (113)..(809)

FEATURE:

NAME/KEY: CDS

LOCATION: (113)..(285)

FEATURE:

NAME/KEY: Inttron

LOCATION: (286)..(412)

FEATURE:

NAME/KEY: CDS

LOCATION: (413)..(809)

US-09-254-733-8

Query Match 19.8%; Score 194.2; DB 3; Length 822;

Best Local Similarity 69.0%; Pred. No. 5,1e-45;

Matches 281; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 286 CTGAACGCAAGACCATCTTGTGAGGGTGTTCACGCAACGCGCAAGCTACCTT 345
Db 402 CTGAACGCAAGGTCATCATCTTCTGGGCAACCTACCAACCCCAACGCGCAAGCTACCTC 461

Qy 346 GCGCTTACGGTTGGAACCCGCAACCCGCTGGTTCAGATTTACATGTCGAGAATTGGC 405
Db 462 TCCGTGTAAGGCTGGTCCGCAACCCCTGTATCGAGTACATGTCGAGAATTGGC 521
Qy 406 ACTATGATTCCTTCTCCGCTGTACAGATCTAGAACTGTGAGTGCAGAGTATC 465
Db 522 ACTTCAACCCGTCACCGGCGCAACAGTGTGGCCAGAGTGAAGTGCAGAGGCGCTC 581
Qy 466 TATGCACTCGGCAAGACCACTCGCGTCAACGCACTTACATGACGCGCAACCTTTC 525
Db 582 TACGACATCTACCGACCAACGCGGTCAACAGCGCTTCATCGAGGCGACCTTTC 641
Qy 526 GACCAATATCTGTCGTCGCGCAGAGCAAGGCGCAACGCGGTACCGTTCAGAGGCGTCG 585
Db 642 TACGATATCTGTCGTCGCGCAGCAACCGCTTCAGCGGCTTCGTAACGCGGCAAC 701
Qy 586 CACTTGCAGCGCTCGGCTCGGCTGTTGAATGTCAACGCTGACCACTACTACGATC 645
Db 702 CACTTCAACGCGGTGGGCTCGCAAGGCTGACGCT---GGGCAACATGATTTACAGATT 758
Qy 646 GTTGCACGAGGCGCTACTTACGACAGCGGTATGCTGCAATCACCGT 692
Db 759 GTTCCCGTGAAGGCGCTACTTACGCTGCTGCTGCTTCCATCACCGT 805

RESULT 9

US-08-121-436A-1

; Sequence 1, Application US/08121436A

; Patent No. 5837515

GENERAL INFORMATION:

APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena

APPLICANT: Saarelainen, Riitta

APPLICANT: Palohelmo, Marja

APPLICANT: Lahinen, Tarja

APPLICANT: Pajunen, Richard

TITLE OF INVENTION: No. 5837515 Enzyme Preparations and Methods

TITLE OF INVENTION: for Their Production

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/121,436A

FILING DATE: 16-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/078,478

FILING DATE: 18-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FI93/00221

FILING DATE: 24-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/889,893

FILING DATE: 29-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/524,308

FILING DATE: 16-MAY-1990

ATTORNEY/AGENT INFORMATION:

NAME: Cimdala, Michele A.

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 1050,008000C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(176..448, 557..952)
US-08-121-436A-1

Query Match 19.3%; Score 190; DB 2; Length 1015;
Best Local Similarity 68.5%; Pred. No. 8.8e-44;
Matches 278; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

QY 287 TGAACGCAAGCCATTCATCTTTGAGGGTGTATTACCAAGGCGCAAGCTTACCTTG 346
DB 546 TAAAAAAGGGGTATCACTTCGCGGAGCTACAAACCCCAAGCGCAAGCTTACCTCT 605
QY 347 CGGTCTACGGTTGACCGCGAACCCGCTGTGAGTATTACATGCTGCAAGAACTTTGGCA 406
DB 606 CGGTGTACGGCTGTGCTCCGCAACCCCTGATCGAGTACTACATGCTGCAAGAACTTTGGCA 665
QY 407 CCTATGATCTTCTCTCCGGTCTACCGATCTAGGAAGTGTGAGCGAGCTAGCATCT 466
DB 666 CCTACAAACCGGTCCACGGGCGCACCAAGCTGGGGAAGTCACTCCGACGGCAGCGCT 725
QY 467 ATCGACTGGCAAGCACTGCGCTGCAAGCACTAGATGAGCGGCAACCAACTTTG 526
DB 726 ACGACATTACCGCAGCGAGCGCGTCAACAGCCCTCATATCGGCAACCGCACTTTT 785
QY 527 ACCAATCTGGTGGTCCGCGCAGCAAGCAAGCGGAGCTGCTGCAAGCGGCTGCTCC 586
DB 786 ACCAGTACTGCTGCTCCGCGCAGCAAGCAAGCGGCTGCTGCTGCTGCTGCTGCTGCT 845
QY 587 ACTTCGACGCTGGGCTGCGCGTGTGTTGAATGTCAACGCTGACCACTACTACGATCG 646
DB 846 ACTTCAGCGGCTGCGCTGAGCAAGCGCTGAGCGCT---CGGAGCATGATTAACGATTTG 902
QY 647 TTGCAAGGAGGCTTACTTTCAGACGCGCTATGCTGCTGCTGCTGCTGCTGCTGCT 692
DB 903 TTGCGGTGAGGGTTACTTTAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948

RESULT 10
US-08-768-373-1
Sequence 1, Application US/08768373

GENERAL INFORMATION:
PATENT NO. 6228629
APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: M NTYL, ARJA
APPLICANT: VEHMANPER, JARI
APPLICANT: LANTTO, RAIIA
APPLICANT: LAHTINEN, TARJA
APPLICANT: PAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC

COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELLE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION: /product= "X1NA"
FEATURE:
NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /product= "X1NA"
US-08-768-373-1

Query Match 18.5%; Score 181.8; DB 3; Length 1281;
Best Local Similarity 65.4%; Pred. No. 2.1e-41;
Matches 283; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

QY 267 AAAGGCTGGAACCCCGGCTGGAACGCAAGAGCCATTCATCTTGAAGGTGTTTCCAGCC 326
DB 478 AACAGGCTGGAACCCCGGTACCGATTAACCGTGTATCAATCAACAGCGCACTACAGAC 537
QY 327 AAAGGCAAGCTTACCTTGGCGGTCTACAGGTTGACCGCAACCCGCTGCTGATTTA 386
DB 538 CAACGGCACTCTTACCTCGCGCTTACAGGCTGGAACCGCAACCCGCTGATCGATCTA 597
QY 387 CATCGTGAAGACTTTGGCACTTATGATCTTCTCCGGTCTACCGATCTAGGAATGT 446
DB 598 CGTGTGAGAGCTTCCGCACTTACAGCCGCTGACGCGGCCACCCGATGGGCAAGCT 657
QY 447 CGAGTGAAGCTGTAGCATCTATGACCTGCGGAAGACCACTGCGCTCAACGCACTAGAT 506
DB 658 GACCAAGCAGCGCGCACTTACCAATCTTACCGACGAGGCGGTCAACGCGCCCTTCAT 717
QY 507 CGAGGCAACCAACTTTCAGCAATCTGCTGCGTCCGAGGACAAGCCGACGAGCGG 566
DB 718 CGAGGCAACCAAGCTTTCAGCAATCTGCTGCGTCCGAGGACAAGCCGACGAGCGG 777
QY 567 TACCGTCAAGCGGAGCTGCACTTGAAGCTGAGCGCTGAGGCTGCGGTTGAAATGTCACGG 626
DB 778 TACGTTTACATGAGCAACCACTTCAATGCTTGGAGGAGGAGGCTGCTGAGCT---GGG 834
QY 627 TGACCACTACTACAGATGCTTGAAGGAGGCTACTTCAAGCAGCGGCTATGCTCGAT 686
DB 835 TTCCATGATATTCAGATGTGCTACTGAGGGTTACTACTGCTGCTGCTGCTGCTGCTGCT 894
QY 687 CACGTTGCTGAC 699
DB 895 CATGTTGCGGCG 907

RESULT 11
US-09-849-242A-1
Sequence 1, Application US/09849242A
Patent No. 6635464
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
HAKOLA, SATU
MONTYLO, ARJA
VEHMANPERO, JARI
LANTTO, RAIIJA
LAHTINEN, TARJA
FAGERSTRIM, RICHARD
SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-MAY-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION: /product= "XLNA"
FEATURE:
NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /product= "XLNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-849-242A-1

Query Match 18.5%; Score 181.8; DB 3; Length 1281;
Best Local Similarity 65.4%; Pred. No. 2.1e-41;
Matches 283; Conservative 0; Mismatches 147; Indels 3; Gaps 1;
267 AAGGGCTGAACCCGGCTGAAGCAGAGCCATCATCTTTAGAGGTGTTTACGAGCC 326

Db 478 AAGAGGCTGAACCCGGCTACCGATTAACCGTGCATCACTACAGACGAGCCGACTACAGACC 537
Qy 327 AAGCGCAACAGCTACCTTGGGCTCTACGTTGAGACCCGCAACCCGCTGCTGAGTATTA 386
Db 538 CAACGGAACTCTTACCTTCGCGCTACGGCTGAGCCGCAACCCGCTGATCGAGTACTA 597
Qy 387 CATCGTCAGAACTTTGCACTTATGATCTTCTCCGGTGTCTACCGATCTAGGAACTGT 446
Db 598 GTGTGTGAGAGCTTCGCACTTACGACCCGTCAACGGGCGCACCCGCACTGGCAGGT 657
Qy 447 CGAGTCGACGCGTAGACTTATCGACTCGGCAAGCACTCGCTCAACGCACTAGCAT 506
Db 658 GACCACGAGCGGCGCACTCAACATCTACCGACGAGGCGCTCAACGCGCCCTCAT 717
Qy 507 CGAGCGCAACCACTTTCAGCACTACTGTGCTCGGCTCGGCAAGACGCAACGCAAGCGG 566
Db 718 CGAGGGCAACCAAGCTTCTACCAATCTGTCTGTGCGCACCTCAAGCGCACCGGCGG 777
Qy 567 TACGTCGACGCGGCTGCCACTTCGACGCGCTGGGCTCGGCTGTGAAATGTCACGCG 626
Db 778 TACTGTTACATGAGCAACCACTTCAATGCTTGAAGCAGGCTGTGACGCT---GGG 834
Qy 627 TGACCACTACTACCAAGATCGTTGCAAGGAGGCTACTTCAGACGCGCTATGCTCGCAT 686
Db 835 TTCCATGATTATCAGATTGTGGCTACTGAGGGGTTACTACTCGTCTGGCGACTGT 894
Qy 687 CACCGTTGCTGAC 699
Db 895 CAATGTTGGCGGC 907

RESULT 12
US-07-744-570B-1
Sequence 1, Application US/07744570B
Patent No. 5202249
GENERAL INFORMATION:
APPLICANT: Kluepfel, D.
APPLICANT: Morosoli, F.
TITLE OF INVENTION: Xylanase for Biobleaching
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael J. Bradley
STREET: 1200 South 47th Street
CITY: Box Number 4023
STATE: Richmond
COUNTRY: California
ZIP: 94804-0023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,570B
FILING DATE: 19910813
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single strand
TOPOLOGY: Circular
US-07-744-570B-1

Query Match 17.1%; Score 168.4; DB 2; Length 675;
Best Local Similarity 60.0%; Pred. No. 1e-37;
Matches 343; Conservative 0; Mismatches 211; Indels 18; Gaps 3;
127 ACAACCCCACTCGAGGCGTGCAGATGTTATTAATTCTGTGTGAGTACGAGT 186

Db 34 ACATCAACAACAACGAGCCGACCGCATGTACTGTTCTGACCGAGCC 93
Qy 187 GAGACGAGGCGACGTAACCAACCTTGAAAGCGGCACTTACGATCAGCTGGAGAT 246
Db 94 GCGGCTCCTCTCTCAATGAGCTCAAGGTGGCGGCACTTACGATCAGCTGGAGAT 153
Qy 247 GCGGCTCCTCTCTCAATGAGCTCAAGGTGGCGGCACTTACGATCAGCTGGAGAT 306
Db 154 TGCGGCAACTCTCTCTCAATGAGCTCAAGGTGGCGGCACTTACGATCAGCTGGAGAT 207
Qy 307 TTTGAGGTGTTTACGACCAAAAGGCAACGCTTACGATCAGCTGGAGAT 366
Db 208 TACAACGCTTACTTCAACCCCGTGGCAACGCTTACGATCAGCTGGAGAT 267
Qy 367 AACCGCTGCTGAGTATTAATCATGCTGCAAACTTTGCACTTACGATCAGCTGGAGAT 426
Db 268 AACCGCTGCTGAGTATTAATCATGCTGCAAACTTTGCACTTACGATCAGCTGGAGAT 321
Qy 427 GCTACCGATCTAGAACTGTGAGTGGACGCTGATCATCTTACGATCAGCTGGAGAT 486
Db 322 GGTACGTACAAAGGACCGCTTCCAGGCGACGAGGCACTTACGATCAGCTGGAGAT 381
Qy 487 GCGCTCAACGCACTAGATGAGGCAACCACTTACGATCAGCTGGAGAT 546
Db 382 CGGTACAAACGCTTCTCGTGGAAAGGCAACCACTTACGATCAGCTGGAGAT 441
Qy 547 CAGGACAAAGGCAACGCTTCTCGTGGAAAGGCAACCACTTACGATCAGCTGGAGAT 600
Db 442 CAGTACGAAAGGCAACGCTTCTCGTGGAAAGGCAACCACTTACGATCAGCTGGAGAT 501
Qy 601 GCTGCGCTGCTTGAATGTCAACGCTGACCACTTACGATCAGCTGGAGAT 660
Db 502 GCGGCGGCGGCACTGATGAGGCACTTACGATCAGCTGGAGAT 561
Qy 661 TACTTACGACGCTGATGCTGCACTACCGT 692
Db 562 TATCAGACGAGTGAAGCTCGAACATCAACGCT 593

RESULT 13
US-08-507-431-5
Sequence 5, Application US/08507431
Patent No. 5693518
GENERAL INFORMATION:
APPLICANT: Kofod, Lene V.
APPLICANT: Kaupinen, Markus S.
APPLICANT: Christgau, Stephan P.
APPLICANT: Heide-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan Q.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 56935180 No. 5693518disk of No. 5693518th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,431
FILING DATE: 15-FEB-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,800
FILING DATE: 25-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3954, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SRO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-08-507-431-5

Query Match 16.8%; Score 165.2; DB 2; Length 927;
Best Local Similarity 57.9%; Pred. No. 9,4e-37; Indels 8; Gaps 3;
Matches 352; Conservative 0; Mismatches 248;

Qy 107 CGAGAGCTCGAAAGCGACAGACCAACCCCACTCGAGAGGCTGGACGATGTTTACT 166
Db 134 CTGCGCTTGCTGGGCGCTGACAGCTGAGCTCACTGGCTACTGGAAGGGTATTACTATA 193
Qy 167 ATTCTGTGAGAGTACGCTGAGAGCGGCACTTACCAACTTGGAAAGGCGCACT 226
Db 194 GCTTCTGAGACGATGAGGCGGCAAGCGGCGATGTGATACACCAACGAGCGGCGGCTCT 253
Qy 227 ACAGAGTCACTGGGAGATGGGCTTAACTGTCGCTGAGAAAGGCTGGAACCCGAGC 286
Db 254 ACAGCGTACCTGCTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCT 312
Qy 287 TGAACGCAAGGCACTTCTGAGGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCT 342
Db 313 AGTGTCTATGACATTTAGTACTCCGCTCTGAGCAAGCAAGCAAGCAAGCAAGCTTAC 372
Qy 343 CTGCGCTTACGCTTGAACCCGCAACCCGCTGCTGAGATTTACATGCTGAGAACTTT 402
Db 373 CTCTCCGCTTACGCTGAGCAACCCGCTCTCTGCTGAGTATTCCTGAGAGACTTAC 432
Qy 403 GGCACCTATGATCTTCTCCGCTGCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCT 462
Db 433 GGGAGTAAACCCCGCTGAGCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCT 492
Qy 463 ATCTATGACTCGGCAAGCACTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCT 522
Db 493 ACATACATATCTTACAGGCGGCAAGCGGCAAGCGGCTTCTGAGCTTCTGAGCTTCTGAGCT 552
Qy 523 TTGACCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
Db 553 TTCAAGGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
Qy 583 TGCACTTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642
Db 613 AACCATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
Qy 643 ATCTTCAACGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGG 702
Db 670 ATCTGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAG 729
Qy 703 GGTAAAG 710
Db 730 CGTGAGA 737

RESULT 14
US-08-902-655A-5

Sequence 5, Application US/08902655A
Patent No. 5885819
GENERAL INFORMATION:
APPLICANT: Kolod, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan Q.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58858190 No. 5885819disk of No. 5885819th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,655A
FILING DATE: 30-July-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl T.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-08-902-655A-5

Query Match 16.8%; Score 165.2; DB 2; Length 927;
Best Local Similarity 57.9%; Pred. No. 9.4e-37;
Matches 352; Conservative 0; Mismatches 248; Indels 8; Gaps 3;

QY 107 CGGAGCTCGAAAACGACAGCAACCCCACTCGGAGGGTGGACAGATGATTACT 166
DB 134 CTGCGCTTGCGGCGCTGCACTGCGAGCTTCAGTCACTGCAAGCGCTATTACTATA 193
QY 167 ATTCCTGATGAGTGAAGCGTGAAGCGGACGATCAACCACTGGAAGCGGCACT 226
DB 194 GCTTCTGAGCGGATGCGGCAAGCGGCGATGTTGAATACAGAAAGCGGCGGCTCT 253
QY 227 ACGAGATCAGCTGGGAGAGTGGCGGTAACTCTGTCGGTGAAGAGGCTGAAACCCGCG 286
DB 254 ACACGCGTACCTGGTCACTCGGCTCGAACTTGTGCGTGAAGAGGCTGGAACCTGG-A 312
QY 287 TGAAGCAAGAGCCATCATCTTTAGAGGTGTTTACCAAGCC-----AAACGGAAGAGTTAC 342
DB 313 AGTGTCTATGACATTAGTACTCGGCTCTCGGACACAGCAAGAAATAGCAAGCTAC 372
QY 343 CTTCGGTCTACGGTTGAGCCGCAACCGGCTGGTCAAGTATTATCATGTCGAAGACTTT 402

DB 373 CTCTCCGCTACGCGTGAACACCGGTCCTCTCGTCGAGTATATATCTGAGAGACTAC 432
QY 403 GGACACCTATGATCTTCTCCGCGTACCGATATAGAACTGTCGAGTCGACGATAGC 462
DB 433 GGGAGTAAACCCCGGCTCAGCTGAGCTTAAAGGCTCGGCTCTGCTCGAGGATCG 492
QY 463 ATCTATGACTCGGCAAGACCACTCGGTCACAGCACTAGCATTCAGCGGCAACCAACC 522
DB 493 ACATCAATATCTACAGGAGGACCCGACCAAGCCCCCTTCATTCAGGGGACCGCACT 552
QY 523 TTGACCAATATCTGTCGATTCGCGAGAGACGACAGCGGTACCGTTCAGACGGGC 582
DB 553 TTACAGGAGTACTGTCATTCGCGACAAAGCGCTCGGCGGTACCGTACGATCGCC 612
QY 583 TGCCATTCGACGCTGGGCTCGGCTGTTTGAATGTCACAGGTACCACTATACAG 642
DB 613 AACATTTCAGTCTGGGAGAACTGGGAATGATCT---GGGACAGCAACATATACAG 669
QY 643 ATGTTGCAACGAGGCTACTTTCAGCAGCGGCTATGCTGATCAACGTTGCTGACGTG 702
DB 670 ATGTCGCTACTGAAAGCTACTCTGTCGGTCTGCTCATTCAGGTTGCTGAGAG 729
QY 703 GGCTAAGA 710
DB 730 CGTGACAG 737

RESULT 15
US-09-116-622-5
Sequence 5, Application US/09116622
Patent No. 6080567
GENERAL INFORMATION:
APPLICANT: Kolod, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan Q.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60805670 No. 6080567disk of No. 6080567th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,622
FILING DATE: 16-July-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-09-116-622-5

Query Match 16.8%; Score 165.2; DB 3; Length 927;
Best Local Similarity 57.9%; Pred. No. 9.4e-37;
Matches 352; Conservative 0; Mismatches 248; Indels 8; Gaps 3;

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QY 107 CGAGCTCGAAGGCGACGACGACCCCACTCGAGGGCTGGACAGATGTTATTACT 166
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DB 134 CTGCCCTTGCTGGGCGCTCGACTGCGACGCTCACTGGCTACTCGAACGGCTATTACTATA 193
    |||||
QY 167 ATTCTGTGAGAGGAGCGGTGAGCGGACGACGACGTAACCACTGGAAGCGGCACT 226
    |||||
DB 194 GCTTCTGACCGATGGCGCAAGCGCGATGTTGAATACAGCAACGCGCCGCGGGGCTCT 253
    |||||
QY 227 ACAGATCAGCTGGGAGAGATGGCGGTAACTCTGTCGTGGAAGGGCTGAAACCCGAGC 286
    |||||
DB 254 ACAGCGTGAAGCTGCTGATCGGCTCGAATCTGTCGTGGAAGGGCTGGAACCTTGG-A 312
    |||||
QY 287 TGAACGAAAGGCGATCCATCTTTGAGGGTGTTAACGAGCC---AAACGCAACGCTAC 342
    |||||
DB 313 AGTCTCATGACATTACGTAATCCGGCTCCGAGCACAGCAAGAAATAGCAACAGCTAC 372
    |||||
QY 343 CTTCGGGCTACGCTGAGACCCGCAACCCGCTGTCGATTAATCTGAGAACTTT 402
    |||||
DB 373 CTCTCCGCTAAGCGGTGACCAACGGTCTCTGTCGAGTACTATATCTGAGAGACTAC 432
    |||||
QY 403 GGCACTATGATCTCTCCGCTGCTACCGATCTAGGAAGTCTGAGTGCAGCGTAGC 462
    |||||
DB 433 GGGGAGTACAAACCCGCTCAGCTGCACTTACAAAGGCTGGTCTACTCCAGGATCG 492
    |||||
QY 463 ATCTATGACTCGGCAAGACCACTGGCTCAACGCACTAGCATGACGCGCAACCAACC 522
    |||||
DB 493 ACATACAAATATCTACACGGGACCGCACCAAGCCCCCTCATCCAGGGCACGGCCACT 552
    |||||
QY 523 TTCAGCCAAATCTGGTCCGTCGCAAGACCAAGCGCAACGATACCGTCCAGACGGGC 582
    |||||
DB 553 TTCAGCGAGTACTGATTCATTGCGCAAGCAAGCGCGTGGCGGTACCGTGAACGACTGCC 612
    |||||
QY 583 TGCCACTTGAAGCGCTGGGCTCGCGCTGTTGAATGTCAACGCTGACCACTACTACCAAG 642
    |||||
DB 613 AACCATTTCAATGCTTGGGCGAAGCTGGGAATGAATCT---GGGACGCAACAATATCAG 669
    |||||
QY 643 ATCGTTGCAACGAGGGGCTACTTTCAGACGCGCTATAGCTCGCATCAACCGTTGCTGACGTG 702
    |||||
DB 670 ATCGTCGCTACTGAAGGCTACTACTGTCGGGTCTGCGTCCATTACGGTTGCTGAGAG 729
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QY 703 GGCTAAGA 710
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DB 730 CGTGCAGA 737
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Job time : 216.809 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:35:33 ; Search time 1023.32 Seconds
(without alignments)
7943.586 Million cell updates/sec

Title: US-09-467-368-1
Perfect score: 983
Sequence: 1 TCGGCCCGACGCTTGCAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_Main:*

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- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 585 | 59.5 | 588 | 6 | US-10-237-386-9 |
| 3 | 374 | 38.0 | 678 | 3 | US-09-803-454-3 |
| 4 | 257.2 | 26.2 | 850 | 8 | US-10-425-115-177283 |
| 5 | 246.6 | 25.1 | 749 | 8 | US-10-425-115-82922 |
| 6 | 240.4 | 24.5 | 818 | 8 | US-10-425-115-37173 |
| 7 | 224.6 | 22.8 | 666 | 5 | US-10-213-990-65 |
| 8 | 223 | 22.7 | 705 | 5 | US-10-213-990-68 |
| 9 | 197.2 | 20.1 | 1375 | 3 | US-09-770-621-1 |
| 10 | 197.2 | 20.1 | 1375 | 6 | US-10-286-993-1 |
| 11 | 190.6 | 19.4 | 739 | 5 | US-10-213-990-67 |
| 12 | 181.2 | 18.4 | 712 | 5 | US-10-213-990-64 |
| 13 | 165.4 | 16.8 | 942 | 5 | US-10-213-990-71 |
| 14 | 155.2 | 15.8 | 978 | 10 | US-11-018-645-21 |
| 15 | 147.2 | 15.0 | 1002 | 5 | US-10-213-990-70 |
| 16 | 146.4 | 14.9 | 596 | 6 | US-10-307-441-39 |
| 17 | 136.8 | 13.9 | 2225 | 3 | US-09-790-070A-8 |
| 18 | 124 | 12.6 | 2898 | 5 | US-10-299-393-1 |
| 19 | 124 | 12.6 | 2898 | 10 | US-11-154-793-1 |
| 20 | 119.2 | 12.1 | 557 | 3 | US-09-970-616-1 |
| 21 | 119.2 | 12.1 | 557 | 9 | US-10-765-716-1 |
| 22 | 119.2 | 12.1 | 642 | 3 | US-09-149-310-31 |
| 23 | 118 | 12.0 | 594 | 10 | US-11-018-645-17 |

| | | | | | | |
|----|-------|------|------|----|---------------------|-------------------|
| 24 | 103.6 | 10.5 | 2054 | 6 | US-10-419-969-5 | Sequence 5, Appli |
| 25 | 101.8 | 10.4 | 643 | 6 | US-10-340-860A-39 | Sequence 39, Appl |
| 26 | 94.2 | 9.6 | 561 | 10 | US-11-018-645-13 | Sequence 13, Appl |
| 27 | 90.2 | 9.2 | 561 | 10 | US-11-018-645-15 | Sequence 15, Appl |
| 28 | 89.4 | 9.1 | 972 | 10 | US-11-018-645-19 | Sequence 19, Appl |
| 29 | 83.6 | 8.5 | 394 | 8 | US-10-425-115-48309 | Sequence 48309, A |
| 30 | 82.6 | 8.4 | 642 | 8 | US-10-626-583-4 | Sequence 4, Appli |
| 31 | 82.6 | 8.4 | 642 | 9 | US-10-626-724-4 | Sequence 4, Appli |
| 32 | 80.8 | 8.2 | 539 | 7 | US-10-437-963-15625 | Sequence 15625, A |
| 33 | 78.4 | 8.0 | 591 | 10 | US-11-018-645-3 | Sequence 3, Appli |
| 34 | 78.4 | 8.0 | 628 | 10 | US-11-018-645-10 | Sequence 10, Appl |
| 35 | 72.4 | 7.4 | 663 | 3 | US-09-909-207-1 | Sequence 1, Appli |
| 36 | 72.4 | 7.4 | 663 | 3 | US-09-909-207-2 | Sequence 2, Appli |
| 37 | 72.4 | 7.4 | 744 | 3 | US-09-909-207-4 | Sequence 4, Appli |
| 38 | 72.4 | 7.4 | 744 | 3 | US-09-909-207-5 | Sequence 5, Appli |
| 39 | 72.4 | 7.4 | 1513 | 3 | US-09-909-207-10 | Sequence 10, Appl |
| 40 | 72.4 | 7.4 | 1513 | 3 | US-09-909-207-11 | Sequence 11, Appl |
| 41 | 71.8 | 7.3 | 642 | 8 | US-10-626-583-6 | Sequence 6, Appli |
| 42 | 71.8 | 7.3 | 642 | 8 | US-10-626-583-12 | Sequence 12, Appl |
| 43 | 71.8 | 7.3 | 642 | 9 | US-10-626-724-6 | Sequence 6, Appli |
| 44 | 71.8 | 7.3 | 642 | 9 | US-10-626-724-12 | Sequence 12, Appl |
| 45 | 71.8 | 7.3 | 645 | 6 | US-10-237-386-10 | Sequence 10, Appl |

ALIGNMENTS

RESULT 1
US-09-467-368-1
; Sequence 1, Application US/09467368
; Patent No. US20020160080A1
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
Mullertz, Peter
Knap, Inge Heimer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. US20020160080A10 No. US20020160080A1disk of No. US200201600
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,368
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Thermomyces lanuginosus

STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705
SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-09-467-368-1

Query Match 100.0%; Score 983; DB 3; Length 983;
Best Local Similarity 100.0%; Pred. No. 7, 8e-305; Indels 0; Gaps 0;
Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCGGCCCCGACGCTTGTGCAATCTTGCAGTGTGCTGCTTACCCCGTTGCCCTTGG 60
DB 1 TCGGCCCCGACGCTTGTGCAATCTTGCAGTGTGCTGCTTACCCCGTTGCCCTTGG 60
QY 61 GCGTTAGCCGCGACCTGGGGCCCTTCCCGCAGAGGAATGCGACGAGCTGAAAAG 120
DB 61 GCGTTAGCCGCGACCTGGGGCCCTTCCCGCAGAGGAATGCGACGAGCTGAAAAG 120
QY 121 CGACAGACAAACCCCACTGGAGGGCTGGCAGTGTATTAATACTATTCCTGGTGAAGT 180
DB 121 CGACAGACAAACCCCACTGGAGGGCTGGCAGTGTATTAATACTATTCCTGGTGAAGT 180
QY 181 GACGCTGAGGCGCAGGCGCAGTACCAACCTGGAGGCGCACCTACGAGATCAGCTGG 240
DB 181 GACGCTGAGGCGCAGGCGCAGTACCAACCTGGAGGCGCACCTACGAGATCAGCTGG 240
QY 241 GGAAGTGGCGGTAACTCTGTGGTGGAAAGGGCTGGAAACCCCGGCTGGAAGCAAGACC 300
DB 241 GGAAGTGGCGGTAACTCTGTGGTGGAAAGGGCTGGAAACCCCGGCTGGAAGCAAGACC 300
QY 301 ATCCACTTGAAGGGTGTATTAACGACCAACGCGCAACGCTTGGCGGTCTACGCTTGG 360
DB 301 ATCCACTTGAAGGGTGTATTAACGACCAACGCGCAACGCTTGGCGGTCTACGCTTGG 360
QY 361 ACCGCGCAACCCGCTGCTGAGTATTAATCTGCAAGAACTTTGGCACTATGATCTTCC 420
DB 361 ACCGCGCAACCCGCTGCTGAGTATTAATCTGCAAGAACTTTGGCACTATGATCTTCC 420
QY 421 TCCGCTGCTACCGATCTAGAACTGTGCAAGTGGCAAGCTTACCTATGACTGGCAAG 480
DB 421 TCCGCTGCTACCGATCTAGAACTGTGCAAGTGGCAAGCTTACCTATGACTGGCAAG 480
QY 481 ACCACTGCGTCAACGCACTAGCATCGACGCGCAACCTTGAACCAATACTGGTGG 540
DB 481 ACCACTGCGTCAACGCACTAGCATCGACGCGCAACCTTGAACCAATACTGGTGG 540
QY 541 GTCCGCGCAGGACCAAGCGACCAAGCGGTACCGTCCAGACGGGCTGCACTTGCAGCTGG 600
DB 541 GTCCGCGCAGGACCAAGCGACCAAGCGGTACCGTCCAGACGGGCTGCACTTGCAGCTGG 600
QY 601 GCTCGCGCTGCTTGAATGTCAACGCTGACCACTACAGATGCTGGTGAACGAGGGCC 660
DB 601 GCTCGCGCTGCTTGAATGTCAACGCTGACCACTACAGATGCTGGTGAACGAGGGCC 660
QY 661 TACTTCAGAGGGCTATGCTGATCAACCGTTCGACGTTGCGAGTGAAGAGTATTC 720
DB 661 TACTTCAGAGGGCTATGCTGATCAACCGTTCGACGTTGCGAGTGAAGAGTATTC 720
QY 721 TGGTATCTCGCGAGGCAACAGCAAGATGTGTCAGATGTGCGGGTGAAGGATTC 780
DB 721 TGGTATCTCGCGAGGCAACAGCAAGATGTGTCAGATGTGCGGGTGAAGGATTC 780
QY 781 ATCAGCATATCTGTCTGCGCTTGGAGTATCTTTGAGAGACTGTGAGAACTTTGGC 840
DB 781 ATCAGCATATCTGTCTGCGCTTGGAGTATCTTTGAGAGACTGTGAGAACTTTGGC 840
QY 841 GAGCTGGCGAGGATCAAGTATGCTTGGCGGTGTTTGGCTCCATTCCTGTAAGAAA 900
DB 841 GAGCTGGCGAGGATCAAGTATGCTTGGCGGTGTTTGGCTCCATTCCTGTAAGAAA 900
QY 901 TTGTTATTGCTTCTGTTCTAGTGTACATAGCGAGCAATTGAGGCTTCAAGCTTGGAAA 960
DB 901 TTGTTATTGCTTCTGTTCTAGTGTACATAGCGAGCAATTGAGGCTTCAAGCTTGGAAA 960
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DB 901 TTGTTATTGCTTCTGTTCTAGTGTACATAGCGAGCAATTGAGGCTTCAAGCTTGGAAA 960
QY 961 AAAAAAAAAAAAAAAAAAAAAA 983
DB 961 AAAAAAAAAAAAAAAAAAAAAA 983
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RESULT 2
US-10-237-386-9
Sequence 9, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
APPLICANT: Sorensen, Jens
TITLE OR INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237, 386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 588
TYPE: DNA
ORGANISM: Thermomyces lanuginosus
US-10-237-386-9

Query Match 59.5%; Score 585; DB 6; Length 588;
Best Local Similarity 100.0%; Pred. No. 5, 7e-177; Indels 0; Gaps 0;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 124 CAGACAAACCCCACTGAGAGGCTGGCAGATGTTATTAATCTTCTGTGAGTGAAC 183
DB 4 CAGACAAACCCCACTGAGAGGCTGGCAGATGTTATTAATCTTCTGTGAGTGAAC 63
QY 184 GGTGAGCGCAGCGCAGTACCAACCTGGAAGGCGGACCTTACGAGTACGCTGGGA 243
DB 64 GGTGAGCGCAGCGCAGTACCAACCTGGAAGGCGGACCTTACGAGTACGCTGGGA 123
QY 244 GATGGCGGTAACTGTCGCTGAGTGAAGGGCTGGAACCCCGGCTGGAACGCAAGACATC 303
DB 124 GATGGCGGTAACTGTCGCTGAGTGAAGGGCTGGAACCCCGGCTGGAACGCAAGACATC 183
QY 304 CACTTGAAGGGTGTTTACAGACCAACGCGCAACGCTTACCTTGCCTTGAAC 363
DB 184 CACTTGAAGGGTGTTTACAGACCAACGCGCAACGCTTACCTTGCCTTGAAC 243
QY 364 CGCAACCGCTGCTGAGTATTAATGTCAGAACTTTGGACCTATGATCTTCC 423
DB 244 CGCAACCGCTGCTGAGTATTAATGTCAGAACTTTGGACCTATGATCTTCC 303
QY 424 GGTGCTACCGATCTAGGAACGTGAGTGGCAGCGTGAATCTATCGACTGGCAAGAC 483
DB 304 GGTGCTACCGATCTAGGAACGTGAGTGGCAGCGTGAATCTATCGACTGGCAAGAC 363
QY 484 ACTGCGCTCAACGCACTAGCATCGACGCGCAACCCAACTTGCACCAATACTGTGCTC 543
DB 364 ACTGCGCTCAACGCACTAGCATCGACGCGCAACCCAACTTGCACCAATACTGTGCTC 423
QY 544 CGCAGAGCAACGCGCAGCGGTACCGTCCAGACGGGCTGCACTTGAAGGCTGGCT 603
DB 424 CGCAGAGCAACGCGCAGCGGTACCGTCCAGACGGGCTGCACTTGAAGGCTGGCT 483
QY 604 CGCGTGGTGAATGTCAAGGTGACCACTTACAGCATGTTGCAACGAGAGGCTAC 663
DB 484 CGCGTGGTGAATGTCAAGGTGACCACTTACAGCATGTTGCAACGAGAGGCTAC 543
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Qy 664 TTCACAGCGGCTATGCTCGCATCACCGTGTCTGAGCTAA 708
Db 544 TTCACAGCGGCTATGCTCGCATCACCGTGTCTGAGCTAA 588

RESULT 3

US-09-803-454-3
; Sequence 3, Application US/09803454
; Publication No. US20030022280A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030022280A1ozymes A/S
; APPLICANT: Takagi, Shinobu
; APPLICANT: Terui, Yuri
; TITLE OF INVENTION: High Expression of Industrial Enzymes
; FILE REFERENCE: 6125-200-US
; CURRENT APPLICATION NUMBER: US/09/803,454
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-803-454-3

Query Match 38.0%; Score 374; DB 3; Length 678;
Best Local Similarity 72.0%; Pred. No. 4.2e-109;
Matches 488; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 31 ATGGTCGGCTTACCCCGCTTGGCGCTTACCGCGGAGCTGGGGCCCTGCGCTTC 90
Db 1 ATGGTCGTTTACTCCAGTGTCTTACCTCTTACGCTACCTGCTTACCTTTC 60
Qy 91 CCGGAGGAAATGCGACGAGACTCGAAAAGCAGACCAACCCCACTCGAGGCTG 150
Db 61 CCACAGGTAATGCTACGTAATGAAAAGACAAACCACTCCAAATTCGAGGTTG 120
Qy 151 CACAGTGTATTAATCTCTGCTGAGTACGCTGAGGCGCAGGCACTACCAAC 210
Db 121 CATATGTTATTAATCTCTGCTGAGTACGCTGAGGCGCAGGCACTACCAAT 180
Qy 211 CTGAAAGCGGACCTACGATCAGCTGGGAGATGGCGGTAACCTCGGTGGAAG 270
Db 181 TTAAAGGTGATCTAATTAATCTGAGTGAATTTAGTGTGTA 240
Qy 271 GCGTGAACCCGCGCTGAACGCAAGACCACTTGAAGGTGTTACCAACCAAC 330
Db 241 GGTGGAATCAAGTTTAAATGCAAGACTATTCATTTTGAAGGTGTTACCAACCAAT 300
Qy 331 GCGAAGCTACTTGGCGCTGACGCTGAGCCGCAACCGCGTGTGAGTATTAATC 390
Db 301 GGTATTTCTTATTAAGCTGTTAGTGTGAGCTGAAATCATTAAGTATTAAT 360
Qy 391 GTGAGAACTTGGCACTATGATCTCTCGGTGATACCGATGAGAACTGTGAG 450
Db 361 GTTAAATTTTGGACTTATGATCACTTCTGCTGATGATTAAGTATGTA 420
Qy 451 TGCAAGCTAGCATCTATGACTCGGCAAGACCACTCGCTCAACGCACTAGATGAC 510
Db 421 TGTATGTTCTATTTAATGATAGTAAATCTATGATTAATGACCACTATGAT 480
Qy 511 GCGACCCAAACTTTCGACCAATAGTGTGCTGCGCCAGCAAGCGCAAGCGGTA 570
Db 481 GGTACTCAACTTTCGATCAATATGCTGTGATGACAAAGATTAAGAACTTCTG 540
Qy 571 GTCAAGCGGCTGCACTTTCGACGCTGCGGTGCTGCTGTTGAATGTAAGTAC 630
Db 541 GTCAAACTGTTGATTTGATGATGCTGCGGTGATGAGCTGTTGAATGTAAGTAC 600
Qy 631 CACTACTACAGATGTTGCAAGGAGGCTACTTACGACGAGGCTATGCTGATCAC 690
Db 601 CACTACTACAGATGTTGCAAGGAGGCTACTTACGACGAGGCTATGCTGATCAC 660

Db 601 CATTATTACAAATTTGTAACGTAAGTATTTCTCTGCTGATGATTAAT 660
Qy 691 GTTGTGACGTGGCTAA 708
Db 661 GTTGTGATGTTGTTAA 678

RESULT 4

US-10-425-115-177283
; Sequence 177283, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 177283
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_93271C.1
US-10-425-115-177283

Query Match 26.2%; Score 257.2; DB 8; Length 850;
Best Local Similarity 64.2%; Pred. No. 1.6e-71;
Matches 420; Conservative 0; Mismatches 228; Indels 6; Gaps 2;

Qy 44 CCCCCTGTCCTTGGCGCTTACCGCGGAGCTGGGCGCTTCCGCGAGGATG 103
Db 139 CCACCGGTGCTCTGCGCGCCCGGTGCTGACGCGACACCACTTGTGAGGCTCCC 198
Qy 104 CCACGAGCTCGAAAACGACAGCAACCCCACTGAGAGGTGCGACATGTTAT 163
Db 199 TCAATGTAATGACTGACAGTCCGCTGACCCCACTCCAGGAGCAACCAACGCT 258
Qy 164 ACTATTCCTGATGAGTGAAGGCTGAGGCGAGGCGATCAACCACTGAAAGGCA 223
Db 259 TCTACTCTGATGAGTGAAGGCTGAGGCGAGGCGATCAACCACTGAAAGGCA 318
Qy 224 CTAAGAGATCAGCTGAGGAGATGCGGTAACTCTGCTGAGTGAAGGCTGAAAC 283
Db 319 AGTACAGGCTCACTGAAAGCGGTGTAATGTTGAGTGAAGGCTGAAACCTG 378
Qy 284 GCTGAAGCGAAGCCATCTTGAAGGCTTTTCAAGCCAAACGCAACGTAAC 343
Db 379 GTGCG--GCGCGACCATCACTCTCGGTACTCAACCCCGCAAGGTAATCTTACC 435
Qy 344 TTGCGGTCTAGGTTGAGCCGCAACCGCGGTGAGTATTCATGCTGAGAACTT 403
Db 436 TTGCAATCTAGGCTGAGCCGCAACCCCGGTGAGTATTCATGCTGAGAACTT 495
Qy 404 GCACTATGATCTTCTCTCGGTGCTACCGATCTGAGAACTGCTGAGTGAAC 463
Db 496 GTACTTACGACCGGTCTCTCGGTGCTACCGATCTGAGAACTGCTGAGTGAAC 555
Qy 464 TCTATGATCTGCGAAGCACTGCTGCTCAACGCACTGATGAGGCAACCACT 523
Db 556 CTTACAAAGATTTGCGCAACCTGAGTGTCAACGCTCTCATGAGGCAACCAAGCT 615
Qy 524 TCGACCAATCTGCTGCTGCTGCGCAAGGCAACGAGGCAACGCTCAAGCGGCT 583
Db 616 TCAACAGTACTGCTGCTGCTGCGCAAGGCAACGAGGCAACGCTCAAGCGGCT 675
Qy 584 GCCACTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643
Db 676 CCGACTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732

Db 573 CAAGACCTTTCAGAGACTGCTGTCTGCGCAAGACAGGCTCCAGCGGATCCGTA 632
Qy 575 AGAGCGGCTGCACCTTTCAGACCTGCGGCTCGGCTGTTGAATCAAGCTGACCACT 634
Db 633 ACATGAAAGACTCACTTCATGCTTGGGCGAGCAAGGAGATGACTCT--TGTAGCCACT 689
Qy 635 ACTACCAAGATGCTTTCAGACGAGGCTACTTCAGACGCGGCTAGTCTGCATCAACCGT 692
Db 690 ACTACCAAGATGCTTTCAGACGAGGAGTACTTCTCAACGCGGCTTCTGCTTACTCTGT 747

RESULT 7

US-10-213-990-65
; Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(666)
US-10-213-990-65

Query Match 22.8%; Score 224.6; DB 5; Length 666;
Best Local Similarity 61.5%; Pred. No. 4.5e-61;

Matches 413; Conservative 0; Mismatches 249; Indels 9; Gaps 3;

Qy 31 ATGTGCGCTTTTACCCCGCTTGCCTTTCGCGCTTTCAGCGGAGCTGGGCGCTTTC 90
Db 1 ATGTGCTATTTCTTCTCTGCTTCTGCTGCTTTCACCGTGGGCTGTAAGCA 60
Qy 91 CCGG--CAGGAAATCCAGAGCTCGAAAAGCGACAGACACCCCACTCGAGGGC 147
Db 61 CCGGCTCGAGCAATACGTGAGCTACCAAGCGGAGCTCACCAAGCTTCAAGCTGGC 120
Qy 148 TGGCAGATGCTTATTAATTTCTGCTGAGTACCGTGGAGCGGAGCGCAAGCAAGTACC 207
Db 121 ACGAATAACGGCTACTTACTCTTCTGACCGAGCGGCGGCAAGTACCTACACC 180
Qy 208 AACCTGAAGCGGAGCTACGAGATCAGCTGGGAGATGGCGGTAACCTGCGTGA 267
Db 181 AACCGCAATGCGGCGCAATACAGTCACTGGAACAACTGCGCACTTTGTGCTGG 240
Qy 268 AAGGCTGGAACCCCGGCTGAACGCAAGCCATTCACCTTGAAGGTATTACAGCA 327
Db 241 AAGGCTGGAACCCGGC--AGCGAAGAACGGTCACTTCAAGCGGCTCTGAGCAACC 297
Qy 328 AACGGAACAGCTACTTGGCGGTCTACAGGTTGACCCGCAACCGGCTGTTGAGTATTAC 387
Db 298 AGCGAAGCGGCTACTCTCGGTGTAAGCGTGAAGCAAGTCCGCTGTGAATTTTAC 357
Qy 388 ATCTGCAAGACTTGTGACCTATGATCTTCTCGGCTGCTACGATCTAGAACTGTC 447
Db 358 ATCTGCAAGACTTGTGACCTATGATCTTCTCGGCTGCTACGATCTAGAACTGTC 417
Qy 448 GAGTGCAGAGCTAGCTATGACTCGGCAAGACCACTCGCTCAACGACCTTAGCATC 507
Db 418 GAGAGCGAGCGGCGGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 477

Qy 508 GACGCAACCCAACTTTCAGCAATGCTGCTGCGGCGAGCAAGCAAGCAAGCGCT 567
Db 478 CAGGCAAGGCTACTTTTGAACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
Qy 568 ACCGTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 627
Db 538 ACTGTACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 594
Qy 628 GACCACTTACAGATGCTTTCAGACGAGGCTACTTTCAGACGCGGCTATGCTGATC 687
Db 595 AACTTGACTTATGATTTGTCAGAGGAGTACCAAGAGCGGCTCTGCTACTATTC 654
Qy 688 ACCGTGCTGA 698
Db 655 ACTGTTCTTA 665

RESULT 8

US-10-213-990-68
; Sequence 68, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(705)
US-10-213-990-68

Query Match 22.7%; Score 223; DB 5; Length 705;
Best Local Similarity 60.5%; Pred. No. 1.5e-60;

Matches 411; Conservative 0; Mismatches 250; Indels 18; Gaps 2;

Qy 29 TGATGCTGCTTTTACCCCGCTTGCCTTTCGCGCTTTCAGCGGAGCTGGGCGCTTTC 88
Db 23 TGCTGCGGTGCTCGGCAATGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 82
Qy 89 TCCCGCAGGGAATGCAAGAGCTCGAAAAGCGACAGACACCCCACTCGAGGGCT 148
Db 83 TCATGAGACTGCTCTTCAATGATTCGCTGAGCGCGCGGACCCCAAGCTTCCACCGCT 142
Qy 149 GGCAGATGCTTATTAATTTCTGCTGAGTACCGTGGAGCGGAGCGGAGCGGAGCGGAG 208
Db 143 GAAACAGGCTTACTTACTCTTCTGACTGATGCGGCGGAGCGGAGCGGAGCGGAGCGG 202
Qy 209 ACTGGAAGCGGAGCTTACGAGATCAGCTGGGAGATGGCGGTAACCTGCTGCTGAA 268
Db 203 ATGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 262
Qy 269 AGGCTGGAACCC-----CGGCTGGAAGCAAGGCTATTCATTTAGG 313
Db 263 AGGCTGGAACCCCTGGAAGGCTAGTACGAGCTTTCATGAGCAATCACTACGAG 322
Qy 314 GTGTTTCAAGCGGCAAGGCAAGCAAGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
Db 323 GCACTTCAACCCCAAGGCGGCAAGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 382
Qy 374 TGCTGAGTATTAATGCTGAGAACTTGGACCTTATGATCTTCTCGGCTGCTACCG 433
Db 383 TGATGAGTACTACGCTTGTGAGTCTGATGATACATCAACCCCGGAGCGGCTGCT 442

Db 937 ACTACCAGATCATGGCGACCGAGGGCTACCAGAGCAGCGGTAGCTCCACCCTTCATCA 996

Db 563 ACCCTTACCCAGTACGTCTGTG

Db 563 ACCTTCACCCAGTACTGTCTGTGCGCACCTCCAGCGTACCGGCGCACTGTCAACCATG 622

Db 623 GCCAACCACTTCAAGCGCTGAGAGACACTGAGCATGAA---CTGGGAATCTACACTAC 679
Qy 640 CAGATCGTTCAGACGAGGGCTACTTCAGACGCGCTATAGCTCGCATACCGCT 692
Db 680 CAGATTGTCCCACTGAGGGTTACCAAGACGCGGATCTGTTCATCATCTGT 732

RESULT 12

US-10-213-990-64
; Sequence 64, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Bussey, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 712
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-64

Query Match 18.4%; Score 181.2; DB 5; Length 712;
Best Local Similarity 57.7%; Pred. No. 4.1e-47;
Matches 412; Conservative 0; Mismatches 253; Indels 49; Gaps 3;

Qy 31 ATGGCGGCTTTACCCCGGTTGCCGCTTACGCGGAGCTGGGGCCCTGGCCCTTC 90
Db 1 ATGGCTCATCTCTCTCTGTTTCGCTGCTCCACCGTTGCGGCTGCTAGTACA 60
Qy 91 CCGG---CAGGGAATGCGACGAGAGCTCGAAAAGCGACAGAACCCCACTCGAGGGC 147
Db 61 CCGGCTCGGAGCAATAGTTGAGCTACCAAGGGGCGACGTCACAGCTCAGACTGGC 120
Qy 148 TGGCAGATGGTTATTACTTCTCTGTGAGTGAAGCGGTGAGCGGACGACCTACACC 207
Db 121 ACGAATACGGGCTACTACTCTCTTGTGACCGACGCGGCGGCGGCAAGTACCTACACC 180
Qy 208 AACCTGGAAGGGCGGACCTAGATGACTGCGGGAGATGGCGGTAACTCTGCGTGA 267
Db 181 AACGGCAATGGGGCGAGATGAGTCACTGGAACAACTGGCGAACCTTGTGTGG 240
Qy 268 AAGGCTGGAACCCCGGCTGAAACGA----- 294
Db 241 AAGGCTGGAACCCCGGCGAGGAAAGATAGGCTCTCTCCCTGTTTGAAGTTCAAGC 300
Qy 295 -----AGAGCATTCACCTTTGAGGGTGTTCACAGCCAAAGCGCAACGTTACT 344
Db 301 TAATGATTCAGAGGGCTACCTACAGGGGCTCTCGGAGACCAAGCGGAAACGCTTACT 360
Qy 345 TGGCGTCAAGGTTGGAACCGGCAACCGGTGTGAGATTACATCGTGAAGATTGG 404
Db 361 CTCCTGTACGGCTGGAAGCAAGTCGCTGTCGAATTCTACATCGTGAAGATTAGG 420
Qy 405 CACCTATGATCTTCTCTCGGTGCTACGATCTAGAACTGTGAGTGAAGTGAAT 464
Db 421 CTCCTATGACCCCTCAAGGGAGCAACCATCTCGGCAACCGTGAAGAGAGGGGCAAC 480
Qy 465 CTATGACTCGGCAAGACCACTCGGTCAAGCACTAGATGACGCGCAACCAACTT 524
Db 481 GTACAACTCTTCAAGAGACGACGCAAGATGCGCGTCACTCAAGGGGCAAGCTTACTT 540
Qy 525 CGAACCAATATGCTGCTCGGCGGCAAGGCAACGCGGTACCGTTCAGACGGGCTG 584
Db 541 TGACCAATATGCTGCTCGGCTTCCGACCCGCGAGAGTGAACCTGTGACGACGAAGA 600

Qy 585 CCACTTCAGCGCTGGGCTGCCGCTGTTGAATGTCAACGGTGAACCACTACTACAGAT 644
Db 601 CCACTTTGAAGCGGTGGAAGAAATGGGCTCTGCAATT---GGGGAACCTTGAATATGAT 657
Qy 645 CGTTGCAAGGAGGGGCTACTTCAGACGCGGCTATAGCTGCATCAGCGTGGTGA 698
Db 658 TGTTCGACGAGAGGGGTACCAAGACGAGCGGCTCTGCTACTATCATCTGTTCTTA 711

RESULT 13

US-10-213-990-71
; Sequence 71, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Bussey, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(942)
US-10-213-990-71

Query Match 16.8%; Score 165.4; DB 5; Length 942;
Best Local Similarity 59.3%; Pred. No. 5.6e-42;
Matches 340; Conservative 0; Mismatches 221; Indels 12; Gaps 3;

Qy 126 GACAACCCCAACTCGAGGGGCTGGCAGATGTTATTACTATTCCTGTGAGTGAACG 185
Db 99 GATCAGCAGCAGCCAGACAGGCAACGCAACAAATGGCTACTACTATTCCTTTCGACCAACGG 158
Qy 186 TGGAGCGGAGCCAGTACACCAACTGGAAGCGGCACTTCAAGATCAGTGGG--- 241
Db 159 TGCCGATCAGTGCAATATCAATATGATGCTGTGGGGAATATGATGAGTGGCGAA 218
Qy 242 --GAGATGGGGGTAAACCTCGGTGGAAGGGCTGGAACCCGCGCTGAACGGAAGC 299
Db 219 CGAAGCGGTGTACTTACTTGTGGAGAGGCTGGAAATCAGG--GAGTGACATGA 275
Qy 300 CATCACTTTGAGGGGTGTTACAGCCAAAGCGCAACGTTACCTTGGGCTTACGCTTG 359
Db 276 CATTACTTCTCTGAGAGCTTCAATCTTCCGGAAGGCTTAACTGATGATG 335
Qy 360 GACCGCAACCCGCTGTGAGTATTAATGCTGAGAACTTTGGCACTTATGATCTTC 419
Db 336 GACTTACCAACCCCTAGTGAATTAATCTCTGAGAACTTATGCAATTCCTGG 395
Qy 420 CTCGGTGTCAACGATCTAGGAACGTGAGTGGAGGCTGAGCACTTATGACTCGGAA 479
Db 396 CTGGGCAATGAGCAAGAGGCAACCGTACCAAGAGATGATCACTTACGACATTTAGA 455
Qy 480 GACCACTGCGCTCAACGCACTTACATGACGAGCAACCAACCTTGAACATATGCTC 539
Db 456 GACCAACAGGTCAACCAAGCTTGTGATGTGGGCAACGCGCACTTCAACCAATCTGCTC 515
Qy 540 GGTTCGCGAGGACAGGCAACGCGGTACCGTCAAGCGGCTGCACTTGAAGCTTG 599
Db 516 CATCGCCAAAACAGGATCAAGCGGCAAGTCAACCAACCTTCAAGGCTTG 575
Qy 600 GGTCTGCGCTGTTTGAATGTCAACGAGTCACTATCAAGATCGTTGACGAGGAG 659
Db 576 GGTATGTCTGGGATGAA---CTGGGTAACCATTAATATCAAGATGTTTCCACTGAGGG 632

QY 660 CTACTTCAGCAGCGGCTATGCTCGCATCACCCT 692
DB 633 ATATGAGAGCAGCGGCTACTCGCATCATCTGT 665

RESULT 14

US-11-018-645-21
Sequence 21, Application US/11018645
Publication No. US20050208178A1
GENERAL INFORMATION:
APPLICANT: Bauer, Michael
APPLICANT: Bedford, Michael
APPLICANT: Pulliam, Derrick
TITLE OF INVENTION: Microbially Expressed Xylanases and Their Use as Feed Additives
TITLE OF INVENTION: Uses
FILE REFERENCE: 703570PCT
CURRENT APPLICATION NUMBER: US/11/018, 645
CURRENT FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: 60/531,404
PRIORITY FILING DATE: 2003-12-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 978
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: XYL1A1E
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(978)
US-11-018-645-21

Query Match 15.8%; Score 155.2; DB 10; Length 978;
Best Local Similarity 56.8%; Pred. No. 1.1e-38;
Matches 327; Conservative 0; Mismatches 243; Indels 6; Gaps 2;

QY 130 ACCCCCACTCGAGGGCTGCGAGTGTATTACTTCCTGCTGAGTGAAGTGGGA 189
DB 19 AGCTGAGCCAGACGGGACCAACAGGCAATTTCTGTTCTGGAAGAAGATCGG 78
QY 190 GCGGAGCCACGTACACCAACCTGGAAGCGGCACTACAGATCAGCTGGGAGATGCG 249
DB 79 GCGAGGTGAATCTCTGATGTATGCGAATGGCGGCTAATCTCACTGAGGGGATC 138
QY 250 GGTAACTCTGCTGGTGAAGAGGCTGGAACCCGCGCTGAAGCGAAGACCATCTTT 309
DB 139 AACAACTGGGTGGGCGGCAAGGGCTGGGCTACCGGCTCAAGCCACAGATCAGTACTCC 198
QY 310 GAGGGTGTTTTACCAAGCGGCAACGCTAATCTTCGGTCTACGTTGGAACCCGCAAC 369
DB 199 GGCAGCTTCAATTCGCG--GGCAACGTTTACTGCGCTGATGCTGAGCCACCAAT 255
QY 370 CCGCTGCTGAGTATTAATCATGTCGAGAACTTTGGCACTATGATCTTCTCGGATGCT 429
DB 256 CCATGCTGAGTACTATCATGTGTCAGACGCTGGGTACTTACCTCCGCGGGGGGCGCAG 315
QY 430 ACCGATTTAGGAATGTCGAGTGGACGAGTGAATCTATGCACTGGCAAGACCACTGCG 489
DB 316 GGTTCATGCGGACGAGTATTAAGCAGCGGGGCGAGTACGATGTAACCGGACGCAACGCG 375
QY 490 GTCAAGCCACTAGCATGACGAGCAACCAACCTTTCAGCAATATCTGGTCTGGCAG 549
DB 376 GTGAACGAGCATCATCATGCGCAACGCGCAAGTTTCAACGATCTGGAAGGTGCGGAG 435
QY 550 GACAAAGCAGCAACGAGTACGCTCAAGCGGGCTGCACTTTCAGCGCTGGGCTCGGCT 609
DB 436 TCGAAGCGCGTGGGCGGCGGACCATACCAATGCGCAACATTTTCAAGCGCTGGGCGCAGCTG 495
QY 610 GGTGTAATGTCAACGCTGACCACTACTACCAATGCTTGGCAAGAGGCTACTTACGC 669
DB 496 GGCATGAA---CTGGGCGGAGCAACATCAAGGTCAATGGCAAGGAGTTACCAAGGC 552

QY 670 AGCGCTATGCTCGCATCACCGTGTGACGTGGC 705
DB 553 AGCGCAGCTTCCGATCATCACCGTGAACCGAAGTGGC 588

RESULT 15

US-10-213-990-70
Sequence 70, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 70
LENGTH: 1002
TYPE: DNA
ORGANISM: Aspergillus
US-10-213-990-70

Query Match 15.0%; Score 147.2; DB 5; Length 1002;
Best Local Similarity 62.2%; Pred. No. 4.1e-36;
Matches 249; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 293 CAAGAGCATCCACTTTGAGGCTGTTTACCAAGCAACGGCAACAGTACTTGGCGTCT 352
DB 329 CTAGTACATTAATCTTCTGCGAGCTTCAATCTTCCGAAATGCTTACTGCTGT 388
QY 353 ACCGTTGGAACCCGCAACCCGCTGTCAGATTAATCATGTCGAGAACTTTGGCACTATG 412
DB 389 ATGATGATGACTACCAACCCCTAGTGAATATCTAATCTTCTGAGAACTATGGAGTTACA 448
QY 413 ATCTTCTCTCGGTGCTACCGATCTAGAACTGTGAGTCGACGCTGAGATCTATGAC 472
DB 449 ATCTGCTGCGGATGACGACCAAGGGCACCGTACACGAGATGATCCACTACGACA 508
QY 473 TCGCAAGACCACTCGGTGTCAGCACTGACATGACCGGCAACCCAACTTGAACCAAT 532
DB 509 TCTATGAGCAACCAAGTCAACGCTTCAATGCTGTGGCAGCGCCACTTCAACCAAT 568
QY 533 ACTGTCGTCGCGCCAGAGCAAGCGGACAGCGGTACCGTCCAGACGGGCTGCACTTGG 592
DB 569 ACTGTCATTCGCGCAAAACAGCGATCCAGCGGCAAGTCAACCGCAATCATCTTCA 628
QY 593 ACCGCTGGGCTCGCGCTGTTTGAATGTCAACGCTGACCACTACTACAGATGTTGCA 652
DB 629 AGGCTGGGCTAATGTTGGGAGTAA---CTGGGTACCCATACTATCAATGTTTCCA 685
QY 653 CGAAGGCTACTTCAAGAGGCGCTATGCTGATCAACCT 632
DB 686 CTGAGGGATATGAGAGCAGGATACCTTCAGCATCACTGT 725

Search completed: February 11, 2006, 23:51:27
Job time : 1025.32 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:37:15 / Search time 314.228 Seconds
(without alignments)
2812.856 Million cell updates/sec

Title: US-09-467-368-1
Perfect score: 983
Sequence: 1 TCGGCGCCGACGCTTTCGCAAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 6240305 seqs, 449581930 residue

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA New:

1: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB_seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB_seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB_seq.*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB_seq.*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB_seq.*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB_seq.*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB_seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB_seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB_seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB_seq.*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB_seq.*
12: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1 | 585 | 59.5 | 588 | 11 US-11-170-653-9 | Sequence 9, App1 |
| 2 | 202.2 | 20.6 | 1008 | 7 US-10-517-939-221 | Sequence 231, App1 |
| 3 | 197.2 | 20.1 | 1375 | 11 US-11-108-1638-1 | Sequence 1, App1 |
| 4 | 190.2 | 19.3 | 663 | 11 US-11-108-1638-5 | Sequence 5, App1 |
| 5 | 190.2 | 19.3 | 906 | 11 US-11-108-1638-4 | Sequence 4, App1 |
| 6 | 187 | 19.0 | 663 | 11 US-11-108-1638-3 | Sequence 3, App1 |
| 7 | 187 | 19.0 | 906 | 11 US-11-108-1638-2 | Sequence 2, App1 |
| 8 | 186.2 | 18.9 | 1059 | 7 US-10-517-939-225 | Sequence 165, App |
| 9 | 185 | 18.8 | 1047 | 7 US-10-517-939-165 | Sequence 159, App |
| 10 | 170 | 17.3 | 1074 | 7 US-10-517-939-199 | Sequence 255, App |
| 11 | 170 | 17.3 | 1137 | 7 US-10-517-939-235 | Sequence 165, App |
| 12 | 165.8 | 16.9 | 1047 | 7 US-10-517-939-169 | Sequence 177, App |
| 13 | 165.6 | 16.8 | 1044 | 7 US-10-517-939-221 | Sequence 195, App |
| 14 | 165.4 | 16.8 | 1299 | 7 US-10-517-939-177 | Sequence 217, App |
| 15 | 164.6 | 16.4 | 1083 | 7 US-10-517-939-217 | Sequence 189, App |
| 16 | 160.8 | 16.4 | 1044 | 7 US-10-517-939-195 | Sequence 235, App |
| 17 | 160.8 | 16.4 | 1083 | 7 US-10-517-939-183 | Sequence 233, App |
| 18 | 156.8 | 15.9 | 1047 | 7 US-10-517-939-253 | Sequence 159, App |
| 19 | 150.8 | 15.3 | 1065 | 7 US-10-517-939-215 | Sequence 159, App |
| 20 | 150.6 | 15.3 | 1071 | 7 US-10-517-939-223 | Sequence 159, App |
| 21 | 150.2 | 15.3 | 1041 | 7 US-10-517-939-159 | Sequence 159, App |

| | | | | | |
|----|-------|------|------|---------------------|-------------------|
| 22 | 146.4 | 14.9 | 1047 | 7 US-10-517-939-299 | Sequence 239, App |
| 23 | 141.8 | 14.4 | 1077 | 7 US-10-517-939-181 | Sequence 181, App |
| 24 | 131.2 | 13.3 | 1047 | 7 US-10-517-939-161 | Sequence 161, App |
| 25 | 128 | 13.0 | 1029 | 7 US-10-517-939-219 | Sequence 219, App |
| 26 | 127.8 | 13.0 | 747 | 7 US-10-517-939-227 | Sequence 227, App |
| 27 | 124 | 12.6 | 1695 | 7 US-10-517-939-217 | Sequence 317, App |
| 28 | 119.2 | 12.1 | 642 | 11 US-11-214-413-31 | Sequence 31, App1 |
| 29 | 118 | 12.0 | 669 | 7 US-10-517-939-167 | Sequence 167, App |
| 30 | 116.4 | 11.8 | 1068 | 7 US-10-517-939-211 | Sequence 211, App |
| 31 | 114.8 | 11.7 | 1068 | 7 US-10-517-939-205 | Sequence 205, App |
| 32 | 109.2 | 11.1 | 1020 | 7 US-10-517-939-153 | Sequence 153, App |
| 33 | 108.4 | 11.0 | 633 | 7 US-10-517-939-207 | Sequence 207, App |
| 34 | 107.2 | 10.9 | 636 | 7 US-10-517-939-197 | Sequence 197, App |
| 35 | 106.8 | 10.9 | 555 | 7 US-10-517-939-251 | Sequence 251, App |
| 36 | 95.4 | 9.7 | 1983 | 7 US-10-517-939-351 | Sequence 353, App |
| 37 | 94.2 | 9.6 | 570 | 7 US-10-517-939-189 | Sequence 189, App |
| 38 | 93.4 | 9.5 | 1068 | 7 US-10-517-939-163 | Sequence 163, App |
| 39 | 92.4 | 9.4 | 1338 | 7 US-10-517-939-167 | Sequence 367, App |
| 40 | 91.8 | 9.3 | 570 | 7 US-10-517-939-177 | Sequence 377, App |
| 41 | 91.4 | 9.3 | 678 | 7 US-10-517-939-171 | Sequence 171, App |
| 42 | 91 | 9.3 | 645 | 7 US-10-517-939-157 | Sequence 157, App |
| 43 | 91 | 9.3 | 1053 | 7 US-10-517-939-191 | Sequence 211, App |
| 44 | 90.2 | 9.2 | 570 | 7 US-10-517-939-175 | Sequence 375, App |
| 45 | 89.8 | 9.1 | 1077 | 7 US-10-517-939-369 | Sequence 369, App |

ALIGNMENTS

RESULT 1
US-11-170-653-9
Sequence 9, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT FILING DATE: US/11/170, 653
PRIOR APPLICATION NUMBER: US/10/237, 386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 588
TYPE: DNA
ORGANISM: Thermomyces lanuginosus
US-11-170-653-9
Query Match 59.5%; Score 585; DB 11; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.9e-148;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 124 | CAGCAACCCCACTGGAGGGCTGACAGATGTTATTAATTCCTGCTGAGAGAC | 183 |
| DB | 4 | CAGCAACCCCACTGGAGGGCTGACAGATGTTATTAATTCCTGCTGAGAGAC | 63 |
| QY | 184 | GATGAGCGGACGACGACCACTGGAAGGCGGACCTTACGAGATCAGCTGGGGA | 243 |
| DB | 64 | GATGAGCGGACGACGACCACTGGAAGGCGGACCTTACGAGATCAGCTGGGGA | 123 |
| QY | 244 | GATGAGCGGACGACGACCACTGGAAGGCGGACCTTACGAGATCAGCTGGGGA | 303 |
| DB | 124 | GATGAGCGGACGACGACCACTGGAAGGCGGACCTTACGAGATCAGCTGGGGA | 183 |

| | | | |
|----|-----|--|-----|
| QY | 304 | CACCTTGAAGGGTGTTTACAGGCAAAAGGCAACACTACCTTGGGGCTACGGTTGGACC | 363 |
| Db | 184 | CACCTTGAAGGGTGTTTACAGGCAAAAGGCAACACTACCTTGGGGCTACGGTTGGACC | 243 |
| QY | 364 | CGCAACCCGGTGGTCGAGTATTACATCGTCGAAACTTTGGACCTTATGATCCTTCTCC | 423 |
| Db | 244 | CGCAACCCGGTGGTCGAGTATTACATCGTCGAAACTTTGGACCTTATGATCCTTCTCC | 303 |
| QY | 424 | GGTGCTACCGATTTAGAACTGTCCGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACC | 483 |
| Db | 304 | GGTGCTACCGATTTAGAACTGTCCGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACC | 363 |
| QY | 484 | ACTCGGCTCAAGCCACTGTCGATTCGACGGGCAACCCAAACCTTGACCAATATCGTGGCTC | 543 |
| Db | 364 | ACTCGGCTCAAGCCACTGTCGATTCGACGGGCAACCCAAACCTTGACCAATATCGTGGCTC | 423 |
| QY | 544 | CGCCAGGACAAAGGCGACACAGCGGTACCGTCCAGAAGGGCTGCGCACTTTCGAGCGCTGGGCT | 603 |
| Db | 424 | CGCCAGGACAAAGGCGACACAGCGGTACCGTCCAGAAGGGCTGCGCACTTTCGAGCGCTGGGCT | 483 |
| QY | 604 | CGCGCTGGTTTGAATGTCAACGGTGACACTTACCAAGATCGTTTGCACGGAAGGCTAC | 663 |
| Db | 484 | CGCGCTGGTTTGAATGTCAACGGTGACCACTACTACAGATCGTTTGCACGGAAGGCTAC | 543 |
| QY | 664 | TTTACGACGCGGCTATGCTCGCAATCAACCGTTGCTGACGAGGGCTAA | 708 |
| Db | 544 | TTTACGACGCGGCTATGCTCGCAATCAACCGTTGCTGACGAGGGCTAA | 588 |

RESULT 2
US-10-517-939-231
; Sequence 231, Application US/10517939
; Publication No. US20060003433A1

```

APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Esteghalalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 564462007901
CURRENT FILING DATE: 2004-12-13
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 231
LENGTH: 1008
TYPE: DNA
ORGANISM: Bacteria
US-10-517-939-231

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| Query Match | 20.6% | Score 202.2 | DB 7 | Length 1008 |
|-----------------------|-------|---|------|----------------------------------|
| Best Local Similarity | 59.1% | Pred. No. 5.7e-45 | | |
| Matches | 386 | Conservative | 0 | Mismatches 258; Indels 9; Gaps 2 |
| QY | 67 | GCCGCGACTGCGGACCCTTGCTTCCCGGCGAGGAATGCGACGAGCTCGAAAAAGCGACG | 126 | |
| DB | 73 | GTCGGCGCTGCGGCGCGCTCGCCGCGTGAATGCTGCCGGGCAACGCCCGACACGCGTC | 132 | |
| QY | 127 | ACAAACCCCACTCGGAGGGCTGGACGATGCTTATTACTTCTGTGAGTACGCGT | 186 | |
| DB | 123 | GTCACGACCAACGAGGAGGACCAACGACGCTACTTACTCTGTTGACCGCAGCG | 192 | |
| QY | 187 | GGAGGCGACGACGTAACCACTCTGGAAGCGGCACTTACGATGACGCTGGGGAGAT | 246 | |
| DB | 193 | CAGGGCACCCTTCCATGAAACATGGGCTCCGGCGGTCACTACAGCACTCTCGTGGGCGAAC | 252 | |

| | | | |
|----|-----|--|-----|
| QY | 247 | GGCGGTAACTCTGTGGTGGTGAAGAGGGCTGGAAACCCCGGCTGAAGACGAAAGACATCCAC | 306 |
| Db | 253 | ACCGGCAACTTGTGTGCGGAGGAGGGCTGGGGCCAACGGGAGCGCCGGG---CCGTGCAG | 309 |
| QY | 307 | TTTGAAGGTGTATTACACAGCCAAACGGCAACAGTCACTTGTGCGGTCTACGGTTGGAACCCGC | 366 |
| Db | 310 | TACTGCGGCAGGTTCAACCCCTCCGGCAACGGGTACTGTGGCGCTCTACGGATGGAGTGTG | 369 |
| QY | 367 | AAACCGCTGTGTGAGTATTATCATGTGTGAGAACTTTGGCACTTAAGATCTTCTTCCTCCGGT | 426 |
| Db | 370 | AAACCGCTGTGTGAGTATTATCATGTGTGACAACTGGGGCACTTACCGGCTCAACGGGCG-- | 427 |
| QY | 427 | GCTACGATCTAGGAACGTGTGAGTGGCAGCGGTATGATCTTATGCACTCGGCAAGACACT | 486 |
| Db | 428 | ----AGTCAAGGGGACCGGTCAACGACGACGCGCGCACTAAGACATCTCAAGAGACGACC | 483 |
| QY | 487 | CGGTCAACGCACTTAGATGAGCGGCAACCCAAACCTTGTGACCAATATCTGTTCGGTCCGC | 546 |
| Db | 484 | CGGTCAACGCAACCGCTTCGTGAGGGGCAACCGGCACTTGTGACAGTATCTGAGAGCGTCCGG | 543 |
| QY | 547 | CAGGCAAGCGCAGCAGCGGCTACGCTTCAGAGCGGGGTGCACTTGCACGCTCGAGGCTCGC | 606 |
| Db | 544 | CAGGCAAGCGGCAACCGGCGGCAACATCAAGACCGGCAACCACTTGCACCGCTGTGGGCCGG | 603 |
| QY | 607 | GCTGTTTGAATGTCAACGGTGAACCACTATCAACGATCGTTGCAACGAGGGGCTTACTTC | 666 |
| Db | 604 | GCGCGGATGCGCGCTCGGCAACTTCAGTACTATCAAGATCATGATGATGCGCCACCGAGGGCTTACAG | 663 |
| QY | 667 | AGCAGCGGCTAATGCTGCATCAACGATGTGACGTGGGGCTAAGACGTAACCTTG | 719 |
| Db | 664 | AGCAGCGGACGCTTCAGCATCAACGTCCGCGGGAGCCGGCCGGCGGCAACAACGG | 716 |

RESULT 3
US-11-108-163B-1
; Sequence 1, Application US/11108163B
; Publication No. US20060014247A1

```

: GENERAL INFORMATION:
: APPLICANT: Paloheimo, Marja
: APPLICANT: Mantyla, Arja
: APPLICANT: Leekinen, Sanna
: APPLICANT: Pagarstrom, Richard
: APPLICANT: Kallio, Jarno
: APPLICANT: Puranen, Terhi
: APPLICANT: Lantto, Raij
: APPLICANT: Suominen, Pirkko
: TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
: TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
: FILE REFERENCE: 1716.03400B/MAC/DUN
: CURRENT APPLICATION NUMBER: US/11/108.163B
: PRIOR FILING DATE: 2005-04-18
: PRIOR APPLICATION NUMBER: US 60/562,692
: PRIOR FILING DATE: 2004-04-16
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: Patenlin version 3.3
: SEQ ID NO 1
: LENGTH: 1375
: TYPE: DNA
: ORGANISM: Nonomuraea flexuosa
: FEATURE:
: OTHER INFORMATION: NE XYLIIA nucleotide sequence (AJ508952), the coding region is
: OTHER INFORMATION: from nt 303 to nt 1337
US-11-108-163B-1

```

| | Query Match | Similarity | Score | 197.2 | DB 11 | Length | 1375 |
|----|-------------|---|--------------|-------|------------|--------|-------------------|
| | Best Local | Similarity | 58.6% | Pred | 1.4e-43 | | |
| | Matches | 403 | Conservative | 0 | Mismatches | 273 | Indels 12; Gaps 3 |
| Qy | 35 | TCGCGCTTACCCCCCGTGGCCCTTACCGCGCCTTAGCCGACATGGGGCCCTTGCCCTTCCCGG | 94 | | | | |
| Db | 349 | TCGGGCTCCGGGCACTGCTGACACAGTGGCTTCGGCCCTTGCGACATGCGCCATGCGCGGTGGGC | 408 | | | | |

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Qy 95 CAGGAAATGCCAGAGCTCGAAAAAGCAGACAAACCCCACTCGAGGGCTGGACG 154
Db 409 TGCTGCCCGGACGCGCCAGCCGACACACCATCATCCAGAACGAGCCGGTACGACA 468
Qy 155 ATGTTATTAATATTTCTGGTGAAGTACCGGTGAGCGCAGCCACGTACACCACTGG 214
Db 469 ACGGCTACTTCTACTCTGTTCTGAGACCGACGCGCCCGGACCGTCTCCATGACCTTCACT 528
Qy 215 AAGCGGACACCTAGAGATCAGCTGAGGGAGATGGCGGTAACTCGTGGTGGAAAGGGCT 274
Db 529 CGGCGGACGATTAACGACCTCTGAGCGAAACCGGGAATTTGTCGCGGCAAGGGCT 588
Qy 275 GAACCCCGGCTGAGCAGAGACCAATCCAATTGAGGGTGTTCACAGCCAAACGCA 334
Db 589 GGTCCACCGGC---GGAACGGGGAACCGTGAACCTCAACCGCTCTTCAACCGTCCGGTA 645
Qy 335 ACAGCTACCTTGGGCTGACGTTGAGACCCGCAACCGGCTGTGAGTATTAATCTGTCG 394
Db 646 ACGCTACCTCAACCTCTACCGCTGACACAGAAACCGCTGTGAGTACTACATCTGTCG 705
Qy 395 AGAATTGGACCTATGATCTTCTCCGGTGTACCGATCTAGGAACGTGCGAGTGGC 454
Db 706 AGACTGGGACCTACCGGCTCAC---GGCACTTCAAGGGACCGTCAACCG 759
Qy 455 ACGGTAGCATCTATCGACTCGGCAAGACCACTCGCTCAACGCACTAGCATCGACGCA 514
Db 760 ACGGCGGACGTAAGACATTAAGAGACTTGGCGGTACAGCCGCTCATTCAGAGGCA 819
Qy 515 CCCAACTTTCGACCAATATCTGTGCGTCCGCAAGACGCAACGAGCGTACCGTCC 574
Db 820 CCCGACCTTCCACAGTCTGAGCGTCCGCGACAGAAACGAGACGAGCCGACCATCA 879
Qy 575 AGAGGGGTGCTGACCTGAGCGCTGGGCTGGCTGTTGAATGTCAACGTGACCACT 634
Db 880 CCATCGGCAACCATCTGACCGCTGGGCTGGGCTGGGCTGATAA---CCTGGGACGCAACG 936
Qy 635 ACTACGAGATGTTGCAACGAGGGCTACTTCAAGACGGCTATGCTGACATCGCTGG 694
Db 937 ACTACGAGATGATGCGACGAGGGCTTACAGAGACGAGGTAGCTCCACCGTCTCCATCA 996
Qy 695 CTGACGTGGCTAAGACGTAACTGTG 722
Db 997 GCGAGGTGGCAACCCGCGCAACCCGGG 1024

RESULT 4
US-11-108-163B-5
; Sequence 5, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; FILE REFERENCE: 1716.034000B/MAC/DON
; CURRENT APPLICATION NUMBER: US/11/108,163B
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Nonomuraea flexuosa
; FEATURE:
; OTHER INFORMATION: am24*, like am24 but 9 codons are changed in the sequence like in

```

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; OTHER INFORMATION: am3* (See Example 10)
US-11-108-163B-5
Query Match 19.3%; Score 190.2; DB 11; Length 663;
Blast Local Similarity 61.2%; Pred. No. 8.6e-42;
Matches 363; Conservative 0; Mismatches 218; Indels 12; Gaps 3;

Qy 130 ACCCCCAACTCGAGGGCTGGACGATGTTATTAATTAATTCCTGAGTGAAGTGA 189
Db 13 ACCGAGAACGAGCCGGCTAGACACGCTACTTCTACTCTGTTCTGACCGAGCCCC 72
Qy 190 GCGAGGCACTGACACCAACTTGAAGCGGCACTTACAGATGACCTGGGAGATGC 249
Db 73 GGCACGCTCTCATGACCTCTCACTCGGGGCGGAGCTACAGACACTGTGGCGCAACC 132
Qy 250 GGTAACTCTGCTGGTGAAGAGGCTGGAACCCCGGCTGAAACGAGACATCACTTT 309
Db 133 GGCAACTTGTGTGGCGGCAAGGGCTGTGCAACGGC---GGCGCGCACGCTCACTTAC 189
Qy 310 GAGGAGTTTACGACCAACGCGCAACAGCTACTTGGCTTACGAGTGGACCCGCAAC 369
Db 190 AAGGCTCTTCAACCGGTGGGTAAAGCTTACCTTACGCTTACGAGCTGACAGAAC 249
Qy 370 CCGGTGTGAGTATTAATCTGTCGAACTTGGCACTTATGATTCCTTCCTCGGTCT 429
Db 250 CCGGTGTGAGTATTAATCTGTCGAAAGCTTGGGCACTTACCGGCCAAC-----GGC 303
Qy 430 ACCGATTTAGAACTGTGAGTGAAGTGAAGCTATCTATGATCTGGCAAGACATCTGC 489
Db 304 ACCTAAAGGAGCCCGTCAACCAACGCGGCGGACGTAACGATCTTACGAGACTTGGCG 363
Qy 490 GTCAAGCACCTATGATCGACGCGCAACCAACTTGAACCAATCTGATGCTGGCGAG 549
Db 364 TACACGCGCTCTCATGAGGAGGACCCGAGCTTTCAGAGATTTGAGAGCTCCGAG 423
Qy 550 GACAAGGCAACAGCGGTACCGTCCAGACGAGCTGCCACTTTCGACGCTGGCTG 609
Db 424 CAGAAGGAGCAAGCGGCAACATCAACATCGGCAACCACTTTCGACGCTGGGCGCGGCC 483
Qy 610 GGTTAATGTCAACGCTGACCACTATCAATGATGTTGCAACGAGAGGCTACTTACG 669
Db 484 GGCATGA---CCTGGGCAACGACGATCAAGATCATGCGACCGAGGGCTTACAGAGC 540
Qy 670 AGCGGCTATGCTGCATCAACGTTTGTGAGTGGGCTTAAGACGTAACTGTG 722
Db 541 AGCGTATGCTCAACGTTCTCATGACGAGGTGGCAACCCCGCAACCGGGG 593

RESULT 5
US-11-108-163B-4
; Sequence 4, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; FILE REFERENCE: 1716.034000B/MAC/DON
; CURRENT APPLICATION NUMBER: US/11/108,163B
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 906
; TYPE: DNA

```

ORGANISM: *Nonomuraea flexuosa*
FEATURE:
OTHER INFORMATION: am35', like am35 but 9 codons are changed in the sequence. See
OTHER INFORMATION: Example 10 (the changes do not alter the encoded amino acid
OTHER INFORMATION: sequence)
US-11-108-163B-4

Query Match 19.3%; Score 190.2; DB 11; Length 906;
Best Local Similarity 61.2%; Pred. No. 9.6e-42;
Matches 363; Conservative 0; Mismatches 218; Indels 12; Gaps 3;

```
QY 130 ACCCCCACTCGAGGGCTGGACAGATGTTATTCTATTCTTGTGTGAGTACGTTGA 189
DB 13 ACCGAGAACGACACCGGCTACGACACGCTACTTCTACTGTTCTGGAACGACGCC 72
QY 190 GCGCAGGCCACGTACACCAACCTGGAAAGCGGACCTACAGATCAGCTGGGAGATGCG 249
DB 73 GGCACCGTCTCCATGACCTCTCACTCGGCGGACGTACAGACCTCGTGGCGAACACC 132
QY 250 GGTAACTGTCGTGGTGAAGGGCTGGAAACCCGGGCTGAACGCAAGAGCCATCACTTT 309
DB 133 GGCACCTTCTGTCGCGCGGACAGGGCTGTCTCAACCGC--GACCGCCGACCGTACCTAC 189
QY 310 GAGGCTGTTTACCAAGCCAAACGCAACAGCTACCTTGCGGTCTACGCTTGGACCCGCAAC 369
DB 190 AAGCCTCTTCAACCCGTCGGGTAAAGCCTTACCTCAAGCTCAAGGCTGAGCAGAGAAC 249
QY 370 CCGCTGTGAGTATTAATCATGTGTGAGAACTTTGGACCTTATGATCTTCTCCGGTGTCT 429
DB 250 CCGCTGTGAGTATTAATCATGTGTGAGAGCTGGGGCACTTACCGGCCACCC--GAC 303
QY 430 ACCGATCTAGGAATGTGAGTGAAGCGTAGCACTATCTATCGACTCGGCAAGACCACTGCG 489
DB 304 ACCTTCAAGGACACCTGTACCAACGACCGGCGGACGTACGACATCTTACGACACTTGGCGG 363
QY 490 GTCAACGCACTTACGATGACGCGACCCAAACCTTTCAGCAATATCTGTGCTCGCCAG 549
DB 364 TACAACGCGCGTCATCGAGGGGACCCGACCTTCCAGAGTTCTGGAAGGTCGCGGAG 423
QY 550 GACAAGCCGACCAAGGATCGGTCCAGACGCGGCTGCCCTTTCAGCGCTGGGGCTCGGCT 609
DB 424 CAGAAAGCGGACGAGGCGGACCATCACTTGGGCAACCTTTCAGCGCTGGGGCTCGGCGC 483
QY 610 GATTGAATGTCAACGCTGACCACTACTACAGATCGTTGCAAGGAGGCTACTTACG 669
DB 484 GGCATGAA---CTGGGACGACGACGATCAATGAGGAGCGGCTTACGAGC 540
QY 670 AGCGCTATGCTCGCATCACCGTTGCTGACGCTGGGCTTAAAGCTTAACTGTG 722
DB 541 AGCGTACCTCAACCGTCTCCATCAGGAGGTGGCAACCCCGGCAACCCGGG 593
```

RESULT 6
US-11-108-163B-3

Sequence 3, Application US/11108163B
Publication No. US20060014247A1

GENERAL INFORMATION:

APPLICANT: Paloheimo, Marja

APPLICANT: Mantyla, Arja

APPLICANT: Leskinen, Sanna

APPLICANT: Paegerstrom, Richard

APPLICANT: Kallio, Jarno

APPLICANT: Puranen, Terhi

APPLICANT: Lantto, Raij

TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of

TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi

FILE REFERENCE: 1716.034008/MAC/DJN

CURRENT APPLICATION NUMBER: US/11/108,163B

PRIOR FILING DATE: 2005-04-18

PRIOR APPLICATION NUMBER: US 60/562,692

PRIOR FILING DATE: 2004-04-16

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.3
SEQ ID NO 3
LENGTH: 663
TYPE: DNA
ORGANISM: *Nonomuraea flexuosa*
FEATURE:
OTHER INFORMATION: am24, shortened form of am35, includes a STOP codon
US-11-108-163B-3

Query Match 19.0%; Score 187; DB 11; Length 663;
Best Local Similarity 60.9%; Pred. No. 6.3e-41;
Matches 361; Conservative 0; Mismatches 220; Indels 12; Gaps 3;

```
QY 130 ACCCCCACTCGAGGGCTGGACAGATGTTATTCTATTCTTGTGTGAGTACGTTGA 189
DB 13 ACCGAGAACGACACCGGCTACGACACGCTACTTCTACTGTTCTGGAACGACGCC 72
QY 190 GCGCAGGCCACGTACACCAACCTGGAAAGCGGACCTACAGATCAGCTGGGAGATGCG 249
DB 73 GGCACCGTCTCCATGACCTCTCACTCGGCGGACGTACAGACCTCGTGGCGAACACC 132
QY 250 GGTAACTGTCGTGGTGAAGGGCTGGAAACCCGGGCTGAACGCAAGAGCCATCACTTT 309
DB 133 GGCACCTTCTGTCGCGCGGACAGGGCTGTCTCAACCGC--GACCGCCGACCGTACCTAC 189
QY 310 GAGGCTGTTTACCAAGCCAAACGCAACAGCTACCTTGCGGTCTACGCTTGGACCCGCAAC 369
DB 190 AAGCCTCTTCAACCCGTCGGGTAAAGCCTTACCTCAAGCTCAAGGCTGAGCAGAGAAC 249
QY 370 CCGCTGTGAGTATTAATCATGTGTGAGAACTTTGGACCTTATGATCTTCTCCGGTGTCT 429
DB 250 CCGCTGTGAGTATTAATCATGTGTGAGAGCTGGGGCACTTACCGGCCACCC--GAC 303
QY 430 ACCGATCTAGGAATGTGAGTGAAGCGTAGCACTATCTATCGACTCGGCAAGACCACTGCG 489
DB 304 ACCTTCAAGGACACCTGTACCAACGACCGGCGGACGTACGACATCTTACGACACTTGGCGG 363
QY 490 GTCAACGCACTTACGATGACGCGACCCAAACCTTTCAGCAATATCTGTGCTCGCCAG 549
DB 364 TACAACGCGCGTCTCATCGAGGGGACCCGACCTTCCAGAGTTCTGGAAGGTCGCGGAG 423
QY 550 GACAAGCCGACCAAGGATCGGTCCAGACGCGGCTGCCCTTTCAGCGCTGGGGCTCGGCT 609
DB 424 CAGAAAGCGGACGAGGCGGACCATCACTTGGGCAACCTTTCAGCGCTGGGGCTCGGCGC 483
QY 610 GATTGAATGTCAACGCTGACCACTACTACAGATCGTTGCAAGGAGGCTACTTACG 669
DB 484 GGCATGAA---CTGGGACGACGACGATCAATGAGGAGCGGCTTACGAGC 540
QY 670 AGCGCTATGCTCGCATCACCGTTGCTGACGCTGGGCTTAAAGCTTAACTGTG 722
DB 541 AGCGTACCTCAACCGTCTCCATCAGGAGGTGGCAACCCCGGCAACCCGGG 593
```

RESULT 7
US-11-108-163B-2

Sequence 2, Application US/11108163B
Publication No. US20060014247A1

GENERAL INFORMATION:

APPLICANT: Paloheimo, Marja

APPLICANT: Mantyla, Arja

APPLICANT: Leskinen, Sanna

APPLICANT: Paegerstrom, Richard

APPLICANT: Kallio, Jarno

APPLICANT: Puranen, Terhi

APPLICANT: Lantto, Raij

TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of

TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi

FILE REFERENCE: 1716.034008/MAC/DJN

CURRENT APPLICATION NUMBER: US/11/108,163B

PRIOR FILING DATE: 2005-04-18

PRIOR APPLICATION NUMBER: US 60/562,692

;; PRIOR FILING DATE: 2004-04-16
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 2
;; LENGTH: 906
;; TYPE: DNA
;; ORGANISM: Nonomurea flexuosa
;; FEATURE:
;; OTHER INFORMATION: am35, Nf xynIIA coding region for the mature Nf XynIIA (AM35)
;; US-11-108-163B-2

Query Match 19.0%; Score 187; DB 11; Length 906;
Best Local Similarity 60.9%; Pred. No. 7e-41;
Matches 361; Conservative 0; Mismatches 220; Indels 12; Gaps 3;

QY 130 ACCCCAACTGGAGGGCTGGACGATGTTATTCTTCTGGTGGAGTACGCTGGA 189
DB 13 ACCCGAAGACGAGCCGGGTACGACAAACGGCTACTTCTACTCGTTCGACCGACGCC 72
QY 190 GCGAGGCGCAGTACCAACCTGGAAAGCGGCACTTACGAGATCAGCTGGGGAATGAC 249
DB 73 GGGACCGTCTCCATGACCTTCCATCTGGGCGGCACTTACAGCAGCTTGGGGAACAC 132
QY 250 GGTAACTCTGCTGGTGAAGGGCTGGAACCCGGCTGGAAGCAAGACCATCTT 309
DB 133 GGGAACTTCTGTCGGCGGCAAGGCTGCTCAACGGC---GGAAGCGGACCTGACCTAC 189
QY 310 GAGGCTGTTTACGAGCCAAACGCAACGCTTCTGGCTTACGCTTGAACCGCAAC 369
DB 190 AACGCTCTTCAACCCGTCGGGTAAACGCTTACCTACGCTTGAACGCTGGAAC 249
QY 370 CCGCTGCTGATTAAGTATGATGTCGAGAACTTTGGCACTTATGATCTTCTCCGGTCT 429
DB 250 CCGCTGCTGATTAAGTATGATGTCGAGAACTTTGGCACTTATGATCTTCTCCGGTCT 429
QY 430 ACCGATCTAGGAAGTGTGAGTGCAGAGTGTAGCATCTTACGCTGGGCAAGCACTGAC 489
DB 304 ACTTACAAAGGACCGCTTACCAACCGACCGGCGCAAGTACGATCTTACGAGACCTGGGCG 363
QY 490 GTCAACGCACTGATGATGACGCAACCCAACTTTCGACCAATCTGTGCTGGTCCGAG 549
DB 364 TACAACGCGCGCTCATGAGGCGACCCGCACTTTCAGAGCTTTCGAGGCTGGGCGAG 423
QY 550 GACAAGCGCACAGGCGTACGTCGACAGCGGCTGCTTTCGAGCTTGGGCTGGCGCT 609
DB 424 CAGAAGCGGACAGGCGGACCATCACTTGGCAACCTTTCGAGCTTGGGCTGGCGCT 483
QY 610 GATTGAATGTCAACGCTGACCACTACTACGATGCTTGGCAAGGAGGCTACTTACG 669
DB 484 GGCATGAA---CTTGGGAGGACGATACGATGATGAGGACCGAGGCTTACCAAGAC 540
QY 670 AGCGGCTATGCTCGCATCACCGTTGCTGACGCTGAGGCTTAAAGCTGAGT 722
DB 541 AGCGGCTATGCTCGCATCACCGTTGCTGACGCTGAGGCTTAAAGCTGAGT 722

RESULT 8
US-10-517-939-225
;; Sequence 225, Application US/10517939
;; Publication No. US20060003433A1
;; GENERAL INFORMATION:
;; APPLICANT: Steer, Brian
;; APPLICANT: Callen, Walter
;; APPLICANT: Healey, Shaun
;; APPLICANT: Hazlewood, Geoff
;; APPLICANT: Wu, David
;; APPLICANT: Belegbalian, Alireza
;; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
;; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
;; FILE REFERENCE: 56462007901
;; CURRENT APPLICATION NUMBER: US/10/517,939

;; CURRENT FILING DATE: 2004-12-13
;; PRIOR APPLICATION NUMBER: PCT/US03/19153
;; PRIOR FILING DATE: 2003-06-16
;; PRIOR APPLICATION NUMBER: 60/389,299
;; PRIOR FILING DATE: 2002-06-14
;; NUMBER OF SEQ ID NOS: 380
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 225
;; LENGTH: 1059
;; TYPE: DNA
;; ORGANISM: Unknown
;; FEATURE:
;; OTHER INFORMATION: Obtained from an environmental sample
;; US-10-517-939-225

Query Match 18.9%; Score 186.2; DB 7; Length 1059;
Best Local Similarity 60.2%; Pred. No. 1.2e-40;
Matches 346; Conservative 0; Mismatches 223; Indels 6; Gaps 2;

QY 130 ACCCCAACTGGAGGGCTGGACGATGTTATTCTTCTGGTGGAGTACGCTGGA 189
DB 88 AGTTCAGCGGAGGAGGACCAACACGCGCACTACTATCTTCTTGGAGAGACATGAC 147
QY 190 GCGAGGCGCAGTACCAACCTGGAAAGCGGCACTTACGAGATCAGCTGGGAGATGAC 249
DB 148 GGCACCGTCACTTCTGATGATGACGCAAGCGGCTTACACTTGAAGAGCGCATC 207
QY 250 GGTAACTCTGCTGGTGAAGGGCTGGAACCCGGCTGGAAGCAAGACCATCTT 309
DB 208 AACAACTGGGTGGCGGCAAGGCTGGCAACCGGCTCACCGCGA---CGATCAGCTAC 264
QY 310 GAGGCTGTTTACGAGCCAAAGGCAACGCTTCTGGCTTACGCTTGAACCGCAAC 369
DB 265 TGGGCTGCTTCACTACCCGCGCAATGTTATCTTCACTGTAAGGTTGACCACTAT 324
QY 370 CCGCTGCTGATTAAGTATGATGTCGAGAACTTTGGCACTTATGATCTTCTCCGGTCT 429
DB 325 CCATTGATGATGATCTATGATGTCGACAACTGGGCGCAAGTACCGGCGCGGAGGCTCG 384
QY 430 ACCGATCTAGGAAGTGTGAGTGCAGAGTGTAGCATCTTACGCTGGCAAGCACTGAC 489
DB 385 GCTTACATGAGGCGGATGACGAGGACCGGCGCACTTTCAGAGCTTTCGAGGCTGGGCGAG 444
QY 490 GTCAACGCACTGATGATGACGCAACCCAACTTTCGACCAATCTGTGCTGGTCCGCGAG 549
DB 445 GTAAACGAGCTTTCATATGAGGACCGGAGCTTTCATCAATCTGAGGCTGGCGAG 504
QY 550 GACAAGCGCACAGGCGTACGTCGACAGCGGCTGCTTTCGAGCTTGGGCTGGCGCT 609
DB 505 CAGAAGCGGACCGGCGGACCATCAACCGGCAATCACTTTCGAGCTTGGGCGGCAATC 564
QY 610 GATTGAATGTCAACGCTGACCACTACTACGATGCTTGGCAAGGAGGCTACTTACG 669
DB 565 GGAATGAA---CTTGGGAGGACGATACGATGATGAGGACCGAGGCTTACCAAGAC 621
QY 670 AGCGGCTATGCTCGCATCACCGTTGCTGACGCTGAGGCTTAAAGCTGAGT 704
DB 622 AGCGGCTATGCTCGCATCACCGTTGCTGACGCTGAGGCTTAAAGCTGAGT 704

RESULT 9
US-10-517-939-165
;; Sequence 165, Application US/10517939
;; Publication No. US20060003433A1
;; GENERAL INFORMATION:
;; APPLICANT: Steer, Brian
;; APPLICANT: Callen, Walter
;; APPLICANT: Healey, Shaun
;; APPLICANT: Hazlewood, Geoff
;; APPLICANT: Wu, David
;; APPLICANT: Belegbalian, Alireza
;; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 165
LENGTH: 1047
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-165

Query Match 18.8%; Score 185; DB 7; Length 1047;
Best Local Similarity 60.6%; Pred. No. 2,66-40;
Matches 340; Conservative 0; Mismatches 215; Indels 6; Gaps 2;

QY 145 GCTGGCAGCATGTTATTCTTCTGAGTGAACGGTGGAGCCGACGCTAC 204
DB 97 GGCAACCAACACGGCTTCTACTATTCTTCTGACCGACGGCGGTCTCCGTCAGTTC 156
QY 205 ACCAACCTGGAAGGCGACCTACGATCACTGCTGGGAGATGGCGGTACCTGCTGGT 264
DB 157 TGCCTGCAATCCGCGCGCGCTACCTTCAGCTGAGCAATGTGGAACTGGGTGCT 216
QY 265 GAAAGGCTGGAACCCGCGCTGAAACGCAAGCCATCACTTGAAGGTGTTTACAG 324
DB 217 GGCAAGGCTGGACAGCCGGGCGCGC---CGCAACATCACTATTCGGGAGCTTCAAT 273
QY 325 CCAAGCGCAACACTTCTGCGGTCTAGCTTGAACCGGACCCGCTGCTGAGTAT 384
DB 274 CCTCGGGTAAACGCTTACCTGCGCTCTATGCTGAGCAAGATCCCTGTTGAGATAC 333
QY 385 TACATGCTGGAACCTTGGGACCTATGATCCTTCTCGGGTCTACCGATCTAGAACT 444
DB 334 TACATGCTGGAACCTTGGGACCTATGATCCTTCTCGGGTCTACCGATCTAGAACT 393
QY 445 GTGAGTCCGACGCTGAGCATCTATGACTCGGCAAGACCACTCGGCTCAACGACTAGC 504
DB 394 GTTGTCAAGATGGGGGACCTAGACGCTTACCGCAAGCAAGGCTCAAGCGCCCTCC 453
QY 505 ATCGACGCAACCAACTTTCAGCAATATCTGCTGCTCCGACAGCAAGCGCACCGC 564
DB 454 ATTCAGGGCAACGCGACCTTCTACAGTACTGAGACGTTCCGCACTGCAAGCGCACCGGT 513
QY 565 GGTACCGTCCAGCGGGGCTGCACTTCAACGCTGGGCTCGGCTGTTGAAATGTCAC 624
DB 514 GGAACCATCTCCACCGGCAACCATTTCAAGGCTGGGCAAGCTTGGGATGAA---CTTG 570
QY 625 GGTGACCACTACTACAGATCTGTTGCAACGAGGGCTACTTTCAGAGCGGCTATGCTGC 684
DB 571 GGAACCTTCAATTAACAGATCTGTTGCAACGAGGGCTATTCAGAGCGGCAATTCGAC 630
QY 685 ATCACGTTGCTGACGTGGC 705
DB 631 ATCACGTTGACGTGGC 651

RESULT 10
US-10-517-939-199
; Sequence 199, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di

APPLICANT: Blum, David
APPLICANT: Etesghalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 199
LENGTH: 1074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-199

Query Match 17.3%; Score 170; DB 7; Length 1074;
Best Local Similarity 57.5%; Pred. No. 2,96-36;
Matches 368; Conservative 0; Mismatches 260; Indels 12; Gaps 3;

QY 59 CGGCTTAGCCGCACTGAGGCTCTGCTTCCCGGAGGAAATGCAAGAGCTCGAAA 118
DB 26 CGGCAAGGCGCGCGTGGCGCGCTGCTGCTTCCCGGCTTACATGCGCGCGCA 85
QY 119 AGCAGACAC-----AACCCTCACTCGAGGCTGACAGATGTTATTCTTCT 172
DB 86 ATGCGCAACCTGATCATCGTACGAGCAAGCGGCAACCAAGGCAACCTATTTCT 145
QY 173 GGTGAGTACCGTGGAGCGGCAAGTACCAACCACTTGAAGCGGCACTACGAGA 232
DB 146 TCTGAAAGACAGCCCGGCAAGTAACTTCTGATGACTCCGCGCGCTACAGCT 205
QY 233 TCAAGTGGAGATGGGCTTAACTCTGCTGTTGAAAGGCTGAAACCCCGCTGAAAG 292
DB 206 CCAACTGAGGCGATCAACAACTGGGTGGCGGCAAGGCTGCAAGCGGCTGCTCC 265
QY 293 CAAGACCATCACTTTGAGGCTTTTACAGCCAAACGCAACGCTACTTGGCTCT 352
DB 266 GCACCGTCTCTTCTCCGCGCAAGTCAATTGCGCG---GGTAAAGGCTTGAAGCTCT 322
QY 353 ACGTGGAGCCCGCAACCGGCTGCTGAGTATTAATGCTGAGAACTTGGCACTATG 412
DB 323 ACGCTGAGCAACCAATCGCTCATGATGATCTGATGATGATGATGATGATGATG 382
QY 413 ATCTTCTCTCCGCTGCTACCATCTGAGAACTGTCAGTGGAGCGTATCTATGAC 472
DB 383 GTCCGCGGCTGGCGAGGCTTCAATGGGCAAGTAAACAGGAGCGGCGCAAGTAC 442
QY 473 TCGCAAGACCACTGCGCTCAAGCAAGCACTGATGAGCGGCAACCAACTTTCAGCAAT 532
DB 443 TCTATGCAACCAACGAGTCAACCAAGCGCTGATGATGAGCGGCGAGTCTTACAGT 502
QY 533 ACTGCTGCTCCGCGCAAGGCAAGGCAACGAGTACCGTCAAGCGGCTGCGCACTCG 592
DB 503 ACTGAGCTGCGGAGTCAAGGCAACGAGGCAACGAGTACCGTCAAGCGGCTGCGCACTCG 562
QY 593 ACGCTGGCTGCGGCTGTTTGAATGTCAGCGTACCACTACTACCAAGATCTGTCGA 652
DB 563 ATGCTGGCGAGCTGCGCATGAA---CTGGGACAGCAACATCAAGATGATGCGCA 619
QY 653 CGAGGCTACTTACGACGCGCTATGCTCCATCACTCGT 692
DB 620 CCGAGGCTTACGAGGAGCGGCGAGCTCGACATCACTCGT 659

RESULT 11
US-10-517-939-255
; Sequence 255, Application US/10517939

Publication No. US20060003433A1
GENERAL INFORMATION:
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 255
LENGTH: 1137
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-255

Query Match 17.3%; Score 170; DB 7; Length 1137;
Best Local Similarity 57.5%; Pred. No. 3e-36;
Matches 368; Conservative 0; Mismatches 260; Indels 12; Gaps 3;
59 CGGCTTAGCCGCGACCTGCGGCTTCCGCGAGGAATCCAGAGCTCCGAAA 118
Db CGGCGAGCGCGCGCTCGCGGCTGCGCTTGCCTTCAATGCGCGCGGA 148
119 AGCGACAGAC-----AACCCCACTCGAGGCGTGGCAAGATGTAATTAATTCCT 172
Db ATGCGCAAACTGCACTACGTGAGCCAGAGCGGCAACAAACGCGCACTTTTCT 208
149 ATGCGCAAACTGCACTACGTGAGCCAGAGCGGCAACAAACGCGCACTTTTCT 208
173 GGTGAGTACGCTGAGAGCGGACGACGTAACCAACCTGAAAGCGGCACTTACGAGA 232
Db TCTGGAAGAGACGCGCGGACGCTGTAATCTTCACTGATGTAACGCGCGCTACAGT 268
209 TCTGGAAGAGACGCGCGGACGCTGTAATCTTCACTGATGTAACGCGCGCTACAGT 268
223 TCACTGAGAGATGAGCGGTAACCTGCTGCTGAGAAAGGCTGAAACCCCGGCTGAAAG 292
Db CCAACTGAGAGCGGCACTCAACAACTGGGTGGCGGCAAGGCTGGGACGCGCTGCTCC 328
269 CCAACTGAGAGCGGCACTCAACAACTGGGTGGCGGCAAGGCTGGGACGCGCTGCTCC 328
293 CAAGAGCATCACTTTGAGGGGTGTTTACAGCCAAACGCGCAAGCTTACGCGCT 352
Db GCACTGCTCTTCTTCCGCGAGCTTCAATTCGCG--GTTAAGGCTTACCTGACGCTCT 385
329 GCACTGCTCTTCTTCCGCGAGCTTCAATTCGCG--GTTAAGGCTTACCTGACGCTCT 385
353 AGGCTTGAACCGCAACCGCTGCTGATGTAATCACTGTCGAGAACTTTGCACTATG 412
Db ACGGCTGAGCAACCAATCGGCTCATGAGTACTGATGTCGAGCAACTGGGCAAGTATC 445
386 ACGGCTGAGCAACCAATCGGCTCATGAGTACTGATGTCGAGCAACTGGGCAAGTATC 445
413 ATCTTCTCTCGGCTGCTACGATCTGAGAACTGTCGAGTGGAGCGGTGATCTATGAC 472
Db GTCCGCGCGGCTGCGGAGGCTTCAATGAGGACGCTGAAACCGCGCGCTGATGAGCA 505
446 GTCCGCGCGGCTGCGGAGGCTTCAATGAGGACGCTGAAACCGCGCGCTGATGAGCA 505
473 TCGGCAAGACCACTGCGCTCAACGCACTAGATGAGGCAACCAACCTTTCGCAAT 532
Db TCTATCGACGCAACGAGTCAACGAGCTGATGATGAGGCAACGCGAGCTTTCACAGT 565
506 TCTATCGACGCAACGAGTCAACGAGCTGATGATGAGGCAACGCGAGCTTTCACAGT 565
533 ACTGCTGCTGCGCGAGCAACGCAACGAGCGTACCGCTCAAGCGGCTGCGCACTTCG 592
Db ACTGAGGCTGCGGAGTCAAGGCGCAACGCGGAGCAATCAACGCGCAACCACTTCA 625
566 ACTGAGGCTGCGGAGTCAAGGCGCAACGCGGAGCAATCAACGCGCAACCACTTCA 625
593 ACGCTTGGGCTGCGGCTGTTGAATGCAACGCTGACCACTTCAACGATTCGTTGCA 652
Db ATGCTTGGGCGAGCTTGGCAATGAA---CTTGGGCAACGCAACCTTCAACGATTCG 682
626 ATGCTTGGGCGAGCTTGGCAATGAA---CTTGGGCAACGCAACCTTCAACGATTCG 682
653 CGAGGAGCTACTTCAAGACGCGCTATGCTCGCATCACTG 692

Db 683 CGAGGAGCTACCAAGACGCGGAGCTCCGACATCACTGCT 722
RESULT 12
US-10-517-939-169
Sequence 169, Application US/10517939
Publication No. US20060003433A1
GENERAL INFORMATION:
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 169
LENGTH: 1041
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-169

Query Match 16.9%; Score 165.8; DB 7; Length 1041;
Best Local Similarity 56.8%; Pred. No. 3.9e-35;
Matches 346; Conservative 0; Mismatches 257; Indels 6; Gaps 2;
97 GGAATGCCACGAGCTCGGAAAGCAAGACAAACCCCACTTGGAGGCTGACGAT 156
Db GGCATTTACCGCGCGGAGCGCAAACTGATCACTTCCAGCCAGACCGGATCCAAAC 111
52 GGCATTTACCGCGCGGAGCGCAAACTGATCACTTCCAGCCAGACCGGATCCAAAC 111
157 GGTATTAATTTCTCTGAGAGTGAAGTGAAGCGGACGACGATCACTTCAACCACTGGA 216
Db GGTATTAATTTCTCTGAGAGTGAAGTGAAGCGGACGACGATCACTTCAACCACTGGA 216
112 GGAATTAATTTCTCTGAGAGTGAAGTGAAGCGGACGACGATCACTTCAACCACTGGA 216
217 GGCAGCACTTACGAGATCACTGAGGAGATGAGCGGTAACCTGCTGAGTGAAGGCTGG 276
Db AATGAGGCTTACCACTTCACTGAGGAGATGAGCGGTAACCTGCTGAGTGAAGGCTGG 231
172 AATGAGGCTTACCACTTCACTGAGGAGATGAGCGGTAACCTGCTGAGTGAAGGCTGG 231
277 AACCCGCGCTGAAAGCAAGAGCCATCACTTGAAGGCTGTTACAGCAACGCGCAAC 336
Db CAGAGGAGCTTCAACCGCAGGTAACCTTCTCC--GTTCTGTTCAATTCGCGGCAAT 288
232 CAGAGGAGCTTCAACCGCAGGTAACCTTCTCC--GTTCTGTTCAATTCGCGGCAAT 288
337 AGCTAAGCTTGGCTTACGCTTGAAGTGAAGCGGCAACCGGCTGAGTATTAATGTCGAG 396
Db GGTATTCACCTTGAAGTGAAGCGGCAACCAATTCATGATGATGATGATGATGATGATG 348
289 GGTATTCACCTTGAAGTGAAGCGGCAACCAATTCATGATGATGATGATGATGATGATG 348
397 AACTTGGCACTTATGATCTTCTCCGCTGCTACGATCTGAGAACTGTCGAGTGGAC 456
Db AGCTGGGCACTTATGATCAACCGCGGAGCGGCAAGGCTTCAATGAGGCAACGTCAGGAT 408
349 AGCTGGGCACTTATGATCAACCGCGGAGCGGCAAGGCTTCAATGAGGCAACGTCAGGAT 408
457 GGTAGCATTTATGATCTTCCGAGAGCACTTCCGCTCAAGCAACCTTATGATGAGGAC 516
Db GCGCGCACTTATGATCACTTACCGCAACGCGGCTGAAACCACTTCAATGATGAGGAC 468
409 GCGCGCACTTATGATCACTTACCGCAACGCGGCTGAAACCACTTCAATGATGAGGAC 468
517 CAATCTTCAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 576
Db GCAAGCTTCAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528
469 GCAAGCTTCAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528
577 ACGGCTGCACTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 636

Db 529 AGCGCAACCACTTCAACGCTGGGCGCACGCTGGGATGAA--CTGGGCGACAGACAAC 585
Qy 637 TACGAGATCGTTGACGAGGAGCTACTTTCAGACGCGGCTATGCTGCATCACCGTGGCT 696
Db 586 TACCAAGTCATGCGCACCGAGGGTTTACAGAGCAATGCGACACTCCGACATCACCGTACC 645
Qy 697 GACGTGGGC 705
Db 646 GAGGCGGCGC 654

RESULT 13
US-10-517-939-221
; Sequence 221, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:

; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-221

Query Match 16.8%; Score 165.6; DB 7; Length 1044;
Best Local Similarity 58.0%; Pred. No. 4.5e-35;
Matches 332; Conservative 0; Mismatches 234; Indels 6; Gaps 2;
Qy 134 CCAACTCGAGGCTGGGACCAATGTTTACTTCTCTGGTGGATGACGTTGAGGCG 193
Db 89 CCAGCAACCGGCGCAACAACGCGCAATTTTTCATCTCGAAGACAACCCGGGCA 148
Qy 194 AGGCCACGTACCAACCTGGAGGCGCACCTTACGATCAGCTGGGAGATGGCGGTA 253
Db 149 CGGTGACCTTTCGATGATGATGCAACGCGCGCTTACACCTCCAACTTGGAGCGGCATCA 208
Qy 254 ACCGTGCGTGGAAAGGCTGGAAACCCCGGCTGAAAGCAAGACCATCCATTGAGG 313
Db 209 ACTGGTGGGTGGCAAGGCTGGCAGACCGGCTCAATGCAAGGTGACTTCTCGGTT 268
Qy 314 GTGTTTACGAGCAACGCGCAACAGCTTCTCGGTCTACGCTTGGAGCCGCGCA 373
Db 269 CGTTCACTCGCC--CGGCAACGGCTTACTCCTGATCGGGTGAACAGAAATCGCG 325
Qy 374 TGTGAGATATTATCATCTGCGAATCTTGGCACTTATGATCTTCTCGGTGCTACCG 433
Db 326 TGATGAGATCTACATCTGCGACAGTGGGGCAGTTATGACCGCGCGCGCGCGAGGCT 385
Qy 434 ATCTAGGAATGTGCGAGTGGCGAGCGGTAGCATCTATGACTGGCAAGCACTGGCTCA 493
Db 386 TCATGGGACCGGTGACGACCGGCGGCACTTACGACATCTATGCGACGCGCGGTGA 445
Qy 494 AGGCACTTGAATGACGCGGCAACCACTTTCGACCAATATCTGCTGGTGGCGCGAGACA 553
Db 446 ACCAGCTTTCATCTGCGACCGGCAAGCTTCTTACAGTATGAGCGGTGCGGAGTGA 505

Qy 554 AGCGCAACCGGTATCCGTCGAAGCGGGCTGCCACTTTCAGCGCTGGGCTCGCGCTGTT 613
Db 506 AGCGGTGGGGGACCATCATCACCGCCAAACACTTCAATGCTGGGCGACGCTGGGCA 565
Qy 614 TGAATGCAACGCGACCACTTACAGATTCGTTGGAAGGAGGCTTACTTCAGCAGCG 673
Db 566 TGA--CTGGGCGCAACAATCTACAGGTCTATGGCCACCGAGGTTTACAGAGACGG 622
Qy 674 GCTATGCTCGCATTCACCGTGGTTCAGCGTGGGC 705
Db 623 GCAGCTCCGACATCACCGTGAACGAGCGGCGC 654

RESULT 14
US-10-517-939-177
; Sequence 177, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:

; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-177

Query Match 16.8%; Score 165.4; DB 7; Length 1299;
Best Local Similarity 56.3%; Pred. No. 5.5e-35;
Matches 351; Conservative 0; Mismatches 266; Indels 6; Gaps 2;
Qy 70 GCGACTGGGCGCTGGCTTCCCGGCAAGGATGCCAGAGCTCGAAAGCGACAGACA 129
Db 28 GCGATTGCTGCGGAGCACTAGCGGTGGCGACTTCCATTCGCTCATGCCAACGCTT 87
Qy 130 ACCCCCACTGGAGGCTGGCAAGATGTTATTAATCTCTGGTGGAGTGAAGGATGGA 189
Db 88 AGCTCAATATGCACTGGAACCAAGATGTACTATATTTGTTTGGAGGATTTCCGAT 147
Qy 190 GCGAGGCGCACTACCAACCTGGAAGCGGCGCACTTACGAGATCAGCTGGGAGATGAGC 249
Db 148 AACGCCACATGACACTCGGTGCGGTGGAATCTTCTATCTGGAACGACGACT 207
Qy 250 GGTAACTGTGCTGGTGAAGAGGCTGGAAACCCCGGCTGAAAGCAAGACCATCCATT 309
Db 208 AACAACTGGTGGCGGTGAAGGCTGAGTGGCGG--TACTCGGCGCAAGTCACTAT 264
Qy 310 GAGGCTGTTTACAGCCAAAGCGCAACGCTTACCTTGGCGGTCTACGTTGAGCCGCGAAC 369
Db 265 TCGGCACTTATAGCGCGAGTGAACAGCTTACCTTTCGACCTTTCAGGCTGGAAC 324
Qy 370 CGGCTGTCGATTAATCATCTGTCGAGAACTTTGGCACTTATGATCTTCTCGGTGCT 429
Db 325 CCGCTGATCAATTTATCATTTGTGAAAACCTGGGTCAATTACATTCCTGCGGCGCA 384

Qy 430 ACCGATCTAGGAAGTGTGAGTGCAGACGGTAGCATCTATCGACTGGCGAAGCACTGCG 489
Db 385 AGCAATTTAGGACCTGTCAATATTTAGACGGACACCTTACAGCTGGCGCGGCGCAACGG 444
Qy 490 GTCAACGCACTTAGATGAGCGGACCCAACTTTCAGCAATATCTGTGGTCCGCCAG 549
Db 445 GTTAATCAGCCATCTATTGAAAGGCAAGGCAAGTTCATCAATATCTGAGTGTGGCGAA 504
Qy 550 GACAGCGCACCGAGCGGTACCGTCCAGACGGGCTGCACCTTGCAGCGCTGGCGCGCT 609
Db 505 AACAGACCGCACCGAGCGGAACATTAATTTAGAGCGCATTTTCAGATGCAATGGGCTGCTGTG 564
Qy 610 GATTGAATGTCAACGGTGAACCATCTACTACAGATCTGTGCAACGAGGCGCTACTTTCAGC 669
Db 565 GCGTTGAA---CCTGGGGGACTCAGATTTATGATTTAGTGGGAGCCGAGGGGTACAGAGC 621
Qy 670 AGCGGCTATGCTCGCATCACCGT 692
Db 622 AGCGGCGCAGTCCATATTCACCGT 644

RESULT 15

US-10-517-939-217
; Sequence 217, Application US/10517939
; Publication No. US20060003433a1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Eareghian, Allreza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 56462007901
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: Fastseq for Windows Version 4.0
; SEQ ID NO: 217
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Unknown
; FEATURES:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-217

Query Match 16.4%; Score 161.6; DB 7; Length 1083;
Best Local Similarity 56.8%; Pred. No. 5.4e-34;
Matches 359; Conservative 0; Mismatches 264; Indels 9; Gaps 3;

Qy 130 ACCCCCACTGGAGAGGCTGGGACGATGTTATTCTATTTCTGTGTGAGTGAACGGTGA 189
Db 100 AGTTCACCGACGACCGGACCAACGGAACCTATTTCTGTGTGAGTGAACGCGCG 159
Qy 190 GCGCAGCGCACGTAACCACTGGAAGCGGACCTTAGAGATCAGCTGGGAGATGGC 249
Db 160 GGCACGGTGAATTTGTGATGTAACCGAATGGCGCTACACTGGAATGGAAGCGGCATC 219
Qy 250 GGTAACTCTGTGTGGAAGAGGCTGGAACCCGGGCTGAAAGCAAGAGCATCTTT 309
Db 220 AACAACTGGGTGGGGGAGGGCTGTGACCGGCTCAGC---CGACCGTCACTAT 276
Qy 310 GAGGTTGTTTACAGCCAAAGCGGAAAGCTTACCTTGGGTGAGGTGAGTGAACCGGAA 369
Db 277 TCGGGACGCTTAATTCGCCCGGCAAGGCTACTGACTCTTACGGGTGAGCAACCAAC 336
Qy 370 CCGCTGTGAGTATTAATGTCGAGAACTTTGGCACTTATGATCTTCTCGGCTGCT 429

Db 337 CCGCTCATCGACTACTACATGTCGAGAACTGGGGTAACTACCGCCGCGGGCGGCGAG 396
Qy 430 ACCGATCTAGGAAGTGTGAGTGCAGACGGTAGCATCTATCGACTGGCGAAGCACTGCG 489
Db 397 GGTATCATGGGAGCGTCAATTTCCAGCGGGCGACCTATGACATTAACCGGACTTTCGG 456
Qy 490 GTCAACGCACTTAGCATGACGCGCA---CCCAAACCTTTCAGCAATATCTGGTCCGTCG 546
Db 457 GACAAACAGCCCTTGATCAACGGGCACTCTGCGCACTTTTACAGTACTGAGAGCTGGCG 516
Qy 547 CAGGAAAGCGCACACCGGTACCGTCAAGCGGCTGCGCACTTTCAGACGCTGGGCTTCG 606
Db 517 CAGTCAAGCGGACAGCGGACCATCAACACGCGCAATCACTTTCGCGGCGTGGAAACAGC 576
Qy 607 GCTGTTGAATGTCAACGGTGAACCATCTACTACAGATCTGTGCAACGAGAGGCTACTTC 666
Db 577 CTGCGCATGAA---CCTGGGCGACAGCAACTTACAGGTCAATGGGCACCGAGGTTACCG 633
Qy 667 AGCAGCGGCTATGCTCGCATCACCGTTCGAGCGTGGGCTTAAGAGTAACTGGTGTGA 726
Db 634 AGCAGCGGCGAGCTTCGACATTCACGTTCAAGAGGCGGCGGCGGACGACGAAATGTGGC 693
Qy 727 TCTGCGAGGCGACAGCGCAAGATGTGTCAG 758
Db 694 AGCAGCAACGCGCGGACAGCAATGGCGGAG 725

Search completed: February 11, 2006, 22:06:15
Job time : 316.228 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:13:38 ; Search time 3493.06 Seconds
(without alignments)
10984.434 Million cell updates/sec

Title: US-09-467-368-1_COPY_31_705
Perfect score: 675
Sequence: 1 ATGCTCGGCTTACCCCGT.....TCACCGTTGTGACGTGGGC 675

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_str:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
|------------|-------|--------------|-------------------|----------------------|
| 1 | 675 | 100.0 | 983 6 AR044575 | AR044575 Sequence |
| 2 | 675 | 100.0 | 983 6 AR157660 | AR157660 Sequence |
| 3 | 582 | 86.2 | 588 6 AX244978 | AX244978 Sequence |
| 4 | 559 | 82.8 | 2460 15 TL035436 | TL035436 Thermomyces |
| 5 | 262.4 | 38.9 | 89019 15 BX842624 | BX842624 Neurospor |
| 6 | 243.6 | 36.1 | 786 15 TRU24191 | TRU24191 Trichoderma |
| 7 | 240.6 | 35.6 | 1039 15 HIXY1 | HIXY1 H. insolens |
| 8 | 239 | 35.4 | 1123 6 165436 | 165436 Sequence 3 |
| 9 | 239 | 35.4 | 1123 6 BD006885 | BD006885 Aspergill |
| 10 | 230.8 | 34.2 | 841 15 AY156910 | AY156910 Trichoder |
| 11 | 228.2 | 33.8 | 672 15 AY320048 | AY320048 Trichoder |
| 12 | 214.6 | 31.8 | 2202 15 AF246830 | AF246830 Fusarium |
| 13 | 214 | 31.7 | 928 15 TVI012718 | TVI012718 Trichoder |
| 14 | 213 | 31.6 | 912 15 AK110604 | AK110604 Oryza sat |
| 15 | 211.4 | 30.3 | 696 15 AY648860 | AY648860 Gibberell |
| 16 | 206.2 | 30.5 | 678 15 AY536639 | AY536639 Aspergill |
| 17 | 205 | 30.4 | 1195 6 E28868 | E28868 Xylanase ge |
| 18 | 205 | 30.4 | 1195 6 E28869 | E28869 Xylanase ge |

| | | | | |
|----|-------|------|--------------------|------------------------------|
| 19 | 204.4 | 30.3 | 816 15 AF490982 | AF490982 Aspergill |
| 20 | 204.4 | 30.3 | 843 15 AY551187 | AY551187 Aspergill |
| 21 | 203.4 | 30.1 | 576 15 SOL292317 | SOL292317 Streptomy |
| 22 | 203 | 30.1 | 696 6 C0786060 | C0786060 Sequence |
| 23 | 201.2 | 29.8 | 300800 1 SC0393112 | SC0393112 Streptomy |
| 24 | 201 | 29.8 | 2208 15 CEMXB2 | CEMBX2 Chaetomium |
| 25 | 200.2 | 29.7 | 1623 15 APE14BXYL | APE14BXYL endo |
| 26 | 199.8 | 29.6 | 1767 1 SPXY1 | SPXY1 Streptomyce |
| 27 | 199.6 | 29.6 | 3173 1 AB110644 | AB110644 Streptomy |
| 28 | 199.6 | 29.6 | 4398 1 STMX1NB | STMX1NB Streptomyce |
| 29 | 199.4 | 29.5 | 1640 15 CCLXYLANAS | CCLXYLANAS Cochliobus |
| 30 | 198.4 | 29.4 | 851 6 A62443 | A62443 Sequence 5 |
| 31 | 198.4 | 29.4 | 949 15 AJ863566 | AJ863566 Gibberell |
| 32 | 198 | 29.3 | 1008 1 AF194025 | AF194025 Streptomy |
| 33 | 196.8 | 29.2 | 687 15 AY578961 | AY578961 Gibberell |
| 34 | 196.2 | 29.1 | 1375 1 AFL508952 | AFL508952 Nontomurae |
| 35 | 196.2 | 29.1 | 1375 6 AR274543 | AR274543 Sequence |
| 36 | 196.2 | 29.1 | 1375 6 AR369734 | AR369734 Sequence |
| 37 | 196.2 | 29.1 | 1375 6 AR441840 | AR441840 Sequence |
| 38 | 194.8 | 28.9 | 2015 15 CEMX1 | CEMX1 Chaetomium |
| 39 | 194.6 | 28.8 | 695 15 CNS01CP8 | CNS01CP8 Botrytis |
| 40 | 191.6 | 28.4 | 1020 15 TRXYNICNA | TRXYNICNA X9573 f. reisel xy |
| 41 | 190 | 28.1 | 1015 6 AR055687 | AR055687 Sequence |
| 42 | 190 | 28.1 | 1075 15 S67387 | S67387 xln2-endoxy |
| 43 | 188.2 | 27.9 | 514 6 E28872 | E28872 Xylanase ge |
| 44 | 187.8 | 27.8 | 2196 1 U01242 | U01242 Thermomonas |
| 45 | 187.8 | 27.8 | 3204 1 AY795559 | AY795559 Thermobif |

ALIGNMENTS

| | | | | | |
|------------|---|------------|-----|--------|-----------------|
| RESULT 1 | AR044575 | 983 bp | DNA | linear | PAT 29-SEP-1999 |
| LOCUS | AR044575 | | | | |
| DEFINITION | Sequence 1 from patent US 5817500. | | | | |
| ACCESSION | AR044575 | | | | |
| VERSION | AR044575.1 | GI:5966040 | | | |
| KEYWORDS | Unknown. | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unclassified. | | | | |
| REFERENCE | 1 (bases 1 to 983) | | | | |
| AUTHORS | Hansen, P. Kamp., Wagner, P., Mullertz, A. and Knap, I. Helmer. | | | | |
| TITLE | Animal feed additives | | | | |
| JOURNAL | Patent: US 5817500-A 1 06-OCT-1998; | | | | |
| FEATURES | Location/Qualifiers | | | | |
| source | 1..983 | | | | |
| ORIGIN | /mol_type="unknown" | | | | |
| | /mol_type="unassigned DNA" | | | | |

| | | | | |
|-----------------------|---------|--|---------------|-------------------|
| Query Match | 100.0% | Score 675; | DB 6; | Length 983; |
| Best Local Similarity | 100.0%; | Pred. No. 4.8e-130; | | |
| Matches | 675; | Conservative 0; | Mismatches 0; | Indels 0; Gaps 0; |
| QY | 1 | ATGCTCGGCTTTACCCCGTTCGCGGCTTTAGCCGGAATGGGCGCTTGCCTTC | 60 | |
| DB | 31 | ATGCTCGGCTTTACCCCGTTCGCGGCTTTAGCCGGAATGGGCGCTTGCCTTC | 90 | |
| QY | 61 | CCGCGAGGAGATGCGAGAGCTGGAAGGAGCAAGCCCACTGGAGAGGCTGG | 120 | |
| DB | 91 | CCGCGAGGAGATGCGAGAGCTGGAAGGAGCAAGCCCACTGGAGAGGCTGG | 150 | |
| QY | 121 | CACGATGTTATTAATTCCTGCTGAGTGAACGCTGAGGAGGACGACGATACCAAC | 180 | |
| DB | 151 | CACGATGTTATTAATTCCTGCTGAGTGAACGCTGAGGAGGACGACGATACCAAC | 210 | |
| QY | 181 | CTGGAAGCGGCGACCTTACGATCACTGGGAGATGCGGTAACCTGCTGGTGAAG | 240 | |
| DB | 211 | CTGGAAGCGGCGACCTTACGATCACTGGGAGATGCGGTAACCTGCTGGTGAAG | 270 | |
| QY | 241 | GGCTGAACCCGCGCTTGAAGGAGGATCATCTTGAAGGCTTTACGACCAAC | 300 | |

Db 271 GGCTGGAACCCCGCTGGAACGGAAGCCATCATCTTGAAGGTTTTCAGACCCAAAC 330
Qy 301 GGCAACAGCTACTCTTGCGGTCTACGGTTGGAACCCGCAACCCGCTGGTGCAGTATTACATC 360
Db 331 GGCAACAGCTACTCTTGCGGTCTACGGTTGGAACCCGCAACCCGCTGGTGCAGTATTACATC 390
Qy 361 GTGAGAACTTTGGCACTATGATCTTCCCTCGGCTGCTACCGATCTAGGAACCTTGAG 420
Db 391 GTGAGAACTTTGGCACTATGATCTTCCCTCGGCTGCTACCGATCTAGGAACCTTGAG 450
Qy 421 TGGCAGCGGTAGCATCTATCGACTCGGCAAGACCACTGCGTCAACGCACTTACATGAC 480
Db 451 TGGCAGCGGTAGCATCTATCGACTCGGCAAGACCACTGCGTCAACGCACTTACATGAC 510
Qy 481 GGCAACCAACCTTGCACCAATATCTGGTGGTCCGCCAGGACCAAGCCGCAAGGCTGAC 540
Db 511 GGCAACCAACCTTGCACCAATATCTGGTGGTCCGCCAGGACCAAGCCGCAAGGCTGAC 570
Qy 541 GTCCAGACGGGCTGCACTTGCACGCGCTGCGCTGCGTGGTTGAATGTCAACGCTGAC 600
Db 571 GTCCAGACGGGCTGCACTTGCACGCGCTGCGCTGCGTGGTTGAATGTCAACGCTGAC 630
Qy 601 CACTACTACCAAGATCGTTGCAACGGAAGGCTACTTTCAGCAAGCGGCTATGCTCGCATACC 660
Db 631 CACTACTACCAAGATCGTTGCAACGGAAGGCTACTTTCAGCAAGCGGCTATGCTCGCATACC 690
Qy 661 GTTGCTGACGTGGGC 675
Db 691 GTTGCTGACGTGGGC 705

RESULT 2
ARI57660
LOCUS ARI57660 983 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6245546.
ACCESSION ARI57660
VERSION ARI57660.1 GI:16218623
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 983)
AUTHORS Hansen, P. Kamp., Wagner, P., Mullertz, A. and Knap, I. Helmer.
TITLE Animal feed additives
JOURNAL Patent: US 6245546-A 1 12-JUN-2001;
FEATURES
Location/Qualifiers
1..983
/organism="Unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 675; DB 6; Length 983;
Best Local Similarity 100.0%; Pred. No. 4.8e-130;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTCGCGCTTTACCCCCCGTGGCCCTTGCGGCTTAGCGCGGACCTGGGGCCCTGGCCCTTC 60
Db 31 ATGTCGCGCTTTACCCCCCGTGGCCCTTGCGGCTTAGCGCGGACCTGGGGCCCTGGCCCTTC 90
Qy 61 CCGGACGGAATGACGAGAGCTCGAAAAAGCAGACACAAACCCCACTCGGAGGGCTGG 120
Db 91 CCGGACGGAATGACGAGAGCTCGAAAAAGCAGACACAAACCCCACTCGGAGGGCTGG 150
Qy 121 CACGATGTTATTACTATTCTCTGTGAGTGAAGCGGTGAGCGGACGCACTGACACCAAC 180
Db 151 CACGATGTTATTACTATTCTCTGTGAGTGAAGCGGTGAGCGGACGCACTGACACCAAC 210
Qy 181 CTGGAAGCGGACCTTACGAGATCAAGCTGGGAGAGTGGCGGTAACTCGTGGTGAAG 240
Db 211 CTGGAAGCGGACCTTACGAGATCAAGCTGGGAGAGTGGCGGTAACTCGTGGTGAAG 270
Qy 241 GGCTGGAACCCCGCTGGAACGGAAGCCATCATCTTGAAGGTTTTCAGACCCAAAC 300

Db 271 GGCTGGAACCCCGCTGGAACGGAAGCCATCATCTTGAAGGTTTTCAGACCCAAAC 330
Qy 301 GGCAACAGCTACTCTTGCGGTCTACGGTTGGAACCCGCAACCCGCTGGTGCAGTATTACATC 360
Db 331 GGCAACAGCTACTCTTGCGGTCTACGGTTGGAACCCGCAACCCGCTGGTGCAGTATTACATC 390
Qy 361 GTGAGAACTTTGGCACTATGATCTTCCCTCGGCTGCTACCGATCTAGGAACCTTGAG 420
Db 391 GTGAGAACTTTGGCACTATGATCTTCCCTCGGCTGCTACCGATCTAGGAACCTTGAG 450
Qy 421 TGGCAGCGGTAGCATCTATCGACTCGGCAAGACCACTGCGTCAACGCACTTACATGAC 480
Db 451 TGGCAGCGGTAGCATCTATCGACTCGGCAAGACCACTGCGTCAACGCACTTACATGAC 510
Qy 481 GGCAACCAACCTTGCACCAATATCTGGTGGTCCGCCAGGACCAAGCCGCAAGGCTGAC 540
Db 511 GGCAACCAACCTTGCACCAATATCTGGTGGTCCGCCAGGACCAAGCCGCAAGGCTGAC 570
Qy 541 GTCCAGACGGGCTGCACTTGCACGCGCTGCGCTGCGTGGTTGAATGTCAACGCTGAC 600
Db 571 GTCCAGACGGGCTGCACTTGCACGCGCTGCGCTGCGTGGTTGAATGTCAACGCTGAC 630
Qy 601 CACTACTACCAAGATCGTTGCAACGGAAGGCTACTTTCAGCAAGCGGCTATGCTCGCATACC 660
Db 631 CACTACTACCAAGATCGTTGCAACGGAAGGCTACTTTCAGCAAGCGGCTATGCTCGCATACC 690
Qy 661 GTTGCTGACGTGGGC 675
Db 691 GTTGCTGACGTGGGC 705

RESULT 3
AX244978
LOCUS AX244978 588 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 9 from Patent W00166711.
ACCESSION AX244978
VERSION AX244978.1 GI:15859703
KEYWORDS
SOURCE Thermomyces lanuginosus
ORGANISM Thermomyces lanuginosus
REFERENCE 1
AUTHORS Slibsezen, O. and Sorensen, J.F.
TITLE Xylanase variants having altered sensitivity to xylanase inhibitors
JOURNAL Patent: WO 0166711-A 9 13-SEP-2001;
FEATURES
Location/Qualifiers
1..588
/organism="Thermomyces lanuginosus"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 86.2%; Score 582; DB 6; Length 588;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 94 CAGACAAACCCCACTCGGAGGCTGGCAGATGTTATTCTATTCTGGTGAAGTAC 153
Db 4 CAGACAAACCCCACTCGGAGGCTGGCAGATGTTATTCTATTCTGGTGAAGTAC 63
Qy 154 GGTGAGGCGAGGACAGTACACCAACTGGAAGGCGGCACTTACGAGATCAGCTGGGGA 213
Db 64 GGTGAGGCGAGGACAGTACACCAACTGGAAGGCGGCACTTACGAGATCAGCTGGGGA 123
Qy 214 GATGCGGTAACTCTGCTGTGGAAGAGGCTGGAACCCCGCTGGAACGCAAGACCAATC 273
Db 124 GATGCGGTAACTCTGCTGTGGAAGAGGCTGGAACCCCGCTGGAACGCAAGACCAATC 183
Qy 274 CACTTTGAGGGTGTTCACCAACCAACGGAACGCTACTCTTGGTGGTGAAGGCTGAC 333
Db 184 CACTTTGAGGGTGTTCACCAACCAACGGAACGCTACTCTTGGTGGTGAAGGCTGAC 243

QY 334 CGCAACCCGCTGGTGCAGTATTACATTCGTGAGAACTTTGGCACTGATCTTCCTCC 393
DB 244 CGCAACCCGCTGGTGCAGTATTACATTCGTGAGAACTTTGGCACTGATCTTCCTCC 303
QY 394 GGTGCTACCGATCTNAGAACTGTGACGTCGACGGTAGCATTTATGCACTCGGCAAGAC 453
DB 304 GGTGCTACCGATCTNAGAACTGTGACGTCGACGGTAGCATTTATGCACTCGGCAAGAC 363
QY 454 ACTGCGTCAACGCACTAGCATTCGACGGCAACCCAACTTTCGACCAATATCGTGGCTC 513
DB 364 ACTGCGTCAACGCACTAGCATTCGACGGCAACCCAACTTTCGACCAATATCGTGGCTC 423
QY 514 CGCCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 573
DB 424 CGCCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 483
QY 574 CGCGCTGTTGTAATGTCAACGGTGAACCACTTACCAAGATGTTGCAACGAGGGCTAC 633
DB 484 CGCGCTGTTGTAATGTCAACGGTGAACCACTTACCAAGATGTTGCAACGAGGGCTAC 543
QY 634 TTGACAGCGGCTATGCTTCGATCAACCGTGTGACGTGGC 675
DB 544 TTGACAGCGGCTATGCTTCGATCAACCGTGTGACGTGGC 585

RESULT 4
LOCUS TLU35436 2460 bp DNA linear PLN 15-NOV-2001
DEFINITION Thermomyces lanuginosus endo-beta-1,4-D-xylanase precursor (xyna)
ACCESSION U35436
VERSION U35436
KEYWORDS U35436.1 GI:2737877

SOURCE
ORGANISM Thermomyces lanuginosus
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
1 (bases 1 to 2460)
REFERENCE
AUTHORS Schlacher, A., Holzmann, K., Hayn, M., Steiner, W. and Schwab, H.
TITLE Cloning and characterization of the gene for the thermostable
xylanase xyna from Thermomyces lanuginosus
J. Biotechnol. 49 (1-3), 211-218 (1996)
JOURNAL
PUBMED 8879171
2 (bases 1 to 2460)
REFERENCE
AUTHORS Schlacher, A., Holzmann, K., Hayn, M., Steiner, W. and Schwab, H.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1995) Institute of Biotechnology, SFB
Biocatalysis, TU-Graz, Petersgasse 12, Graz 8010, Austria
FEATURES
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969..976
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/note="determined by homology"
2106
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polyA_site

ORIGIN

Query March 82.8%; Score 559; DB 15; Length 2460;
Best Local Similarity 86.4%; Pred. No. 5.6e-106;
Matches 675; Conservative 0; Mismatches 0; Indels 106; Gaps 1;

QY 1 ATGTCGCGCTTTACCCCGGTGACCTTGCGGCTTACCGCGACTGGGGCCCTGGCTTC 60
DB 1065 ATGTCGCGCTTTACCCCGGTGACCTTGCGGCTTACCGCGACTGGGGCCCTGGCTTC 1124
QY 61 CGGCGAGGAAATGCCACGAGACTCGAAAAGCGACAGACACCCCACTCGAGGGCTGG 120
DB 1125 CGGCGAGGAAATGCCACGAGACTCGAAAAGCGACAGACACCCCACTCGAGGGCTGG 1184
QY 121 CACGATGTTATTTACTATTCCTGCTGAGTACGCTGAGAGGCGACCGTACCAAC 180
DB 1185 CACGATGTTATTTACTATTCCTGCTGAGTACGCTGAGAGGCGACCGTACCAAC 1244
QY 181 CTGGAAGCGGCACTACGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAG 240
DB 1245 CTGGAAGCGGCACTACGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAG 1304
QY 241 GGTGGAACCCCGGCTGAACGCA----- 264
DB 1305 GGTGGAACCCCGGCTGAACGCAAGGATCGTCCCAAGAGATACCAATAGTA 1364
QY 265 ----- 264
DB 1365 ATCCGTCGCGTTGATTTGAATCGTTGAACCTTCTCACCCCAACGAGTACGTACC 1424
QY 265 -----AGAGCCATTCACCTTTGAGGGGTGTTTACGAGCCAAACGCAACAGTACCT 314
DB 1425 TGTATGATGACAGACCATTCACCTTTGAGGGGTGTTTACGAGCCAAACGCAACAGTACCT 1484
QY 315 TGGGCTTACGCTTGAACCCGCGCAACCCGCTGGTGAATTTACATGCTGAGAACTTTGG 374
DB 1485 TGGGCTTACGCTTGAACCCGCGCAACCCGCTGGTGAATTTACATGCTGAGAACTTTGG 1544
QY 375 CACCTATGATCTTCTCTCCGGTGTACCGATCTTGAACCTGTGAGTGGCCAGCTAGCAT 434
DB 1545 CACCTATGATCTTCTCTCCGGTGTACCGATCTTGAACCTGTGAGTGGCCAGCTAGCAT 1604
QY 435 CTATGACTCGGCAAGACCACTCGCTGCAACGCACTAGTACGAGCAACCAACCTT 494
DB 1605 CTATGACTCGGCAAGACCACTCGCTGCAACGCACTAGTACGAGCAACCAACCTT 1664
QY 495 CGAACCAATATCTGTCGTCGCGCAGACCAAGCGCAACGCGTACCGTACGAGCGGCTG 554
DB 1665 CGAACCAATATCTGTCGTCGCGCAGACCAAGCGCAACGCGTACCGTACGAGCGGCTG 1724
QY 555 CCACTTGAACGCTGGGCTGGGCTGGTGTGAATGTCAACGCTGACCACTTACACGAT 614
DB 1725 CCACTTGAACGCTGGGCTGGGCTGGTGTGAATGTCAACGCTGACCACTTACACGAT 1784
QY 615 CGTTGCAACGAGGGCTACTTACAGAGGGCTATGCTGCATCACCGTTGCTGACGTGG 674
DB 1785 CGTTGCAACGAGGGCTACTTACAGAGGGCTATGCTGCATCACCGTTGCTGACGTGG 1844
QY 675 C 675
DB 1845 C 1845

RESULT 5
BX842624/c 89019 bp DNA linear PLN 17-APR-2005
LOCUS Neurospora crassa DNA linkage group I BAC clone B10D6.
DEFINITION BX842624
ACCESSION BX842624
VERSION BX842624.1 GI:38566913
KEYWORDS
SOURCE Neurospora crassa
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE
AUTHORS 1 Schulte,U., Aign,V., Hoheisel,J., Brandt,P., Partmann,B.,
Holland,R., Nyakatura,G., Mewes,H.W. and Mannhaupt,G.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 89019)
AUTHORS German Neurospora genome project.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-2003) MIPS, Institut fuer Bioinformatik,
Gef-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,
Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:
G.Mannhaupt@gef.de Project Coordinator: Ulrich Schulte, Institute
of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,
E-mail: ulrich-schulte@uni-duesseldorf.de
BAC clone 10D6 (strain OR74A) is available at the Fungal Genetic
Stock Center, http://www.fgsc.net
Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
http://www.mwgdna.com
Information on performance of analysis and a more detailed
annotation of this entry and other sequences can be viewed at:
http://mips.gsf.de/proj/neurospora.
FEATURES
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exon
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14173.. 14195, 14433.. 14924, 14995.. 15128, 15186.. 15281,
15411.. 15458)
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15411.. 15458)
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gene:CG11008, Drosophila melanogaster, TREMBL:AE003540_19"
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QKSGQFAPAPAPAPITLHTCTETSHAPIFQPTSHPTPPTRLPLHCRKRYKTDIA
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Query Match 38.9%; Score 262.4; DB 15; Length 89019;
Best Local Similarity 65.3%; Pred. No. 1.7e-44;
Matches 418; Conservative 0; Mismatches 216; Indels 6; Gaps 2;

24 CTTGCGGCTTAAGCCGGACTGGGGCCCTTGCCGCGAGGAATGCCAGAGACT 83
39342 CCTCCTCGGCGCTGCGCGGTGCTGTATGCTCCCTTCAACGCCACCGAGTTCCTGAGCT 39283
84 CGAAAGGACAGACACCCCAACTCGAGAGCTCGGACAGATGTTATTAATCTCTG 143
39282 CGCCAGGCTGAGCGGTACCCCAAGACAGACCGGCTTCAACACGCTTACTACTCTT 39223
144 GTGAGTGACCGGTGAGCGGACAGCACTACCAACCACTGGAAGCGGCACTACGAGAT 203

Db 39222 CTGACCGAACAACGCGGCAATGTCACCTACGCAACGCGCGGCGGCTTACTCTGT 39163
Qy 204 CAGCTGGGAGATGCGGTAACTCTGTCGTGGTGAAGAAGGCTGGAACCCCGGCTGAAAGC 263
Db 39162 GAACCTGGCAAGAACCGCGCAACTTGTGCGCGGAAGGCTGGAAACCCCGTTG---GC 39106
Qy 264 AAGACCATCACTTGAAGGGTGTTTTACAGCCAAACGGCAACGATACCTTGGGCTCTA 323
Db 39105 TCGCAACATCACTACTCGGTAACCTTACAGACCTCGGCGCAACGGCTACTCTGCTCTA 39046
Qy 324 CGTTTGAACCCGCAACCCGCTGTCAGATATTACATGTCGAGAACTTTGGACCTTATGA 383
Db 39045 CGGCTGACCTGCAACCCGCTTTCAGTACTAGTGTGAGAACTTTGGCTCTTACAA 38986
Qy 384 TCTTCTCGGTGCTACCATCTAGGAATCTGTGAGTGGACGCTAGCATTTTCACT 443
Db 38985 CCTTTCGTGGGCGCCCAAGCTTCGATCGCTTACACGACGCTCCACCTTCGACAT 38926
Qy 444 CGGCAAGCACTGCGCTTCAACGCACTTACATGACGCGCAACCCAACTTCGACCAATA 503
Db 38925 CTAAAGACCAACCGCTTCAACACGCGCTTCATTTAGCGCACCCGCACTTCAACAGTA 38866
Qy 504 CTGTCGTGTCGCGCAGACCAAGCGCAACGCGTACCGTCCAGACGCGCTGCCACTTGA 563
Db 38865 CTGGTCGCTGCGCAGCAGAAAGCGCACCGGTGTACCGTCAACATGGCAACCACTTCAA 38806
Qy 564 CGCTGGGCTCGCGCTGCTTTGAATGTCAACGCTGACCACTACTACAGATCTTGCAC 623
Db 38805 CGCTGGGCGCAAGGCTGCGCTGCA---CTGGGCAACCAACATCAAGATCGTGGCAC 38749
Qy 624 GAGGCGTACTTTCAGCAGCGGCTATGCTCGCATCACCGTT 663
Db 38749 TGAAGATACCAAGACGATGCTTGGCCAGATCACGTT 38709

RESULT 6
TRU24191
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

TRU24191 786 bp mRNA linear PLN 25-MAR-1997
Trichoderma reesei beta-xylanase (XYN2) mRNA, complete cds.
U24191.1 GI:780815

Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 786)
la Grange, D.C., Pretorius, I.S. and van Zyl, W.H.
Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
Saccharomyces cerevisiae
Appl. Environ. Microbiol. 62 (3), 1036-1044 (1996)
8975597
2 (bases 1 to 786)
van Zyl, W.
Direct Submission
Submitted (06-APR-1995) Willem H. van Zyl, University of
Stellenbosch, Microbiology, Victoria Street, Stellenbosch, 7600,
South Africa

FEATURES
source
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105..776
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/codon_start=1
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/protein_id="AB50278.1"
/db_xref="GI:780816"

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mat_peptide 204..773
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/product="beta-xylanase"

ORIGIN

Query Match 36.1%; Score 243.6; DB 15; Length 786;
Best Local Similarity 61.7%; Pred. No. 2.1e-40;
Matches 406; Conservative 0; Mismatches 249; Indels 3; Gaps 1;
QY 5 TCGGCTTAAACCCCGCTTGCCCTTGAAGCCGACCTGGGGCCCTTGCCCTTCCCGG 64
DB 115 TCACCTCCCTCCTCGCCGCGCTCGCCCATCTCGGGCGTCTTGCGCTCCGCGCGG 174
QY 65 CAGGGAATGCCAGGAGCTCGAAAAGGACAGACAAACCCCACTCGGAGGGCTGGACG 124
DB 175 AGGTGAAACCGGTGCTGTGAGAAAGCCCAAGATTCAGCCGCGACGGGCTTACAA 234
QY 125 ATGGTTATTACTTATTCCTGTGTGAGTGAAGCGGTGAGCGACGACGTAACCAACTGG 184
DB 235 ACGGCTACTTCACTCGTACTGTAAGAAAGATGCGACGGGGGGGTGACGTAACCAATGGTC 294
QY 185 AAGCGGCACTTACAGATTCAGCTTGGGAGATGGCGGTACCTGCTGCTGGTGGAAAAGGGCT 244
DB 295 CCGGCGGGCAGTCTCCGTCACCTGTGTCAACTCGGGCAACTTTGTGCGCGGCAAGGAT 354
QY 245 GGAACCCCGGCGCTGAAGCAAGAGCCATCCACTTTGAAGTGTATTACCAAGCCAAAGGCA 304
DB 355 GCGACGCCGGAACCAAGAACAGGTCAATCACTTCGCGGACGTAACAACCCCAAGGCA 414
QY 305 ACAGCTACTTTCGCGTCTACGCTTGAAGCCCGCAACCCGCTGATGAGTATTATTCGTCG 364
DB 415 ACAGTACTCTCGGTGTACGAGCTGTGTCCCGCAACCCCTGATGAGTACTACATCGTCG 474
QY 365 AGAATTTTGGCACTTATGATCTTCTCGGTGTCAACCGATCTAGGAACCTGCAAGTGGC 424
DB 475 GGAATTTTGGCACTTACAAACCGGTCAAGGGGGCCCAAGCTGGGCGAGGTCACTTCG 534
QY 425 ACGGATGATCTATGATCTCGGCAAGACCACTCGGCTCAACGACCTAGATTCAGGCA 484
DB 535 ACGGACGCTGTACGACATTTTACCGACGCAAGCGGTCAACGACCTGATCATCGGCA 594
QY 485 CCCAAACCTTGCACCAATATCTGTGCGTCCGCGCAAGACGCAACGCGGTACCGTCC 544
DB 595 CCGGCACTTTTACAGATTAAGTGTCCGTCCGCGCAACCGCTCGAGCGGCTCCGTCA 654
QY 545 AGACGGGCTGCCACTTTCAGACGCTGGGCTCGGCGCTGGTTTGAATGTCAACGTTGACACT 604
DB 655 ACACGGCAACCACTTCAACGCGGTGCTCAAGCAAGGCGCTGACGCT---CGGAGAGATGG 711
QY 605 ACTACCAAGTGGTTCAGACGAGGGCTACTTCAGACGAGGCTATCTGCACTACCGT 662
DB 712 ATTACCAAGTGTGTCCGCTGAGGGTTACTTTAGCTTGGCTCTGCTTCATCAACCGT 769

RESULT 7
LOCUS H1XYL1 1039 bp mRNA linear PLN 18-APR-2005
DEFINITION H. insolens XYL1 mRNA for endoglucanase.
ACCESSION X76047
VERSION X76047.1 GI:505260
KEYWORDS endoxylanase; xyl1 gene.
SOURCE Humicola insolens
ORGANISM Humicola insolens
REFERENCE 1 (bases 1 to 1039)
AUTHORS Dalboege,H. and Hansen,H.P.H.

TITLE A novel method for efficient expression cloning of fungal enzyme
JOURNAL Genes
PUBMED Mol. Gen. Genet. 243 (3), 253-260 (1994)
8190078
REFERENCE 2 (bases 1 to 1039)
AUTHORS Dalboege,H.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1993) H. Dalboege, Manager GeneExpress, Novo
Nordisk A/S, Sydbroen, Fruelervej 3, 2100 Copenhagen OB, DENMARK
FEATURES
source location/Qualifiers
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ORIGIN

Query Match 35.6%; Score 240.6; DB 15; Length 1039;
Best Local Similarity 64.6%; Pred. No. 8.4e-40;
Matches 392; Conservative 0; Mismatches 209; Indels 6; Gaps 2;

QY 57 CTTCGCGGCAAGGAAATGCAACGAGCTCGAAAAGCGACAGAACCCCAACTCGAGGG 116
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QY 117 CTGGCAGATGTTATTACTATTCCTGTGAGTGAAGCGGTGAGCGGACGACGTACAC 176
DB 178 CTGGCAACAAGGCTACTTCTACTCTGTGTGTGTCGACGCGGAGGACGAGTTCACTACAC 237
QY 177 CAACCTGGAAGCGGCACTTACAGATCAGCTGGGAGATGCGGCTAACCTGTCGTGG 236
DB 238 CAACCTGGAAGGCGGCTTACAGATCAGTGTGAGTGAACCGGCAACTTCGTGCGTGG 297
QY 237 AAAGGGCTGGAACCCCGGCGTGAAGCGCAAGGCAATCACTTGAAGGTGTTTACAGCC 296
DB 298 TAAAGGTTGGAACCCGAG--AACCGGCGGACATCAACTACGCGGCTACTTCAACC 354
QY 297 AAAGGCAACGACTACCTTGGGCTTACGCTTGAACCGCAACCGCGTGTGAGATTA 356
DB 355 CCAAGGCAAGGCTTACCTGCGCGCTACAGGTGACACCGGCAACCGGCTCGTCAAGTACTA 414
QY 357 CATGTGAGAACTTTGGCACTTATGATCTTCTCGGTGCTACCAATCTTAGAACTGT 416
DB 415 TGTCAATGAGTGTGACGCAAGTACCAATCCCGGACGAGGCTAGTCAAGGGGACATT 474
QY 417 CGAGTGGAGGTTGACATCTATGACTCGGCAAGCACTGCGGTCAACGCACTAGCAT 476
DB 475 CTATACCAAGGCGCAATCAGTATGACATTTTGTGAGCACCCGCTTACACAGCCAGCAT 534
QY 477 CGAGGCAACCAACTTTCGACCAATATCTGTGCGGTCCGCGGAGGACAGCGCACCGGCG 536
DB 535 CGAGGCAACCGGCACTTTCGACGAGTACTGTCTATCGGCAAGAAAGCGGTGCGAGG 594
QY 537 TACGTCAGACGAGGCTGCCACTTTCAGACGCTCGGAGCTCGCGCTGTTGAATGTCAACG 596

Db 595 CTCGGTCAACATGCAAGAACCACTTCAAGCCGTGGAGAGACGACCGGAATGCCGCT---CGG 651
Qy 597 TGACCACTACTACCAAGATCGTTTGCAACGAGGCGTACTTCAAGCGGCTATGCTCGCAT 656
Db 652 CCAGCACTACTACCAAGGTCGTCCGACCGAGGCGTACAGAGCATGTGCGAGTCCGACAT 711
Qy 657 CACCGTT 663
Db 712 CTATGTT 718

RESULT 8
LOCUS 165436 1123 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5667990.
ACCESSION 165436
VERSION 165436.1 GI:2482006
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1123)
AUTHORS Berka, R., Michael, J., Yoder, W., Takagi, S. and Boomlathnan, K. Chettler.
TITLE Aspergillus expression system
JOURNAL Patent: US 5667990-A 3 16-SEP-1997;
FEATURES
Source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 35.4%; Score 239; DB 6; Length 1123;
Best Local Similarity 64.4%; Pred. No. 1.8e-39;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

57 CTTCCCGGAGGAGATGCGACGAGCTCGAAGAGGACAGCAACCCCACTCGAGAGG 116
Db 197 CGTTCCTCGGAGCACTGACGCGCCCTTCAAGCTCGACAGGTGACCCCAACGCGAGAGG 256
Qy 117 CTGGCAGCATGTTATTAATTCCTGCTGAGTGAAGTGAAGTGAAGCGGACGACGTAAC 176
Db 257 CTGGCAGCAACGCGTACTTCTAATCGTGTGTCGACAGCGCGGAGCGGAGTTCAGTACAC 316
Qy 177 CAACCTGGAAGCGGCGACCTACAGAGATAGCTGGGAGATGCGGTAACTCTGCTGCTG 236
Db 317 CAACCTCGAGGCGACGCGCTACAGGTCAAGTGGGTAAACCGGCAACTTCTGCTGCTG 376
Qy 237 AAAGGCTGGAACCCCGGCTGAAGCGAAGCCATCACTTTGAGGGTGTTCACAGCC 296
Db 377 TAAAGGTTGAAACCCGGG---AACCGCGCGACAGTCACTACGCGGCTACTTCAACCC 433
Qy 297 AAAGCGCAACAGTACTCTTGGGCTTACGTTTGAACCGCAACCGGCTGCTGAGTATTA 356
Db 434 CCAAGGCAACGCGTACTTCTGCGCTTACGCTGAGACCGGCAACCGGCTGCTGAGTACTA 493
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Db 494 TGTCACTCAAGTCTGACGCACTGTAACATCCCGGACGCGAGGCTAGTACAGGGCACATT 553
Qy 417 CGAGTGGCAGGATGATCTATTCAGCTGGGAGCACTGCGGCTCAACGCAAGCACTAGAT 476
Db 554 CTATACCGACGCGATCAGTATGACATTTTGTGAGCACCGGCTACCAACGACCGCAT 613
Qy 477 CGAGCGCAACCAACCTTGAACATATCTGCTGCTGCGGACGAGCAAGCGCACAGCGG 536
Db 614 CGAGGCAACCGGAGCTTCAAGCACTATGATCTATCGCAAGAAAGAGGTGTCGAGG 673
Qy 537 TACGCTCAAGACGGGCTGCTGAGAGCTTGGGCTGCGGCTGTTGAATGTCACAG 596
Db 674 CTCGCTCAACATGCAAGAACCACTTCACGCTGGGAGAGCAAGCAAGTATGCGGCT---CGG 730
Qy 597 TGACCACTACTACCAAGATCGTTTGCAACGAGGCGTACTTCAAGCGGCTATGCTCGAT 656

Db 731 CCAGCACTACTACCAAGTCTCTCGCAACGAGGCTACAGAGCATGTGCGAGTCCGACAT 790
Qy 657 CACCGTT 663
Db 791 CTATGTT 797

RESULT 9
LOCUS BD006885 1123 bp DNA linear PAT 31-JAN-2002
DEFINITION Aspergillus expression system.
ACCESSION BD006885
VERSION BD006885.1 GI:18635256
KEYWORDS JP 2001025393-A/2.
SOURCE Humicola insolens
ORGANISM Humicola insolens
REFERENCE 1 (bases 1 to 1123)
AUTHORS Berka, R.M., Yoder, W., Takagi, S. and Boomlathnan, C.C.
TITLE Aspergillus expression system
JOURNAL Patent: JP 2001025393-A 2 30-JAN-2001;
COMMENT
NOVO NORDISK BIOTECH INC
OS Humicola insolens
PN JP 2001025393-A/2
PD 30-JAN-2001
PF 17-MAY-2000 JP 2000185449
PR 01-DEC-1993 US 08/161675
PI RANDY M BERKA, MENDY YODER, SHINOBU TAKAGI,
PI CARAPAPAN CHELYER BOOMINAZAN
PC C12N15/09, C12N1/15, C12P21/02// (C12N15/09, C12R1:66), (C12N15/09,
PC C12R1:685)
PC (C12N15/09, C12R1:69), (C12N1/15, C12R1:66), (C12P21/02, C12R1:66),
PC C12N15/00,
PC (C12N15/00, C12R1:66), (C12N15/00, C12R1:685), (C12N15/00, PC
C12R1:69)
CC
FH Key Location/Qualifiers
FT CDS (126)..(806).

ORIGIN
Query Match 35.4%; Score 239; DB 6; Length 1123;
Best Local Similarity 64.4%; Pred. No. 1.8e-39;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

57 CTTCCCGGAGGAGATGCGACGAGCTCGAAGAGGACAGCAACCCCACTCGAGAGG 116
Db 197 CGTTCCTCGGAGCACTGACGCGCCCTTCAAGCTCGACAGGTGACCCCAACGCGAGAGG 256
Qy 117 CTGGCAGCATGTTATTAATTCCTGCTGAGTGAAGTGAAGTGAAGCGGACGACGTAAC 176
Db 257 CTGGCAGCAACGCGTACTTCTAATCGTGTGTCGACAGCGCGGAGCGGAGTTCAGTACAC 316
Qy 257 CTGGCAGCAACGCGTACTTCTAATCGTGTGTCGACAGCGCGGAGCGGAGTTCAGTACAC 316
Db 177 CAACCTGGAAGCGGCGACCTACAGAGATAGCTGGGAGATGCGGTAACTCTGCTGCTG 236
Qy 317 CAACCTGGAAGCGGCGACCTACAGAGATAGCTGGGAGATGCGGTAACTCTGCTGCTG 376
Db 177 CAACCTGGAAGCGGCGACCTACAGAGATAGCTGGGAGATGCGGTAACTCTGCTGCTG 236
Qy 317 CAACCTGGAAGCGGCGACCTACAGAGATAGCTGGGAGATGCGGTAACTCTGCTGCTG 376
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Qy 177 CAACCTGGAAGCGGCGACCTACAGAGATAGCTGGGAGATGCGGTAACTCTGCTGCTG 236
Db 317 CAACCTGGAAGCGGCGACCTACAGAGATAGCTGGGAGATGCGGTAACTCTGCTGCTG 376
Qy 297 AAAGCGCAACAGTACTCTTGGGCTTACGTTTGAACCGCAACCGGCTGCTGAGTATTA 356
Db 377 TAAAGGTTGAAACCCGGG---AACCGCGCGACAGTCACTACGCGGCTACTTCAACCC 433
Qy 237 AAAGGCTGGAACCCCGGCTGAAGCGAAGCCATCCTTTGAGGGTGTTCACAGCC 296
Db 377 TAAAGGTTGAAACCCGGG---AACCGCGCGACAGTCACTACGCGGCTACTTCAACCC 433
Qy 297 AAAGCGCAACAGTACTCTTGGGCTTACGTTTGAACCGCAACCGGCTGCTGAGTATTA 356
Db 614 CGAGGCAACCGGAGCTTCAAGCACTATGATCTATCGCAAGAAAGAGGTGTCGAGG 673
Qy 537 TACGCTCAAGACGGGCTGCTGAGAGCTTGGGCTGCGGCTGTTGAATGTCACAG 596
Db 674 CTCGCTCAACATGCAAGAACCACTTCACGCTGGGAGAGCAAGCAAGTATGCGGCT---CGG 730
Qy 597 TGACCACTACTACCAAGATCGTTTGCAACGAGGCGTACTTCAAGCGGCTATGCTCGAT 656

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|----|--|-----|
| Qy | CGAGTGGGAGGGGTGAGCATCTATTCAGCTCGGCAAGACACTGGCGTCAACGCACTAGCAT | 476 |
| | | |
| Db | CTATACCGACGGCCGATCAGTATGACATCTTTGTGTAGCACCCGCTACAAACGACCCAGCAT | 613 |
| | | |
| Qy | CGACGGCACCCMAACTTTCGACCAATACTGTGTGGTTCGGCAGGACAAAGCGCACACGG | 536 |
| | | |
| Db | CGACGGCACCCGAGCTTCCAGCAGTACTGTGTCTTTCGGCAAGAACAAAGCGTGTCCGAGG | 673 |
| | | |
| Qy | TACCGTCGAGACGGGCTGGCACTTCGAGCCCTGGGCTGGCGCTGTGATGTCAACGG | 596 |
| | | |
| Db | CTGGGTCAACATGCAAGACCACTTCAACGGCTGGGACGACGACCGGAATGCCGCT---CGG | 730 |
| | | |
| Qy | TGACCACTACTACAGATCGTTGCACGAGAGGCTACTTCAAGCAGCGGCTATGTCCGAT | 656 |
| | | |
| Db | CCAGCACTACTACAGATCGTTCGCCACGAGGGCTAACAGAGCAGTGGCGAGTCGACAT | 790 |
| | | |
| Qy | CACGGTT 663 | |
| | | |
| Db | CTATGTT 797 | |

| RESULT 10 | | | | | |
|------------|-------------|-------------|---------------------------------|--------|-----------------|
| AY156910 | AY156910 | 841 bp | mRNA | linear | PLN 11-DEC-2002 |
| LOCUS | Trichoderma | sp. | SY xylanase mRNA, complete cds. | | |
| DEFINITION | AY156910.1 | GI:26514829 | | | |
| ACCESSION | | | | | |
| VERSION | | | | | |

SOURCE ORGANISM

| REFERENCE | AUTHORS | TITLE |
|--------------------|--|---|
| 1 (bases 1 to 841) | Min, S.-Y., Kim, B.-G., and Ahn, J.-H. | Purification, Characterization, and cDNA Cloning of Xylanase from Fungus <i>Trichoderma Strain SY</i> |

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 841)
 AUTHORS Min.S.Y., Kim,B.G. and Ahn,J.-H.
 TITLE Direct Submission
 JOURNAL Submitted (30-SEP-2002) Forest and Environmental Science, Konkuk University, 1 Hwayang-Pong, Kwangjin-Gu, Seoul 143-701, South Korea
 FEATURES Location/Qualifiers
 SOURCE 1. 841

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ORIGIN

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| Query Match | 34.2%; | Score 230.8; | DB 15; | Length 841; |
| Best Local Similarity | 60.8%; | Pred. No. 9.3e-38; | | |
| Matches 395; | Conservative | 0; | Mismatches 252; | Indels 3; |
| | | | | Gaps 1 |

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| Qy | 24 | CCTTGC | CGCTT | AGCCG | CACTGG | GGCCCT | CTGAC | CTTCC | GGCAG | GGATGCC | ACGAG | CT | 83 |
| Db | 80 | CTTCC | CGGCTT | TGGCG | CTGTG | CCGAG | CTCTG | TCTTAC | TGAAG | AGGTCA | CACT | 139 | |
| Qy | 84 | CGAAA | AGCG | CAGACA | CCCCA | CTCG | AGGG | CTTG | CGATG | GTATT | TACTAT | TCTG | 143 |
| Db | 140 | CGAAA | AGCG | CTAG | GTCTAT | TGGCC | CGGCA | CTGG | CTTCA | CAACG | GGTTAC | TACTAC | 199 |

| | | | |
|----|-----|---|-----|
| OY | 144 | GTGAGTGAACGATGGAACCGACGGCACGTACCAACCTTGAAAGGCGGCACCTACAGAT | 203 |
| Db | 200 | CTGGAACGACGGCCATCCCGCGGTGATTTACCAACGAGCGGTGGCGGGTGTCAACGT | 259 |
| OY | 204 | CAGCTGGGAGATGGCGGTAACTCTGTCGGTGGAAAGGGCTGGAAACCCCGGCTGAACGC | 263 |
| Db | 260 | CAACTGGGCGCAACTCGGGCAACTTTGTGGAGGCGAAGGATGGAAACCCGGGCAAGACAC | 319 |
| OY | 264 | AAGAGCATCACTTTAGAGGGGTGTTTACGAGCCAAACGGCAACAGTACCTTGGCGGTCTA | 323 |
| Db | 320 | CAGAACCATCACTTCTCCGGCAGCTACAGCCCAAGAACAGCTACCTCTCCGTCTA | 379 |
| OY | 324 | CGGTTGGAACCCGCAACCCCGCTGGTGGAGTATTAATCTGTGAGAACTTTGGCACTTATGA | 383 |
| Db | 380 | CGGCTGGCTCAAGAAACCCGCTCACTGAGTACTAATATGTGAGAACTTTGGCACTTCAAA | 439 |
| OY | 384 | TTCCTTCCCTCGGATGCTACCGATCTAGAGAACTGTGAAGCGACGGTATGATCTATGACAT | 443 |
| Db | 440 | CCCGTCAAGGCGCGCACACAGCTGGGCGAGGTACGCTGACGGCAGCGCTTACGACAT | 499 |
| OY | 444 | CGGCAAGACCACTCGGTCAAACGCACTGACATGACGCGCACCCAAACTTTGACCAATA | 503 |
| Db | 500 | TTACCGCACGACGAGCGGTCAAACGCGGTCCATCATCGGCAACCGCACCTTTTACCAATA | 559 |
| OY | 504 | CTGATCGGTCCGCGACAGAACAAAGCGCACAGCGGTACCGTCCAGACGGGCTGCCACTTGA | 563 |
| Db | 560 | CTGGTCGGTGGCGCGACGCAACCGCTCCAGGGGCTCGGTCAACGTGGCAACCACTTCA | 619 |
| OY | 564 | CGCCTGGGCTCGCGCTGGTTGAAATGTCAACGATGACCACTACCAAGATCGTTGCAAC | 623 |
| Db | 620 | TGCGTGGGCAATCTCGGCTGACGCT---GGACAGGTGATCAACAGATTAATTTGCGGT | 676 |
| OY | 624 | GAGGGGCTACTTTCAGACAGCGGTATGCTCGATACAGCTGTCTACCGTG | 673 |
| Db | 677 | GAGGGGATATTTCAGCTCTGGCAACGGCCAAATTTAAGTCAAGTAAAGTGG | 726 |

| | |
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| RESULT 11 | |
| AY320048 | AY320048 |
| LOCUS | 672 bp mRNA linear PLN 14-JUL-2003 |
| DEFINITION | Trichoderma viride strain YNCC0183 endo-1,4-beta-xylanase mRNA, |
| | complete cds. |
| ACCESSION | AY320048 |
| VERSION | AY320048.1 GI:32481056 |
| KEYWORDS | |
| SOURCE | Trichoderma viride |

| ORGANISM | Trichoderma viride |
|---|--------------------|
| Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes | |
| Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; | |
| Trichoderma; Trichoderma viride species complex. | |
| 1 (bases 1 to 672) | |

REFERENCE

| AUTHORS | TITLE |
|---|---|
| Li, W. P., Zhang, Q., Liao, C. L., Zhou, J. G., Yang, Y. H., Liu, W. J. and Yang, Z. W. | Cloning and characterization of endo-1,4-beta-xylanase from <i>Trichoderma viride</i> YN00C0183 |

JOURNAL
REFERENCE
AUTHORS

2 (bases 1 to 672)
Li, W.P., Zhang, Q., Liao, C.L., Zhou, J.G., Yang, Y.H., Liu, W.J. and Yang, Z.W.

TITLE Direct Submission
JOURNAL Submitted (10-JUN-2003) Key Laboratory of Industrial Microbiology & Fermentation Technology of Yunnan, School of Life Science, Yunnan University, 2 North Road, Green Lake, Kunming, Yunnan 650091, China
FEATURES Location/Qualifiers

FEATURES

Source

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ORIGIN

Query Match 33.8%; Score 228.2; DB 15; Length 672;
Best Local Similarity 60.6%; Pred. No. 3.3e-37;
Matches 393; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

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15  CCCCCTGACCTTCGCGGCTTAGCCGCGGACTGGGCCCCCTCCCGGCGAGGAGTGC 74
Db  CTTGCGCGGCTTCGTGCTGTTACCGAGTCTCTGCTCCCACTGAGAACGTGAGGT 80
Qy  75  CACGAGCTCGAAAAGCAGACAAACCCCACTCGAGGGCTGCGACGATGTTATTA 134
Db  81  CGTGGAGGTGAGAAAGGCCAGACGATTTGGCCCGGCACTGGCTTCAACACGCTACTA 140
Qy  135  CTATTCCTGGTGAAGTACGCTGAGCGCAGCGCACTGACCAACCTGAAAGCGGCAC 194
Db  141  CTACTCGTACTGGAACGATGGCCATTCCGCGCTGACATACCAACGCTGCTGGCGCTC 200
Qy  195  CTACGAGATACGCTGGGAGATGGCGGTACCTGTCGCTGGAAGAGGCTGGAACCCCGG 254
Db  201  ATTACGCTCACTGGGCAAACTCGGCGCACTTGTGGAAGGCAAGGATGGAACCCCGG 260
Qy  255  CCTGAACGCAAGACCACTCCACTTTGAGGAGTGTATACAGCAACCAACAGCTACT 314
Db  261  CAGAGCTCCAGGGTCACTCACTTCTGCGAGCTACCAACCCCAAGCGCACTAGCTACT 320
Qy  315  TGGCGTCTACGCTTGAACCCGCAACCGCTGCTGAGTATTATCACTGTCGAACTTTGG 374
Db  321  CTCAGTCTATGGCTGTCGCAAGAAACCTCTCATGAGTACTACCTGTTGAGAACTTTGG 380
Qy  375  CACCTATGATCTCTCCGCGTGTACCGATCTAGAACTGTGAGTGGCGACCGTTACAT 434
Db  381  AACCTACACCCATCGACCGGACACCAACGCTGGGCGAGGTGACCTCTGACGGCAGCT 440
Qy  435  CTATGACTCGGCAAGACCACTCGCGTCAACGCACTAGACTGACGGGCAACCAACCTT 494
Db  441  CTACGACATCTACCGGACGACGACGATCAACACCTTCACTATCGAAACCGCACTT 500
Qy  495  CGACCAATACTGTCGTGCTCGCGCAGAACAGCGGACGAGCTGTCACAGCGGCTG 554
Db  501  TTACCACTACTGTCGTGCTCGCGCAGAACACCGCTCCAGCGGCTCGGTCAAGGTTGGA 560
Qy  555  CCACTTGAGAGCGCTGGGCTGCGGCTGTTGAATGTCAACGCTGACCACTACTACGAT 614
Db  561  CCACTTGAGAGCGGCTGGGCAACCTGGGCTTGA---CCCTGGAAACCTTGGACTACGAT 617
Qy  615  CGTTGCAACGAGGCTACTTACAGACGAGGCTATGCTCGATCAACGCTT 663
Db  618  CATTGCGGTGAGGCTACTTACCTGCTGTTACGCGCAACATTACGTT 666

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RESULT 12
AF246830 2202 bp DNA linear PLN 20-FEB-2002
LOCUS Fusarium oxysporum f. sp. lycopersici xylanase 5 protein (xyl5)
DEFINITION gene, complete cds.
ACCESSION AF246830
VERSION AF246830.1 GI:13491872
KEYWORDS
SOURCE Fusarium oxysporum f. sp. lycopersici
ORGANISM Fusarium oxysporum f. sp. lycopersici
Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE
1 (bases 1 to 2202)

AUTHORS Gomez-Gomez, B., Isabel, M., Roncero, G., Di Pietro, A. and Hera, C.
TITLE Molecular characterization of a novel endo-beta-1,4-xylanase gene from the vascular wilt fungus *Fusarium oxysporum*
JOURNAL Curr. Genet. 40 (4), 268-275 (2001)
PUBMED 11795847
REFERENCE 2 (bases 1 to 2202)
AUTHORS Hera, C., Gomez-Gomez, B. and Roncero, M.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-2000) Departamento de Genetica, Universidad de Cordoba, Avda. San Alberto Magno s/n, Cordoba 14071, Spain
FEATURES
source Location/Qualifiers
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SENQPDQEDITRANPCQ"

CDS

ORIGIN

Query Match 31.8%; Score 214.6; DB 15; Length 2202;
Best Local Similarity 64.7%; Pred. No. 2e-34;
Matches 377; Conservative 0; Mismatches 159; Indels 47; Gaps 2;

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132  TTACTATTCTGTGAGTACGCTGAGCGGACGCGCACTACCAACCTGGAAGCGG 191
Db  870  TGACTTATATATGATGATGATGCGGTGCGGATGCCACTTACCAACGATGAGGAGG 929
Qy  192  CACCTACGAGATCAGCTGGGAGATGGCGGTAACTGTCGTGGAAGGCTGGAACCC 251
Db  930  TTCTTACTCATGAGATGGAAGATGGCGCAACGTGCTGATGAGGTTGCTCTC 989
Qy  252  CGGCTGAAAC-----GCAGA 267
Db  990  TGGAAAGCCCGGTATAGTACAAATAAGCTTACATGCCCCCTGCTAATACCTGTAGA 1049
Qy  268  GCCATCACTTTAGAGGATTTTACCAAGCCAAACGCAACGCTAGCTTGGGTTACGGT 327
Db  1050  ACCATCTGTACAGAGGAGATCAAGCCCAACGCAACGCTACCTCTGTCTACGGT 1109
Qy  328  TGAACCCGCAACCCGCTGCTGATATTAATGTTGAGAACTTTGGCACTATGATCCT 387
Db  1110  TGAACCCGAAACCTCTGCTGATATTAATGTTGAGAACTTTGCTTCAACACCC 1169
Qy  388  TCCTCGGATCTACCATTTAGGAATGTCGATGAGCGGTGAGCATCTATGACTCGG 447
Db  1170  TCCAGCGGTGCTACCAAGAAAGGCACTGTTAGAGCCGATGACGACCTACGACATCTTC 1229
Qy  448  AAGACCACTTCGCTCAACGCACTAGCATGACGGAACCCAACTTTCAGCAATATG 507
Db  1230  GAGACCACTGACCAACGCCCCCTTCATATGACGATACGACTTCCAGCAGTACTGG 1289
Qy  508  TCGGTCCGCAAGACCAAGCGCAGTACCTGTCACAGCGGCTGCCACTTTCAGCGC 567
Db  1290  TCTGTTCCGACAGACGACGCTTACTGAGGCTGACACGCTGCTTCAATTCGATGCC 1349
Qy  568  TGGGCTCGGCTGTTGAATGTCAACGCTGACCACTACTACAGATCTGTGCAACGAG 627

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Db 1350 TGGGAGAGGCGCGCATGAAAGCT---CGTACTCAGCACTACAGATCCTCGCTACTGAG 1406

Qy 628 GGCTACTTCAGCAGCGGCTAATGCTGCATCAGCGTGTGACG 670

Db 1407 GGTTACTTCAGCAGCGGATCTCTCCACATGACCGCTCTTGAGG 1449

RESULT 13
TVI012718

LOCUS TVI012718 928 bp mRNA linear PLN 15-APR-2005

DEFINITION Trichoderma viride mRNA for endo-1,4-beta-xylanase.

ACCESSION AJ012718.1 GI:6434132

VERSION AJ012718.1

KEYWORDS endo-1,4-beta-xylanase.

SOURCE Trichoderma viride

ORGANISM Trichoderma viride

REFERENCE 1 Fuman-Matarazo, N., Cohen, E. and Avni, A. Mutations in the Active Site of the Ethylene Inducing Xylanase Elicitor Inhibits the D-1-4-Endoxylanase Activity But Not the Elicitation Activity Unpublished

REFERENCE 2 (bases 1 to 928)

AUTHORS Avni, A.

TITLE Direct Submission

AUTHORS Submitted (10-NOV-1998) Avni, A., Plant Sciences, Tel-Aviv University, Tel-Aviv University, Tel-Aviv, 69978, ISRAEL

JOURNAL Location/Qualifiers

FEATURES

Source 1..928

CDS

1..928

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/mol_type="mRNA"

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63..734

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ORIGIN

Query Match 31.7%; Score 214; DB 15; Length 928;

Best Local Similarity 60.2%; Pred. No. 2,9e-34;

Matches 390; Conservative 0; Mismatches 255; Indels 3; Gaps 2;

Qy 15 CCCCCTTGCCTTGGCGCTTAGCCGCGACTGGGGCCTTGGCCTTCCCGGAGGGAATGC 74

Db 83 CCTCGCAGGCTTTCGCTGCTTACCGGAGTTCTGCTCCCTCCACTGAGACCGTGAAGT 142

Qy 75 CACGAGCTCGAAAAGCAGACACCCCACTCGAGGGCTGGCGACGATGTTATTA 134

Db 143 CGTGACGTGAGAAAGCCGACAGACATTTGGCCCCGCGACTGGCTTCAACAACGGCTACTA 202

Qy 135 CTATTCCTGTGAGTGAAGTGAAGCGCAGCGCAGTACCAACTGGAAGCGGAC 194

Db 203 CTACTCTTACTGGAAGATGGCATTCGGCGGTGACATACACCAACGGTGTCTGGCGCTC 262

Qy 195 CTACAGATCAGCTGGGAGATGGCGGTAACTCTCGGTGAGAAAGGCTGGAACCCCGG 254

Db 263 ATTACGCTGCACTGGGCAAACTCGGCAACTTTGTCGAGGCGAAGGATGAACTCTGG 322

Qy 255 CTTGAACGAAAGACCATCCACTTTTGAAGGTGTTTACAGCCAAACGGCAACGTAACCT 314

Db 323 CACAGCTCCAGAGTATCAACTTCTCTGACACTTCAACCCCAACGGCAACGTAACCT 382

Qy 315 TGGGCTTACGTTTGAACCCGCAACCGCTGTGAGTATTACATGTGCAAACTTTGG 374

Db 383 CTCAGCTATAGCTGTGCTCCAAAGAACCCCTTCATCGAGTACTAATTTGTGAACTTTGG 442

Qy 375 CACTTATGATCTCTCTCCGCTGTCTACCGATCTAGAACTGTGAGAGCGGAGTACAT 434

Db 443 AACCTCAACCACTGACATGCGACACCAAGCTGGGTGAGTACCTCTTACCGACCT 502

Qy 435 CTATGCACTGCGAAGACCACTGCGTCAACGCACTGAGTACGCGCAACCAACTT 494

Db 503 CTACGACATTTACCGCAGCAGAGAGTCAACAGCTTTCATGATGGAACGGCACTT 562

Qy 495 CGAACCAATCTGCTGCTGCGCCAGACAAAGCGCAACGCGTACCGTCCAGACGGCTG 554

Db 563 TTACACGACTGCTGTCTGCTCGCGCAACCA-CGCTCCAGCGCTGCTGCTACGGTTGCAA 621

Qy 555 CCACTTGCAGCCTGCGCTGCGCTGCTGTTTGAATGCAAGGTCACGCACTACAGAT 614

Db 622 CCACTTGCAGCCTGCGCTGCGCTGCTGTTTGAATGCAAGGTCACGCACTACAGAT 679

Qy 615 CGTTGCAACGAGGCTACTTTCAGCAGCGGCTATGCTGCGATCAGCT 662

Db 680 CATTGCGGTGAGGCTACTTATGCTGTTAGCGCAATTAAGCT 727

RESULT 14
AKI10604

LOCUS AKI10604 912 bp mRNA linear PLN 24-JUN-2003

DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-168-G08, full insert sequence.

ACCESSION AKI10604

VERSION AKI10604.1 GI:32995813

KEYWORDS FLI cDNA; oligo capping.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otono, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tanoda, Y., Kuroseki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Naitaka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, D., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matubara, K., RIKEN; Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Komori, H., Miyazaki, A., Otsu, N., Oka, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y. Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice Science 301 (5631), 376-379 (2003)

JOURNAL JOURNAL

REFERENCE PUBMED 12869764

AUTHORS 2 (bases 1 to 912)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, P., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,

Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurotaki, T., Kusnegg, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Miura, T., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikkura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Oosato, N., Ota, Y., Otsomo, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Takaki, Y., Tagami, M., Tagami, T., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yabagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Title
Journal
Submitted (27-AUG-2002) Shoichi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@ias.affrc.go.jp).
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 2K full-length cDNA clones from japonica

FEATURES

Source

ORIGIN

| | | | | |
|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 31.6% | Score 213; | DB 15; | Length 912; |
| Best Local Similarity | 62.8% | Pred. No. 4.6e-34; | | |
| Matches 365; Conservative | 0; | Mismatches 210; | Indels 6; | Gaps 2; |

| | | | |
|----|-----|--|------|
| Qy | 82 | CTGGAAAAGGACAGACAACATCCCAACTGGAGGGCTGGACAGATGGTTATTACTATTC | 14.1 |
| Db | 159 | CTTGAGAGGGGCCAGTCCACCGCAACTAGTCGGAATCAACAACGGTACTTTTACTCG | 21.8 |
| Qy | 142 | TGGTGAAGTGAACGCTGTGAGCGACAGCGCACTTCAACAACCTGGAAGCGGACCTACGAG | 20.1 |
| Db | 219 | TGGTGAACCGATGAGCGGCGGCTCTGCCAATATACACATGAGGCGGCTCCAACTACACT | 27.8 |
| Qy | 202 | ATCAGCTGGGAGATGCGCGTAACTCTGTCGGTGAAGAGGCTGGAACCCCGGCTGGAAC | 26.1 |
| Db | 279 | GTCACAGTGGGCAACCTGGCAACTTCTGCTGGTGGGAAGGATGGAACCCGAG---AACC | 33.5 |

| | | | |
|----|-----|---|-----|
| Oy | 262 | GCAAGAGCATCCACTTTGAGGGGTTTACGAGCAAAAGGCAACAGTACTCTTGCGGTC | 321 |
| Db | 336 | GGCCGCACATCAACTAGGCGGGCTAGCTCAACTTCCAGGCAACGGCTTACTCGCATTCC | 395 |
| Oy | 322 | TACGGTTGSAACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACCTTTGGCACTTAT | 381 |
| Db | 396 | TACGGCTGGAACCCGCAACCCGCTGGTCGAGTATTACGAGTATCGAGAACCTTACCGGACCTTAC | 455 |
| Oy | 382 | GATCTTCTCTCCGGTGTACCGATCTAGAACTGTCCAGTCCGACGGTAGCATCTATCGA | 441 |
| Db | 456 | AAACCCGCGAAGCGGCGCCAGGTGCGGGAACTTCTCGAACCGATGGGCGGCAGTACGAG | 515 |
| Oy | 442 | CTCGGCAAGACACTCGCGGTCAACGCAACTGACATCGACGGCACCAACCTTGACCA | 501 |
| Db | 516 | GTTGCGCTTTGACCCGCTACACACAGCCCTCCATCGACGCAAGTCGACCTTTACACAG | 575 |
| Oy | 502 | TACTGTGTCGTCCGCCAGAGCAAGCGCAACGCGGTACCGTCCAGACGGGCTGCGCACTTC | 561 |
| Db | 576 | TACTGTGTCGTCCGCCACTGCGAAGCGTACCGGGGGTAGCGTCAACATGACAGCGGCACTTC | 635 |
| Oy | 562 | GAGCCCTGGGCTCGCGCTGTTTGAATGTCAACGCTGACACTACTACAGATGTTGCA | 621 |
| Db | 636 | AACAGTGGGCTAAGTATGACATGAAA--CTTGGGTGAGCACTTACTACCAATATGTGCTCT | 692 |
| Oy | 622 | ACGGAAGGCTACTTCAGACAGCGGCTATGCTTCGATCAACCGT | 662 |
| Db | 693 | ACCGAAGGCTTACAGAGCAAGTGTATCTCTGAGATCTATGT | 723 |

JOURNAL Submitted (09-JUN-2004) Laboratoire de Phytopathologie, UMR 7100 - IFR 85 - ESBS - UIP, Boulevard Sebastien Brant - BP10413,

FEATURES

Bouyce

gene

CDS

ORIGIN

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 GSFPNGNGILCYCHTRGRLPVEIYVIBSYGSLNPGSOAQHCTVYTDGDYIDLNMST
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|-----------------------|--------------|------------------|-----------------|-------------|
| Query Match | 31.3%; | Score 211.4; | DB 15; | Length 696; |
| Best Local Similarity | 62.3%; | Pred. No. 1e-33; | | |
| Matches 367; | Conservative | 0; | Mismatches 216; | Indels 6; |
| | | | | Gaps 2; |

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| QY | 7 | CCACGAGGCTCGAAAAGCAGACAGACACCCCACTCGAGAGGGCTGGCAGCATGGTATT | 133 |
| Db | 101 | CCTCGGCTCCTCGAGGCTCGCCAAATCACTGGGACAGTGAAGTTACCAACAACGGTTACT | 160 |
| QY | 134 | ACTATTCTTGTTGAGTGAACGGTGGAGCGCAGACGCAACGTACCAACTGGAAAGCGCA | 193 |
| Db | 161 | TCTATCTTGTGTGTCTGATTTGGTGGTATTAGTCAATACGTATGGGTAGAGGACGCC | 220 |
| QY | 194 | CCTACGAGATCAGCTGGGGAGATGGCGGTAACTCTGTGGGTGGAAAGGGCTGGAAACCCCG | 253 |
| Db | 221 | ACTACCAAGGTGTGATTGGCGCAACACTGGTAACTTTGTGGGTGAAAGGAAGAAACCTTG | 280 |
| QY | 254 | GCCTGAACGCAAAAGGCATCCACTTTTGAAGGGGTTTACAGCAAAACGGCAACAGTACC | 313 |
| Db | 281 | G---TACTGGCCGAACCATCTAATCAACGAGAGTTCTTCAACCTTCAGGATTAACGATACC | 337 |
| QY | 314 | TTGGGCTCTACGGTTGGAGCCCGCAACCGCTGTCAGATATTACAATGTCGAGAACTTTG | 373 |
| Db | 338 | TTTGGCTTTACGATGAGACCGCGGGTCCCTCGTCGAGATCACTAGTCATCGAGAGTTACG | 397 |
| QY | 374 | GCACTTATGATCCTTCTCGCGGTGCTAACGATCTTAGAACTGTGCAATGTCGACGGTTAGCA | 433 |
| Db | 398 | GTCTTTACAAACCCCGCAGCAGAGCTCAGACACGAGTAAACGCTTACACCAACGCTAGCA | 457 |
| QY | 434 | TCTATGCACTCGGCAAGACCAACTCGCGTCAACGCAACCTAGACTCGACGGCAACCCAACT | 493 |
| Db | 458 | CTTACGATCTCTTATATGTCAACCCGTTACCAACAGCTTCGATCGACGGGTTTTAGACT | 517 |
| QY | 494 | TCGACCAATATCGTGTGCTCCGCGCAGAGCAAGACGCAACGCGGTACCGTCCAGACGGGCT | 553 |
| Db | 518 | TCAACCAAGTACTGTGCATCCGCGCGAACAAGGATACAGGGGCTCGGTCAACATGACAGA | 577 |
| QY | 554 | GCCACTTTCGACGCGCTGGGCTCGCGCTGTGTTGAATGTCAACGATGACCACTTACTACAGA | 613 |
| Db | 578 | ACCACCTTCAATGCTTGGAGATCTGCTGGCATGAAA--CCTCGAACAACCACTTACACAGA | 634 |
| QY | 614 | TGCGTTGCAAGAGGGCTACTTACAGAGGGGCTAATGCTGCATCAACCGT | 662 |
| Db | 635 | TTCTGGCACTAGAGGTTACAGAGCATGGCTCACTTCTTATCTATGT | 683 |

Search completed: February 11, 2006, 20:54:07
Job time : 3495.06 secs

CC This sequence represents the coding sequence for the xylanase from
CC Thermomyces lanuginosus strain DSM 4109. The encoded xylanase, and
CC xylanases derived from Humicola, Thermosaurus, Chaetomium, Mucor,
CC Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssoschlamus or
CC Paecilomyces strains can be used in the monocomponent xylanase
CC preparations of the invention. The xylanase preparations and the
CC recombinant Thermomyces xylanase are useful as animal feed additives,
CC which promote in-vivo breakdown of plant cell wall material and thus
CC improve digestibility, growth rate and/or feed conversion

XX Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 675; DB 2; Length 983;

Best Local Similarity 100.0%; Pred. No. 2,6e-174;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 31 ATGGTCGGCTTTTACCCCCCGTTGCGGCTTTAGCCCGGACTGGGGCCCTTGCTTC 90
QY 61 CCGGCAAGGGAATGCGACGAGAGCTGAAAAGGACAGACAAACCCCAACTGGAGGGCTGG 120
DB 91 CCGGCAAGGGAATGCGACGAGAGCTGAAAAGGACAGACAAACCCCAACTGGAGGGCTGG 150
QY 121 CACGATGGTTATTAATACTTCTCGGTGAGTAGACGATGAGCGACGACGCCACCTACCAAC 180
DB 151 CACGATGGTTATTAATACTTCTCGGTGAGTAGACGATGAGCGACGACGCCACCTACCAAC 210
QY 181 CTGAAAGCGGACACCTTACGAGATCACTGGGAGAGATGGCGGTTAACTCTGTCGTGGAAG 240
DB 211 CTGAAAGCGGACACCTTACGAGATCACTGGGAGAGATGGCGGTTAACTCTGTCGTGGAAG 270
QY 241 GGCCTGGAACCCCGGCTGAAAGCAAGAGACCACTTGAAGGGTTTACAGCCAAAC 300
DB 271 GGCCTGGAACCCCGGCTGAAAGCAAGAGACCACTTGAAGGGTTTACAGCCAAAC 330
QY 301 GGCACACAGCTACTTTCGGCTCTACGCTTGGAACCCGCAACCCGCTGCTGAGTATTATC 360
DB 331 GGCACACAGCTACTTTCGGCTCTACGCTTGGAACCCGCAACCCGCTGCTGAGTATTATC 390
QY 361 GTCGAGAACTTTGGCACTTATGATCTTTCCTCGGCTGCTACCGATCTTGAACCTGTGAG 420
DB 391 GTCGAGAACTTTGGCACTTATGATCTTTCCTCGGCTGCTACCGATCTTGAACCTGTGAG 450
QY 421 TGGCAGCGTAGCATATGATGACTGGGCAAGACCACTGCGGTCAACGCACTTAGCATGAC 480
DB 451 TGGCAGCGTAGCATATGATGACTGGGCAAGACCACTGCGGTCAACGCACTTAGCATGAC 510
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DB 511 GGCACCCAAACCTTTCGACCAATACTGTCTGCTCCGCGCGCAGACCAAGCGACGCGGTACC 570
QY 541 GTCCAGACGGGCTGCGCACTTTCGACGCGCTGGGCTCGCGCTGTTGATGATCAAGGTGAC 600
DB 571 GTCCAGACGGGCTGCGCACTTTCGACGCGCTGGGCTCGCGCTGTTGATGATCAAGGTGAC 630
QY 601 CACTACTTACCGATGCTTGGCAACGAGAGGCTTACACTCAAGCGGTATGCTCGCATCACC 660
DB 631 CACTACTTACCGATGCTTGGCAACGAGAGGCTTACACTCAAGCGGTATGCTCGCATCACC 690
QY 661 GTTGCTGACGTGGGC 675
DB 691 GTTGCTGACGTGGGC 705
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RESULT 2
AAT43010
ID AAT43010 standard; cDNA; 983 BP.

XX AAT43010;

AC AAT43010;
XX 16-OCT-2003 (revised)
DT 22-FEB-1997 (first entry)

XX Endo-1,4-beta-D-xylanase gene.

DE Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;

KW Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;

KW Flour; Baking; dough; ss.

XX Thermomyces lanuginosus; (strain DSM 4109).

OS Key Location/Qualifiers

FT 5'UTR 1..30

FT CDS /*tag= a

FT /*tag= b

FT /product= "Endo-1,4-beta-D-xylanase"

FT /note= "EC-3.2.1.8"

FT 3'UTR 709..983

FT /*tag= c

PN WO632472-A1.

PN 17-OCT-1996.

XX 11-APR-1996; 96WO-DK000171.

XX 11-APR-1995; 95DK-00000435.

XX (NOVO) NOVO-NORDISK AS.

XX Jorgensen OB, Si JQ, Jakobsen TS;

XX WPI: 1996-477123/47.

DR P-PSDB; AAM05187.

XX Bread improving additive contg. xylanase from Thermomyces - and opt.

PT alpha-amylase, increases volume, improves anti-staling properties etc.

XX Claim 7; Page 30-31; 41pp; English.

XX The sequence encodes an endo-1,4-beta-D-xylanase from Thermomyces

CC lanuginosus (Humicola lanuginosa), which may be used as a bread-

CC improving additive. The enzyme may be expressed recombinantly from a

CC plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (clamed),

CC and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour,

CC optionally along with other enzymes (amylase, maltogenase, lipase,

CC cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase,

CC protease and/or peroxidase). The enzyme combines particularly well with

CC amylolytic enzymes, and may be used to improve baking properties of flour

CC softness, freshness and anti-staling properties, while improving dough

CC machinability and stability. (Updated on 16-OCT-2003 to standardise OS

CC field)

XX Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 675; DB 2; Length 983;

Best Local Similarity 100.0%; Pred. No. 2,6e-174;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGGTCGGCTTTTACCCCCCGTTGCGGCTTTAGCCCGGACTGGGGCCCTTGCTTC 60
DB 31 ATGGTCGGCTTTTACCCCCCGTTGCGGCTTTAGCCCGGACTGGGGCCCTTGCTTC 90
QY 61 CCGGCAAGGGAATGCGACGAGAGCTGAAAAGGACAGACAAACCCCAACTGGAGGGCTGG 120
DB 91 CCGGCAAGGGAATGCGACGAGAGCTGAAAAGGACAGACAAACCCCAACTGGAGGGCTGG 150
QY 121 CACGATGGTTATTAATACTTCTCGGTGAGTAGACGATGAGCGACGACGCCACCTACCAAC 180
DB 151 CACGATGGTTATTAATACTTCTCGGTGAGTAGACGATGAGCGACGACGCCACCTACCAAC 210
QY 181 CTGAAAGCGGACACCTTACGAGATCACTGGGAGAGATGGCGGTTAACTCTGTCGTGGAAG 240
```

D 211 CTGGAAGCGCGCACTACGAGATCAGCTGGGAGATGGCGGTAACTTCGTGCTGGAAG 270
Q 241 GCGTGAACCCCGCTTGAAGCAAGCAATCCATCTTGGAGGGTGTACACCAAC 300
D 271 GCGTGAACCCCGCTTGAAGCAAGCAATCCATCTTGGAGGGTGTACACCAAC 330
Q 301 GCGAAGAGCTACTTGGCGGTCTACGGTTGGAACCGCAACCGCTGTGAGTATTAC 360
D 331 GCGAAGAGCTACTTGGCGGTCTACGGTTGGAACCGCAACCGCTGTGAGTATTAC 390
Q 361 GTCGAGAACTTTGGCACTTATGATCTTCTCCGCTGACCGATCTAGAACTGTGAG 420
D 391 GTCGAGAACTTTGGCACTTATGATCTTCTCCGCTGACCGATCTAGAACTGTGAG 450
Q 421 TGGCAAGCTAGCATCTATGACTGGGGAAGCACTGCGCTGACCGCATAGCATGAC 480
D 451 TGGCAAGCTAGCATCTATGACTGGGGAAGCACTGCGCTGACCGCATAGCATGAC 510
Q 481 GGCACCCCAACCTTTCGACCAATATCTGTGCGTCCGCAAGCAAGCGACGCGTACC 540
D 511 GGCACCCCAACCTTTCGACCAATATCTGTGCGTCCGCAAGCAAGCGACGCGTACC 570
Q 541 GTCGAGAGGGCTGCACTTTCGACCGCTGGCTGCGCTGATGATGCAACGCTGAC 600
D 571 GTCGAGAGGGCTGCACTTTCGACCGCTGGCTGCGCTGATGATGCAACGCTGAC 630
Q 601 CACTTACTACGATCTTTCGACCGGAGGCTTACAGACCGCTATGCTGCATACC 660
D 631 CACTTACTACGATCTTTCGACCGGAGGCTTACAGACCGCTATGCTGCATACC 690
Q 661 GTTGTGACGTGGGC 675
D 691 GTTGTGACGTGGGC 705

RESULT 3

AAS13813
ID AAS13813 standard; DNA; 588 BP.

AC AAS13813;

DT 18-DEC-2001 (first entry)

DE DNA encoding Thermomyces lanuginosus xylanase A.

XX xylanase A; plant cell wall; baking; cereal; starch production; wood;
KM wood pulp bleaching; hemicellulose; arabinoxylan; foodstuff; bread; ds.

XX Thermomyces lanuginosus.

OS WO20016711-A1.

PN 13-SEP-2001.

PD 08-MAR-2001; 2001WO-1B000426.

PF 08-MAR-2000; 2000GB-00005585.

PR 27-JUN-2000; 2000GB-00015751.

XX (DANI-) DANISCO AS.

PA Slibesen O, Sorensen JF;

PI WPI, 2001-596834/67.

XX Novel variant xylanase polypeptide or its fragment useful for degrading
PT or modifying plant cell wall, comprises amino acid modifications such
PT that the polypeptide has altered sensitivity to xylanase inhibitor.

XX Disclosure, Page 64; 70pp; English.

XX The invention relates to a variant xylanase polypeptide (I) or its
CC fragment having xylanase activity, comprising one or more amino acid

CC modifications such that (I) or its fragment has an altered sensitivity to
CC a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or
CC its coding sequence (II) is useful for degrading or modifying plant cell
CC wall or for processing a plant material by contacting the plant cell wall
CC or plant material with (I) or (II). (I) is useful for modifying plant
CC materials, and in baking, processing cereals, starch production,
CC processing wood and enhancing the bleaching of wood pulp. (I) is useful
CC for altering the viscosity derived from the presence of hemicellulose or
CC arabinoxylan in a solution or system comprising plant cell wall material.
CC (I) is useful for preparing a foodstuff such as bread, pretzels,
CC tortillas, cakes, cookies, biscuits or crackers. The present sequence
CC represents the coding sequence of Thermomyces lanuginosus xylanase A as
CC described in the method of the invention

XX Sequence 588 BP; 131 A; 178 C; 168 G; 111 T; 0 U; 0 Other;

Query Match 86.2%; Score 582; DB 5; Length 588;
Best Local Similarity 100.0%; Pred. No. 6,1e-149;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q 94 CAGCAACCCCAACCTGGAGGGCTGGCAAGATGTTATTAATCTTCCTGGTGAAGTAC 153
D 4 CAGCAACCCCAACCTGGAGGGCTGGCAAGATGTTATTAATCTTCCTGGTGAAGTAC 63
Q 154 GATGAGAGGAGGCAAGTACCAACCTGGAAGGCGGCACTTACGAGATCAGTGGGA 213
D 64 GATGAGAGGAGGCAAGTACCAACCTGGAAGGCGGCACTTACGAGATCAGTGGGA 123
Q 214 GATGAGAGGAGGCAAGTACCAACCTGGAAGGCGGCACTTACGAGATCAGTGGGA 273
D 124 GATGAGAGGAGGCAAGTACCAACCTGGAAGGCGGCACTTACGAGATCAGTGGGA 183
Q 274 CACTTGAAGGAGGTTTACCAAGCCAAAGCAAGCTTACGAGATCAGTGGGA 333
D 184 CACTTGAAGGAGGTTTACCAAGCCAAAGCAAGCTTACGAGATCAGTGGGA 243
Q 334 CGCAACCCGCTGTCGAGTATTAATCATGTCGAGAACTTTGGCACTTATGATCTTCCTCC 393
D 244 CGCAACCCGCTGTCGAGTATTAATCATGTCGAGAACTTTGGCACTTATGATCTTCCTCC 303
Q 394 GGTGCTACCGATCTAGGAACCTGTCAGTGCAGCGGAGCATCTATGCACTGGCAAGAC 453
D 304 GGTGCTACCGATCTAGGAACCTGTCAGTGCAGCGGAGCATCTATGCACTGGCAAGAC 363
Q 454 ACTGCGTCAACGCACTTACGATGAGAGGCAACCACTTTCGACCAATCTGTGCTC 513
D 364 ACTGCGTCAACGCACTTACGATGAGAGGCAACCACTTTCGACCAATCTGTGCTC 423
Q 514 CGCAGGACAAGGCGCACGAGCGTACCGTCAAGCGGAGCTGCCACTTGCAGCGCTGGGCT 573
D 424 CGCAGGACAAGGCGCACGAGCGTACCGTCAAGCGGAGCTGCCACTTGCAGCGCTGGGCT 483
Q 574 CGCGCTGTTGAATGTCAACCGTGAACCACTTACCAAGATCGTTGCAACGAGAGGCTAC 633
D 484 CGCGCTGTTGAATGTCAACCGTGAACCACTTACCAAGATCGTTGCAACGAGAGGCTAC 543
Q 634 TTCAAGCAGCGCTATGCTCGCATACCGTGTGCTGACGTGGGC 675
D 544 TTCAAGCAGCGCTATGCTCGCATACCGTGTGCTGACGTGGGC 585

RESULT 4

AAD17927
ID AAD17927 standard; DNA; 678 BP.

AC AAD17927;

DT 10-DEC-2001 (first entry)

DE Thermomyces lanuginosus codon optimised xylanase gene.

XX xylanase; Pichia cell; heterologous nucleotide; codon optimisation; ds.

OS Thermomyces lanuginosus.
 OS Synthetic.
 PN W0200166693-A1.
 PD 13-SEP-2001.
 XX
 PF 09-MAR-2001; 2001WO-DK000154.
 XX
 PR 10-MAR-2000; 2000DK-00000392.
 PR 15-MAR-2000; 2000DK-00000419.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Takagi S, Terui Y, Teutsami N, Taira R;
 DR WPI; 2001-582273/65.
 XX
 PT Novel Pichia cell useful for producing polypeptide of interest, comprises
 PT a copy of heterologous nucleotide sequence encoding polypeptide of
 PT interest.
 XX
 PS Claim 14; Page 38-39; 61pp; English.
 XX
 CC The invention relates to a Pichia cell comprising at least one copy of
 CC heterologous nucleotide sequence encoding a polypeptide of interest,
 CC where the codon usage of the sequence has been adjusted to match the
 CC preferred codon usage of P. methanolica. The invention also relates to a
 CC method for producing high yields of heterologous codon optimised
 CC polypeptide in a Pichia cell. The Pichia cell is useful for producing a
 CC polypeptide of interest, where the polypeptide is encoded by a nucleotide
 CC sequence heterologous to P. methanolica. The present sequence is
 CC Thermomyces lanuginosus codon optimised xylanase gene which is the
 CC heterologous DNA used in the invention
 CC
 XX
 SQ Sequence 678 BP; 180 A; 89 C; 152 G; 257 T; 0 U; 0 Other;
 Query Match 55.1%; Score 371.6; DB 4; Length 678;
 Best Local Similarity 72.0%; Pred. No. 2,2e-91;
 Matches 485; Conservative 0; Mismatches 189; Indels 0; Gaps 0;
 QY 1 ATGGTCGGCTTTACCCCGGTTGCGGCGCTTACCGCGACTGGGGCCCTGGCCCTTC 60
 DB 1 ATGGTTGGTTTATCTCCAGTTGCTTAGCTGCTTAGCTGCTGCTTAGCTTTC 60
 QY 61 CCGGCAAGGAATGCCAGGACTCGAAAAGGACAGAACCCCAATCCGAGGGGCTGG 120
 DB 61 CCAGCAGGTAATGCTACTGAATTAGAAAAAGACAAACCACTCCAAATTCGAAGGTTGG 120
 QY 121 CACGATGGTTATTAATCTATTCCTGCGTAGTACGCGTAGCGGACGACGATACCAAC 180
 DB 121 CATGATGGTTATTAATCTATTCCTGCGTAGTACGCGTAGCGGACGATACCAAT 180
 QY 181 CTGAAAGCGGACCTACGAGATCAGCTGGGAGATGCGGCTGCTGCTGGTGAAG 240
 DB 181 TTAGAAGGTGGTACTATGAATTTCTGGGGTGAATGTTGAATTTAGTGGTGA 240
 QY 241 GGCCTGAACCCCGGCTGAAGCAGACCACTCCCTTGAAGGTTTACCAAGCAAC 300
 DB 241 GGTGGAAATCCAGGTTTAAATGCAAGACTATTCATTTTGAAGGTTTATCAACCAAT 300
 QY 301 GGCACACGCTACCTTGGGCTCTACGCTTGGGACCCGCAACCGGCTGGTGAATTAATC 360
 DB 301 GGTATTTCTTATTAATGCTGTTTATGCTTGAATCAATTCATTTGTTGAATTTATTT 360
 QY 361 GTCCGAACTTTGGACCTTATGATCTTCTCCGCTGCTACCGATCTAGAACTGTGAG 420
 DB 361 GTTGAATAATTTTGTACTTATGATCATCTTCTGCTGCTACGATTTAGTACTGTGA 420
 QY 421 TCGCAGCGTAGATCTATGAGATCGGCAAGACCACTCGCTGAAGCACTAGATCAGAC 480
 DB 421 TGTGATGGTTCTTATTTATGATTTAGATTAGTAAACTACTAGAGTTTAAAGCACTATTTAT 480

QY 481 GGACCCCAACCTTGCAGCAATATCTGTGCTCCGCCAGGACAGCGCACCAAGCGTACC 540
 DB 481 GGTACTCAACCTTTCATCATATATGTTGCTGTAGACAGATATAAGAACTTCTGTACT 540
 QY 541 GTCCAGACGGGCTGCCACTTCCAGCGCTGGGCTCGGCTTGAATGCAACGGTAC 600
 DB 541 GTTCAACCTGGTGTATTCGATGCTGGGCTGAGCTGGTGAATGTTAATGGTACT 600
 QY 601 CACTACTACGAGATCGTTGCAACGAGGCGTACTTCCAGCAGCGCTATGCTCCGATACC 660
 DB 601 CATTTATTTCAATTTGTGTGCAACTGAAGTTATTTCTTCTGTATATGCTAGATTA 660
 QY 661 GTTCTGACGTGGG 674
 DB 661 GTTGTGATGTTGG 674
 RESULT 5
 AAQ74098
 ID AAQ74098 standard; DNA; 1123 BP.
 XX
 AC AAQ74098;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 14-NOV-1995 (first entry)
 XX
 DE Humicola xylanase gene.
 XX
 KM xylanase; vector; pAXX40-1-1; Aspergillus foetidus; ss.
 OS Humicola insolens.
 XX
 FH Key Location/Qualifiers
 FT CDS 126..809
 FT /*tag= a
 XX
 XX W09515390-A1.
 PN
 XX
 PD 08-JUN-1995.
 XX
 PF 29-NOV-1994; 94MO-US013612.
 PR 01-DEC-1993; 93US-00160591.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PI Berka RM, Yoder W, Takagi S, Boominathan K;
 DR WPI; 1995-215270/28.
 DR P-PSDB; AAR75421.
 XX
 XX Aspergillus foetidus cells expressing heterologous enzyme - partic.
 PT Fungal lipase or xylanase, provide high yield without significant prodn.
 PT of protease or mycotoxin.
 PS
 PS Disclosure; Page 35-36; 47pp; English.
 XX
 CC A DNA fragment (AAQ74098) encoding H. insolens xylanase (AAR75421) was
 CC isolated from PYBS (DSM 6595) and inserted into pHD414 (contg. the TATA
 CC promoter and AMG terminator) to form pAXX40-1-1-1. This plasmid and
 CC pJAL77 (impacting hygromycin B resistance) were used to transform
 CC protoplasts of A. foetidus NO953. The xylanase yield was 0.12 g/l.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX
 SQ Sequence 1123 BP; 249 A; 342 C; 293 G; 239 T; 0 U; 0 Other;
 Query Match 35.4%; Score 239; DB 2; Length 1123;
 Best Local Similarity 64.4%; Pred. No. 4.7e-55;
 Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;
 QY 57 CTTCCGGCAGGGAATGCCAGGAGCTCGAAAAGCAGACCAACCCCAACTCGGAGGG 116

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Db 197 CGTTCCTCGGAGCAACTCGACGCGCCCTTCAGGCTCGACAGGAGACCCCAACGCGAGAGG 256
Qy 117 CTGGACCAATGTTATTACTATTCTGTGAGATGACGCTGAGAGCGGACGATAC 176
Db 257 CTGGACCAATGTTATTACTATTCTGTGAGATGACGCTGAGAGCGGACGATAC 316
Qy 177 CAACCTGGAAGGCGGACCTACGAGATGAGCTGGGAGATGGCGGTAACTCTGTGAGG 236
Db 317 CAACCTGGAAGGCGGACCTACGAGATGAGCTGGGAGATGGCGGTAACTCTGTGAGG 376
Qy 237 AAAGGCTGGAACCCCGGCTGAAAGCAAGACCACTTCATTTAGGGTGTTCACACC 296
Db 377 TAAAGGTTGAAACCCGGG---AACGGCGGACGATCAACAGCGGCTTCAACCC 433
Qy 297 AAAGGCAACGCTACCTTGGGCTTACGCTTGAAGCCGCAACCGCTGTGAGATTA 356
Db 434 CCAAGGCAACGCTACCTTGGGCTTACGCTTGAAGCCGCAACCGCTGTGAGATTA 493
Qy 357 CATGCTGAGAACTTTGGACCTATGATCTTCTCCGGGTGTAACCGATTAAGAACTGT 416
Db 494 TGTATCGAAGTCTACGACGATCAATCCGCGACAGGCTTCATTAAGGCACTT 553
Qy 417 CGAGTGCAGCGGTAGCATCTATCGACCTGCGAAGACACTGCGCTCAACGACCTAGAT 476
Db 554 CTATACCGAAGCGGATGATGATGATCTTTGTGAGACCGCGCTACAAACGACGAT 613
Qy 477 CGAGGCAACCCAACTTTCGACCAATACTGCTGCTCCGCGAAGCAAGCGGACGAT 536
Db 614 CGAGGCAACCCGAGCGGTTCAGCACTGCTGCTTCTTCCGCAAGAACTGTCGAGG 673
Qy 537 TACGCTCAGACGCGGCTGCACTTTCGAGCGGCTGCGGCTGTTGAATGTCACAG 596
Db 674 CTCGCTCAACATGCAAGCACTTTCAGCGGCTGCGGACGACGAGATGCGCT---CGG 730
Qy 597 TGACCACTACTACGAGATGCTTTCGACGAGGCGCTACTTTCAGCGGCTATGCTCGAT 656
Db 731 CCAAGCACTACTACGAGATGCTTTCGACGAGGCGCTACGAGGCGTACGAGGCGATGCTCGAT 790
Qy 657 CACCGTT 663
Db 791 CTATGTT 797

RESULT 6
AAQ94952 standard; DNA; 1123 BP.
AC AAQ94952;
XX
DT 25-MAR-2003 (revised)
DT 02-DEC-1995 (first entry)
XX
DE Humicola insolens xylanase.
XX
KW Xylanase; DSM 6995; ss.
XX
OS Humicola insolens.
XX
FH Key Location/Qualifiers
FT CDS 126..806
FT /*tag= a
XX
PN MO9515391-A2.
XX
PD 08-JUN-1995.
XX
PE 29-NOV-1994; 94MO-US013613.
XX
PR 01-DEC-1993; 93US-00161675.
XX
PA (NOVO ) NOVO NORDISK BIOTECH INC.
XX
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PI Berka RM, Yoder W, Takagi S, Boomnathan K;
XX WPI: 1995-215271/28.
DR P-PSDB; AAR78231.
XX
PT Aspergillus japonicus-type cells expressing heterologous protein - esp.
PT fungal enzyme, provide high yields without significant prodn. of protease
PT or mycotoxin.
PS Example; Page 39-40; 50pp; English.
XX
CC A strain of E. coli contg. the approx. 1,100 bp xylanase HindIII/ XbaI
CC cDNA fragment in pYES is deposited in DSM as DSM 6995. The xylanase cDNA
CC fragment is isolated from one of the clones. The sequence of the xylanase
CC gene and protein are given in AAQ94952 and AAR78231 and the gene is
CC deposited as DSM 6995. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 1123 BP; 249 A; 342 C; 293 G; 239 T; 0 U; 0 Other;

Query Match 35.4%; Score 239; DB 2; Length 1123;
Best Local Similarity 64.4%; Pred. No. 4.7e-55;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

Qy 57 CTTCCCGCAGGAGATGCAAGAGCTGAAAAGCAGACAAACCCCACTCGAGGG 116
Db 197 CGTTCCTCGGAGCAACTCGACGCGCCCTTCAGGCTCGACAGGTGACCCCAACGCGAGGG 256
Qy 117 CTGGACCAATGTTATTACTATTCTGTGAGATGACGCTGAGAGCGGACGATAC 176
Db 257 CTGGACCAATGTTATTACTATTCTGTGAGATGACGCTGAGAGCGGACGATAC 316
Qy 177 CAACCTGGAAGGCGGACCTACGAGATGAGCTGGGAGATGGCGGTAACTCTGTGAGG 236
Db 317 CAACCTGGAAGGCGGACCTACGAGATGAGCTGGGAGATGGCGGTAACTCTGTGAGG 376
Qy 237 AAAGGCTGGAACCCCGGCTGAAAGCAAGACCACTTCATTTAGGGTGTTCACACC 296
Db 377 TAAAGGTTGAAACCCGGG---AACGGCGGACGATCAACAGCGGCTTCAACCC 433
Qy 297 AAAGGCAACGCTACCTTGGGCTTACGCTTGAAGCCGCAACCGCTGTGAGATTA 356
Db 434 CCAAGGCAACGCTACCTTGGGCTTACGCTTGAAGCCGCAACCGCTGTGAGATTA 493
Qy 357 CATGCTGAGAACTTTGGACCTATGATCTTCTCCGGGTGTAACCGATTAAGAACTGT 416
Db 494 TGTATCGAAGTCTACGACGATCAATCCGCGACAGGCTTCAATCAAGGCACTT 553
Qy 417 CGAGTGCAGCGGTAGCATCTATCGACCTGCGAAGACACTGCGCTCAACGACCTAGAT 476
Db 554 CTATACCGAAGCGGATGATGATGATCTTTGTGAGACCGCGCTACAAACGACGAT 613
Qy 477 CGAGGCAACCCAACTTTCGACCAATACTGCTGCTCCGCGAAGCAAGCGGACGAT 536
Db 614 CGAGGCAACCCGAGCGGTTCAGCACTGCTGCTTCTTCCGCAAGAACTGTCGAGG 673
Qy 537 TACGCTCAGACGCGGCTGCACTTTCGAGCGGCTGCGGCTGTTGAATGTCACAG 596
Db 674 CTCGCTCAACATGCAAGCACTTTCAGCGGCTGCGGACGACGAGATGCGCT---CGG 730
Qy 597 TGACCACTACTACGAGATGCTTTCGACGAGGCGCTACTTTCAGCGGCTATGCTCGAT 656
Db 731 CCAAGCACTACTACGAGATGCTTTCGACGAGGCGCTACGAGGCGTACGAGGCGATGCTCGAT 790
Qy 657 CACCGTT 663
Db 791 CTATGTT 797

RESULT 7
ABQ80362 standard; cDNA; 666 BP.
XX
ID ABQ80362
XX
AC ABQ80362;
```

XX 11-AUG-2003 (first entry)
DT
XX
XX A. fumigatus AFXYL1 cDNA.
DE
XX
XX Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KM beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KM polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KM glucose; oxygen; myo-inositol phosphate; laccase; tea leaf; sucrose;
KM glyceride; starch; maltodextrin; oxidated phenolic compound;
KM polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
XX textile; tea liquor; cleaning ability; ss.
XX
XX Aspergillus fumigatus.
OS
XX
XX Key Location/Qualifiers
FH 1..666
FT CDS /*tag= a
FT /product= "xylanase 1"
FT
XX
XX WO2003012071-A2.
XX
XX
XX 13-FEB-2003.
PD
XX
XX 05-AUG-2002; 2002MO-US024842.
PR
XX 03-AUG-2001; 2001US-0309870P.
PA (ELIT-) ELITRA PHARM INC.
XX
XX Jiang B, Storms R, Roemer T, Bussey H;
PI WPI; 2003-332729/31.
XX P-PSDB; ABB80185.
DR
XX
XX Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.
XX
XX
XX Claim 2; Page 163-64; 169pp; English.
PS
XX
XX The sequences given in AB080319-66 encode enzymatic proteins derived from
CC A. fumigatus. The resulting proteins display the catalytic activity of an
CC enzyme such as tannase, cellulase, glucose oxidase, glucoamylase,
CC phytase, beta-galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylase are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC laccase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonase
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanase are useful for modulating the amount of xylan or xylo-oligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A.fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers

CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC renase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions
XX
XX Sequence 666 BP; 142 A; 199 C; 192 G; 133 T; 0 U; 0 Other;

| | | | | |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match | 33.3% | Score 224.6; | DB 10; | Length 666; |
| Best Local Similarity | 61.5%; | Pred. No. 3.5e-51; | | |
| Matches 413; Conservative | 0; | Mismatches 249; | Indels 9; | Gaps 3; |

| | | | |
|----|-----|--|-----|
| Qy | 1 | ATGTCGAGCTTTACCCCGTGGCCCTTGCGGACCTTAAGCCGGACTGGGGCCCTGGCTTC | 60 |
| Db | 1 | ATGATCTCATTTCTTCTCTCGTTCTCGCTGCCTCCACCGTTGCTGGGTGTAGTTACA | 60 |
| Qy | 61 | CCGG--CAGGAAATGCCACGAGCTGGAAAGCGACAGACACACCCCACTCGAGGGC | 117 |
| Db | 61 | CCCCGCTCGGAGCATACGTTGAGCTAGCCAAAGCGGACGCTCACAGCTCTGAGACTGGC | 120 |
| Qy | 118 | TGGACAGATGATTTATTAATTCTTCGTGGAGATGACGAGTGGAGCGGCAAGGCAAGTACAC | 177 |
| Db | 121 | ACGAATAAGGCTACTACTTCTCTCTGGACCAAGCGCGGCGGCAAGTATGACTACAC | 180 |
| Qy | 178 | AACCTGGAAAGCGGCACTTACAGATCAGCTGGGGAGATGGCGTTAAGCTCGTGGTGA | 237 |
| Db | 181 | AACGGCAATGGCGGCGCCAGTATCAGGTGCACTGGAAACAATCGCGGCAACTTTGTGCTGGG | 240 |
| Qy | 238 | AAGGGCTGGAAACCCCGGCTGTAAGGCAAGACCATCACTTTGAGAGGTGTTAACAGCA | 297 |
| Db | 241 | AAGGGCTGGAAACCGGCGC--AGCAGAAAGCGGTCACTACAGCGGCTCTGGCAGACC | 297 |
| Qy | 298 | AACGGCAACAGCTACCTTTCGCTCTACGTTTGAACCCGCAACCCGCTGGTGGATTTAC | 357 |
| Db | 298 | AGCGGAAACGGCTACCTTCCTCGTGTACGGCTGAGCAGCACAGTCCGCTGGTGCATTTCTAC | 357 |
| Qy | 358 | ATGCTCGAAGACTTTGSCACTTATGATCTTCTCTCGGTGCTTACCGATTTAGAACTGTC | 417 |
| Db | 358 | ATCTGTGAGATTAAGGCTCTCTATGACCCCTTCCAGGGAGCCACCATTTCTGGCACTGTC | 417 |
| Qy | 418 | GAGTGCAGCGGTAGCATCTATTCGACTCGGCAAGACCACTCGGCTCAACGCACTAGCATC | 477 |
| Db | 418 | GAGAGCAAGGGGGCAACGTACAACCTTACAAGAGAGAGCGGGAAGCATGCGCGTCAATC | 477 |
| Qy | 478 | GACGGCAACCAACTCTTGACCAATATCTGTCGTTCGCGCAGAGCAAGCGCACACGGT | 537 |
| Db | 478 | CAGGGCAACGGCTACTTTTGAACAGATACGTGTGCTTGGACTTTCGACCGGAGATGGA | 537 |
| Qy | 538 | ACCGTCAAGAGGGGTGCACTTCGACGCTGGGCTCGCGCTGATTGAATGCAACGGT | 597 |
| Db | 538 | ACTGTGACGAGAAAGAACCACTTTGATGTCGTGGAAGAAATGCGGGTCTGCATTT--GGGG | 594 |
| Qy | 598 | GACCACTACTACAGATGTTTGCACACGAGAGGCTTACTTACAGAGCGGCTATGCTCGCATC | 657 |
| Db | 595 | AACTTTGACTATATGATATTGTTCGACGAGAGGGGTACAGAGCAGCGGCTCTGACTATAC | 654 |
| Qy | 658 | AACGTTGCTGA 668 | |
| Db | 655 | ACTGTTTCTTA 665 | |

RESULT 8
ABQ80364
ID ABQ80364 standard; cDNA; 705 BP.

AC ABQ80364;

DT 11-AUG-2003 (first entry)

DE A. fumigatus AfXYL2 cDNA.

Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;

activity enhances cleaning ability of detergent compositions

XX

| FH | Key | Location/Qualifiers |
|-----|-----|---------------------|
| 1 | 1 | 1 |
| 2 | 2 | 2 |
| 3 | 3 | 3 |
| 4 | 4 | 4 |
| 5 | 5 | 5 |
| 6 | 6 | 6 |
| 7 | 7 | 7 |
| 8 | 8 | 8 |
| 9 | 9 | 9 |
| 10 | 10 | 10 |
| 11 | 11 | 11 |
| 12 | 12 | 12 |
| 13 | 13 | 13 |
| 14 | 14 | 14 |
| 15 | 15 | 15 |
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```

FT CDS 298..993
FT /*cag= a
FT /gene= "Xyng"
FT /product= "xylanase"
FT sig_peptide 298..417
FT /*cag= b
FT mat_peptide 418..990
FT /*cag= c
FT /note= "mature peptide is claimed"
XX
XX JP11266873-A.
XX
XX 05-OCT-1999.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX (NORO ) NORINSUISANSO SHOKUJIN SOGO.
XX (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
XX WPI; 1999-613780/53.
XX P-PSDB; AAY44183.
XX
XX A xylanase gene, contiguous with a vector and a transformant - used for
XX pulp-bleaching.
XX
XX Claim 1; Page 5-6; 10pp; Japanese.
XX
XX This sequence corresponds to a degenerate sequence encoding a xylanase
XX precursor from Streptomyces olivaceoviridis. The sequence can be inserted
XX into the plasmid pOB60 to generate plasmid FERM P-16713 for expression in
XX e.g. E.coli. The xylanase is useful for the preparation of xyl-
XX oligosaccharide from xylan and for pulp-bleaching. (Updated on 27-AUG-
XX 2003 to correct OS field.)
XX
XX Sequence 1195 BP; 230 A; 457 C; 333 G; 174 T; 0 U; 1 Other;
SQ
Query Match 30.4%; Score 205; DB 2; Length 1195;
Best Local Similarity 62.9%; Pred. No. 9.5e-46;
Matches 354; Conservative 0; Mismatches 200; Indels 9; Gaps 2;
QY 100 ACCCCCACTCGAGAGGCTGACAGATGTTATTACTTCTCGTGGATGACGGTGA 159
DB 430 ACCACCAACAGACCGGACCAACACGAGTTCTACTCTCTGGACCGAGCGGC 489
QY 160 GCGAGGCAAGTACCAACCTGGAAGCGGACCTTCGAGTACGCTGGGAGATGC 219
DB 490 GATTGCTCTGATGACCTGAACTCGGCGCAACTACACACTCGTGAACGAACTGC 549
QY 220 GATAACCTGTCGATGAAAGGCTGAAACCCGGCTGAAAGCAAGCACTCACTTT 279
DB 550 GGGAACTTCTGCGCGGCAAGGCTGAGCAACGGCGAAGC---AGAAAGTGAGTAC 606
QY 280 GAGGCTGTTTACCAACCAACGCAAGCTTCTGCTGACGTTGACGTTGACCCGCAAC 339
DB 607 TCGGGACAGCTTCTACCTCGCGCAACGAGTACCTGCGGTGACGAGTGAACCTCGAAC 666
QY 340 CCGCTGCTGAGTATTACATGTCGAACACTTGGACACTTATGATCTTCTCCGGTCT 399
DB 667 CCGCTGCTGAGTATTACATGTCGAACACTTGGGCAACTACCGGCAAC---GGA 720
QY 400 ACCGATTTAGAACTGTGAGTGAAGGCTGATCTATCTGACCTGGGCAAGCACTGC 459
DB 721 ACGTACAAGGGGACGCTACCAACGCAAGGCGGCACTGACGATCTTACCAACGAGCGG 780
QY 460 GTCAACGCACTGATGACGACGCAACCAACCTTGAACCAATACTGTCGTCGCGCAG 519
DB 781 TACAACGCCCCCTCGTGAAGGACCAAGACCTTCAACAGTACTGAGAGCGTCGCGGAG 840
QY 520 GACAAGGCAACGAGGATACCTTCAGACAGGCTGCACTTGAAGCCTGGGCTGCGCT 579
DB 841 TCCAAGCGGACCGGCGGACCATCAACACGGCAACCACTTGAAGCCTGGGCTGCGCTAC 900

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QY 580 GATTGAATGTCACGGTGACCACTACCAAGATGTTGCAACGAGGCTTACTTACG 639
DB 901 GGATGCAACTGGGACGCTTACAGCTACTACATGATGAGCCACCGAGGCTACAGAGC 960
QY 640 AGCGGCTATGCTCGCATCAACCGT 662
DB 961 AGCGGCTCTTCAACCTCAACGCT 983

RESULT 10
AAZ28865
ID AAZ28865 standard; DNA; 1195 BP.
XX
XX AAZ28865;
XX
XX 27-AUG-2003 (revised)
XX 01-FEB-2000 (first entry)
XX
XX Streptomyces olivaceoviridis xylanase (Xyng) gene.
XX
XX Xylanase; plasmid; expression; E.coli; xyl-oligosaccharide; xylan;
XX pulp-bleaching; de.
XX
XX Streptomyces olivaceoviridis.
XX
XX Key Location/Qualifiers
XX CDS 298..993
XX /*cag= a
XX /gene= "Xyng"
XX /product= "xylanase"
XX sig_peptide 298..417
XX /*cag= b
XX mat_peptide 418..990
XX /*cag= c
XX /note= "mature peptide is claimed"
XX
XX JP11266873-A.
XX
XX 05-OCT-1999.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX (NORO ) NORINSUISANSO SHOKUJIN SOGO.
XX (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
XX WPI; 1999-613780/53.
XX P-PSDB; AAY44183.
XX
XX A xylanase gene, contiguous with a vector and a transformant - used for
XX pulp-bleaching.
XX
XX Claim 4; Page 6-7; 10pp; Japanese.
XX
XX This sequence corresponds to the complete sequence encoding a xylanase
XX precursor from Streptomyces olivaceoviridis. The sequence can be inserted
XX into the plasmid pOB60 to generate plasmid FERM P-16713 for expression in
XX e.g. E.coli. The xylanase is useful for the preparation of xyl-
XX oligosaccharide from xylan and for pulp-bleaching. (Updated on 27-AUG-
XX 2003 to correct OS field.)
XX
XX Sequence 1195 BP; 230 A; 457 C; 333 G; 175 T; 0 U; 0 Other;
SQ
Query Match 30.4%; Score 205; DB 2; Length 1195;
Best Local Similarity 62.9%; Pred. No. 9.5e-46;
Matches 354; Conservative 0; Mismatches 200; Indels 9; Gaps 2;
QY 100 ACCCCCACTCGAGAGGCTGACAGATGTTATTACTTCTCGTGGATGACGGTGA 159
DB 430 ACCACCAACAGACCGGACCAACACGAGTTCTACTCTCTGGACCGAGCGGC 489

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QY 160 GCGAGGCGCAGTACACCACTGMAAGCGGCACTTACGATCAGCTGGGAGATGCG 219
DB 490 GATTCCGCTGATGATGACCTTGAACCTCGGGCGGCACTTACGACCTGTGGACGAACTGC 549
QY 220 GGTAACTCTGCTGGTGGAAAGGCTGGAAACCCCGGCTGAAAGCAAGACCTCACTTT 279
DB 550 GGGAACTTCTGCTGGCGGCGMAAGGCTGGAGCAACGCGGACGC---AGGAACGTGCAGTAC 606
QY 280 GAGGCTGTTTTCAGAGCCAAACAGCTACCTTGCGGTCTACGCTTGGACCCGCAAC 339
DB 607 TCGGGACAGCTTCTACCCGCTCGGCAACGCTACCTGGCGCTGTACGGGTGGACCTCGAAC 666
QY 340 CCGCTGTGAGTATTAATCATGTGCAAGAACTTTGCACTTATGATCTTCTCCGTGCT 399
DB 667 CCGCTCGTGAATCTACATGTGCAACACTGGGGCAACTACGGGCCAAC-----GGA 720
QY 400 ACCGATCTAGAACTGTGAGTGGAGCGGTAGCATCTATCGACTTCGGCAGACACTGCG 459
DB 721 ACGTACAAAGGCGCGCTACCGAGCGCGGCAAGTACAGCTCTACCAAGACGACGCG 780
QY 460 GTCAAGCACTTACGATCGAGCGGACCGCAACCTTCAACCAATATGCTGCTCGGCGAG 519
DB 781 TACACGCGCCCTCTCGTGAAGGCAACCAAGCTTCAACGATCTGAGGCTCGGCGAG 840
QY 520 GACAAAGCGCACCAAGCGTACCGTCAAGCGGGCTGGCACTTCAAGCGCTGGGCTCGGCT 579
DB 841 TCCAAAGGAGACCGGCGGCAACATCAACCGGCAACCACTTCAAGCGCTGGGCGGCTAC 900
QY 580 GATTGAATGTCAACGCTGACCACTACTACCAAGTCTTGGCAAGAGGCTACTTCAAC 639
DB 901 GGCATGCAACTGGGCACTTCACTACTACATGATCAATGCGCAACGAGGCTACCAAGGC 960
QY 640 AGCGGCTATGCTCGCATCACCGT 662
DB 961 AGCGGCTCTTCAACCTCACCGT 983

RESULT 11

ADK70798
ID ADK70798 standard; DNA; 576 BP.

AC ADK70798;

DT 06-MAY-2004 (first entry)

DE Streptomyces olivaceoviridis xylian enzyme encoding DNA SEQ ID NO:1.

KM Streptomyces olivaceoviridis; xylian enzyme; feed additive;

KW animal feed; gene; ds.

OS Streptomyces olivaceoviridis.

Key Location/Qualifiers

FT CDS 1..576
/*CDS= a
/product= "xylian enzyme"

XX CN1405304-A.

XX 26-MAR-2003.

XX 14-SEP-2001, 2001CN-00142163.

XX 14-SEP-2001, 2001CN-00142163.

XX (FODD-) FODDER INST CHINESE ACAD AGRIC SCI.

XX Yao B, Fan Y, Zhang H;

XX WPI, 2003-514374/49.

XX P-PSDB; ADK70799.

PT Heat-resisting, antiprotease acidic-neutral xylenase and its gene.

XX Claim 3; SEQ ID NO 1; 21pp; Chinese.
PS The present sequence encodes the Streptomyces olivaceoviridis xylian
XX enzyme. The xylian enzyme has good heat stability, high activity under
CC acidic and neutral pH. The xylian enzyme can be used as a feed additive
CC and can be widely used in animal feed.
XX
SQ Sequence 576 BP; 125 A; 207 C; 165 G; 79 T; 0 U; 0 Other;

Query Match 30.1%; Score 203.4; DB 10; Length 576;

Best Local Similarity 62.7%; Pred. No. 2.1e-45;

Matches 353; Conservative 0; Mismatches 20; Indels 9; Gaps 2;

QY 100 ACCCCCACTCGAGGCTGCGCAAGTGTATTAATTCCTGCTGAGTACGAGTGA 159
DB 13 ACCACCAACAGACCGGCAACCAAGGCTTACTACTCTTGTGACCGAGCGGC 72
QY 160 GCGAGGCGCAGTACCAACCTGGAAGCGGCACTTACGAGATCAGCTGGGAGATGCG 219
DB 73 GATTGCTCTGATGACCTTGAACCTCGGCGGCACTTACGACCTGTGGACGAACTGC 132
QY 220 GGTAACTCTGCTGGTGGAAAGGCTGGAAACCCCGGCTGAAAGCAAGACCTCACTTT 279
DB 133 GGGAACTTCCGCGCGGCAAGGCTGGAGCAACGCGGAGC---AGGAACGTGCAGTAC 189
QY 280 GAGGCTGTTTTCAGAGCCAAACGCTACCTTGGCTTACGCTTGGACCCGCAAC 339
DB 190 TCGGCGAGCTTCAACCGCTCGGCAACGCTTACCTGCGCTGTACCGGTGGACCTCGAAC 249
QY 340 CCGCTGTGAGTATTAATCATGTGCAAGAACTTTGCACTTATGATCTTCTCCGTGCT 399
DB 250 CCGCTCGTGAATCTACATGTGCAACACTGGGGCAACTACGGGCCAAC-----GGA 303
QY 400 ACCGATCTAGAACTGTGAGTGGAGCGGTAGCATCTATCGACTTCGCAAGACCACTGCG 459
DB 304 ACGTACAAAGGCGCGCTACCGAGCGGCGGCAAGTACAGCTCTACCAAGACGACGCG 363
QY 460 GTCAAGCACTTACGATCGAGCGGACCGCAACCTTCAACCAATATGCTGCTCGGCGAG 519
DB 364 TACACGCGCCCTCTCGTGAAGGCAACCAAGCTTCAACGATCTGAGGCTCGGCGAG 423
QY 520 GACAAAGCGCACCAAGCGTACCGTCAAGCGGGCTGGCACTTCAAGCGCTGGGCTCGGCT 579
DB 424 TCCAAAGGAGACCGGCGGCAACATCAACCGGCAACCACTTCAAGCGCTGGGCGGCTAC 483
QY 580 GATTGAATGTCAACGCTGACCACTACTACCAAGTCTTGGCAAGAGGCTACTTCAAC 639
DB 484 GGCATGCAACTGGGCACTTCACTACTACATGATCTTGGCAAGGCTTACCAAGGC 543
QY 640 AGCGGCTATGCTCGCATCACCGT 662
DB 544 AGCGGCTCTTCAACATCACCGT 566

RESULT 12

ADL23221
ID ADL23221 standard; cDNA; 696 BP.

AC ADL23221;

DT 20-MAY-2004 (first entry)

DE A. niger (hemi) cellulase NB5021 coding sequence.

KM ss; gene; A. niger; (hemi)cellulase; filamentous fungus; dough; bread;

KW biscuit; elasticity; stability; stickiness; extensibility; machinability;

XX crumb structure; softness; flavour.

XX Aspergillus niger.

Key Location/Qualifiers

FT CDS 1..696

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FT      /*tag= a
XX      /product= "(Hemi)cellulase NBE021"
PN      NO2004018662-A2.
XX
XX      04-MAR-2004.
XX
XX      15-AUG-2003; 2003WO-EP009147.
XX
XX      19-AUG-2002; 2002EP-00102152.
XX      19-AUG-2002; 2002EP-00102150.
XX      19-AUG-2002; 2002EP-00102151.
XX      30-AUG-2002; 2002EP-00102245.
XX      03-SEP-2002; 2002EP-00102279.
XX      03-SEP-2002; 2002EP-00102298.
XX
XX      (STM ) DSM IP ASSETS BV.
XX
XX      Fokkers U, Fritz A, Gerhard B, Klugbauer S, Spreafico F,
PI      Wagner C, Boer DL, Meima RB;
XX
XX      WPI: 2004-226842/21.
XX      P-PSDB; ADL23222.
XX
XX      Novel hemi-cellulase NBE012, NBE021, NBE022, NBE064, NBE075 or NBE092
PT      derived from Aspergillus niger, useful for preparing dough and/or baked
PT      product.
XX
XX      Disclosure; SEQ ID NO 5; 92pp; English.
XX
XX      This sequence encodes an A. niger (hemi) cellulase NBE021. The
CC      (hemi)cellulase coding sequences of the invention are derived from a
CC      filamentous fungus, preferably Aspergillus niger. The (hemi)cellulase is
CC      useful in producing dough, which is useful for preparing a baked product
CC      such as bread, biscuits from the dough. Fragments of the (hemi)cellulase
CC      DNA are useful as probes and primers for detecting the expression of
CC      (hemi)cellulose mRNA in a biological sample such as a tissue. They are
CC      also useful as query sequences to identified other family members or
CC      related sequences. Anti-(hemi)cellulase antibodies are useful for
CC      qualitative or quantitative determination of a polypeptide in a
CC      biological sample. These antibodies are also useful in diagnosing
CC      organism is infected with Aspergillus. The dough prepared by using the
CC      inventive (hemi)cellulase has increased strength, elasticity, stability,
CC      reduced stickiness, improved extensibility and machinability. The
CC      prepared baked product has improved crumb structure, softness and
CC      flavour. The (hemi)cellulase has higher specificity towards the
CC      substrate, is less antigenic and produces less undesirable side
CC      activities.
XX
XX      Sequence 696 BP; 143 A; 221 C; 192 G; 140 T; 0 U; 0 Other;
SQ
Query Match      30.1%; Score 203; DB 12; Length 696;
Best Local Similarity 59.7%; Pred. No. 2.9e-45;
Matches 398; Conservative 0; Mismatches 260; Indels 9; Gaps 3;
```

```
Db      241 AAGGTTGGAACCCGGGC---AGTGCTCAGAGCCGCTTACTTACACCGGATCATGGGAAAC 297
Qy      298 AACGGCAACAGTACCTTGGGCTCTACGGTTGAGACCGCAACCGGCTGTCAGATATTAC 357
Db      298 GACGCCAAGCCCTACTCTGCTCCGTTACGGTTGAGACCACTCCCTTGGTGGAAATTTAT 357
Qy      358 ATGCTGAGAACTTTGGCACTTATGATCCTTCTCCGGTGTCTACCGTATAGAACTGTTC 417
Db      358 ATGCTGACAAAGTACGGTGTATGACACCCCTCTGGGCTGTACCGAGCTCGGCAACGTC 417
Qy      418 GATGTGAGAGGTGACATCTATGACTCGGCAAGACCACTGGCTCAACGCACTAGATC 477
Db      418 GACAGCAGACGAGAACTTCAAGATCTTCAAGACCACTCGTAGAGAGCGCACTCAATC 477
Qy      478 GACGGCAACCAACTTTCGACCAATATCTGGTCCGTCGCGCAGGACCAACGACGCGT 537
Db      478 GAAGGCACTGCCACTTCAAGCACTGCTCGGTGGCACTAGAGGCGGTATTGGTGA 537
Qy      538 ACCGTCAAGCGGAGCTGCGCACTTCGACGCGCTGCGCTGGTTGAAATGTCACGCT 597
Db      538 ACCGTCAACGACGAGAACTTCGATGCTGGGAGAACCTTGGTCTGAGACT---GGGT 594
Qy      598 GACCACTACTACGAGATCGTTGCAACGAGGCTACTTTCAGACGCGGCTATGCTCGATC 657
Db      595 ACCTTCAACTTACATGATGTTGCAACGAGGATACGAGAGACGCGGCTGCCACATC 654
Qy      658 ACCGTTG 664
Db      655 ACCGTTG 661

RESULT 13
ADJ35015
ID      ADJ35015 standard; DNA; 1008 BP.
XX
XX      ADJ35015;
XX
XX      22-APR-2004 (first entry)
XX
XX      DNA encoding xylanase from an environmental sample seq id 231.
XX
XX      antibacterial; fungicide; thermostable xylanase activity;
XX      dough conditioning; beverage production; nutritional supplement;
XX      animal feed; lignin reduction; wood product; xylan; bacterial infection;
XX      fungal infection; coccidiosis; gene; ds.
XX
XX      Unidentified.
XX
XX      WO2003106654-A2.
XX
XX      24-DEC-2003.
XX
XX      16-JUN-2003; 2003WO-US019153.
XX
XX      14-JUN-2002; 2002US-0389299P.
XX
XX      (DIVE-) DIVERSA CORP.
XX
XX      Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
PI      Beeghlylalan A;
XX
XX      WPI: 2004-099016/10.
XX      P-PSDB; ADJ35016.
XX
XX      Novel xylanase recombinant polypeptide useful for improving textile
PT      texture, treating paper, eliminating microorganisms.
XX
XX      Claim 1; SEQ ID NO 231; 570pp; English.
XX
XX      The invention describes an isolated or recombinant polypeptide (I),
CC      having 50% or more identity to 190 300-1200 residue amino acid sequences
CC      (SI), given in the specification, over a region of 100 or more residues
CC      and the polypeptide as thermostable xylanase activity. (I) is useful for:
```

CC dough conditioning; beverage production; as a nutritional supplement in
CC animal feed; reducing lignin in a wood or a wood product; and for
CC eliminating and protecting animals from a microorganism comprising xylan.
CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
CC acid encoding a polypeptide having a xylanase activity which involves
CC amplification of a template nucleic acid with a primer pair capable of
CC amplifying (II) or its subsequence. (I) is useful for treating and
CC preventing bacterial infection and fungal infection e.g. coccidiosis.
CC This sequence encodes xylanase protein isolated from an environmental
CC sample.

XX Sequence 1008 BP; 192 A; 362 C; 331 G; 123 T; 0 U; 0 Other;

Query Match 29.8%; Score 201.2; DB 12; Length 1008;

Best Local Similarity 59.9%; Pred. No. 9.9e-45;

Matches 376; Conservative 0; Mismatches 243; Indels 9; Gaps 2;

```
QY 37 GCGCGAGCTGGGGCCCTTGGCTTCCGCGAGGAAATGCCACGAGCTCGAAAAGCGACAG 96
DB 73 GTGCGGTGGGGCGGCTCGCGCGCTGATGCTGCGGGGACCGCCAGGCGGACAGGTC 132
QY 97 ACAACCCCACTGGAGGGCTGGCAAGATGTTATTAATTTCTGTGAGATGAGCGT 156
DB 133 GTCAACGACCAACGAGGAGGACCAACACGCTACTACTGTTCTGACGACGACAGC 192
QY 157 GAGCGGAGGCGGACGTAACCAACCTGGAGGCGGACCTACGAGATCAGCTGGGAGAT 216
DB 193 CAGGGACCGTCTCATGAGAAATGGGCTCCGGCGGTCAATACAGACCTCTGGCGCAC 252
QY 217 GCGCGTAACCTGTCGTGGTGAAGAGGGCTGAACCCCGGCTGAACGCAAGAGCCATCAC 276
DB 253 ACCGGCAACTTTCGTGGGGGCAAGGGCTGGGCAACCGCGGCGCGCGGCGGCGGCGG 309
QY 277 TTGAGGGTGTATTCACGACCAAGGCAACGCTACTCTGGGTCTACGCTTGAACCGCC 336
DB 310 TACTCGGGCAGCTTCAACCCCTCCGCGCAACGCTACCTGGGCTCTACGATGAGCGTCG 369
QY 337 AACCGGCTGGTGAATTAATCATGTCGAGAACTTTGGGACCTTAATGATTCCTCGGCT 396
DB 370 AACCGGCTGGTGAATTAATCATGTCGAGAACTTTGGGACCTTAATGATTCCTCGGCT 427
QY 397 GCTACCATCTAGGAATGTCGAGTGGGACGCTAGCACTTATCGACTCGGCAAGACCAT 456
DB 428 ----AGTACAAAGGACCGTACACGAGGAGCGGGGACCTTACGACATCTTACAAAGAC 483
QY 457 GCGGTCAACGACCTAGCATGACGCAACCAACCTTTCGACCAATACTGGTGGTCCG 516
DB 484 CGCGTCAACGACCGCTCGTCGAGGGGACCGGCACTTTCGACAGTACTGGAGCGTCCG 543
QY 517 CAGGCAAGGCGCACGAGGCTACGTCGAGCGGGGCGGCACTTTCGAGCGCTGGGCTCCG 576
DB 544 CAGGCAAGGCGCACGAGGCTACGTCGAGCGGGGCGGCACTTTCGAGCGCTGGGCTCCG 603
QY 577 GCTGGTGAATGTCACGCTGACCACTACTACGATCGTTGGCAAGGAGCTACTTC 636
DB 604 GCGGGATGCGGCTCGGCACTTACGCTACATGATCATGGGCAACGAGGCTTACAG 663
QY 637 AGCAGCGGCTATGCTCGCATCACCGTTG 664
DB 664 AGCAGCGGCTATGCTCGCATCACCGTTG 691
```

RESULT 14

AA63044 standard; cDNA; 851 BP.

AA63044;

17-OCT-2003 (revised)

22-JUL-1997 (first entry)

Apergillus niger xylanase cDNA.

KW Endoxylanase; xylanase; protein detection; enzyme detection;
XX library screening; ds.
XX

OS Apergillus niger; strain N400 (CBS120.49).

PH Key Location/Qualifiers

FT CDS 30..707

/*tag= a

PN W09713853-A2.

PD 17-APR-1997.

PF 14-OCT-1996; 96WC-BP004510.

PR 13-OCT-1995; 95EP-00202777.

PA (KONN) GIST-BROCADES BV.

PI Van Den Broeck HC, De Graaff LH, Visser J, Van Ooyen AJJ;

DR WPI; 1997-235889/21.

DR P-PSDB; AAW14597.

PT Identifying DNA fragments encoding proteins, e.g. for new enzyme
PT discovery - by direct screening of a cDNA library in bacteria transformed
PT with DNA from eukaryotic organism producing the protein.

PS Claim 6; Page 19-20; 30pp; English.

CC A cDNA clone (AA63044), deposited as CBS 590.95, codes for a xylanase
CC (AAW14597) of *Apergillus niger* N400 (CBS120.49). It was isolated using a
CC method for identifying a DNA fragment encoding a protein of interest. The
CC method involves the direct screening of a cDNA library prepd. in bacteria
CC (e.g. *E. coli*) transformed with DNA from a eukaryotic organism (e.g. *A.*
CC *niger*) that produces the protein. Screening for xylanase-producing clones
CC can be performed on agar plates containing oat spelt xylan and RBB-xy12an.
CC The method was utilized in the identification of cDNA clones (AA63042-
CC 46) coding for *A. niger* cellulase, xylanase and arabinoxylan degrading
CC enzymes (AAW14595-99). (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 851 BP; 201 A; 244 C; 224 G; 182 T; 0 U; 0 Other;

Query Match 29.4%; Score 198.4; DB 2; Length 851;

Best Local Similarity 61.5%; Pred. No. 5.5e-44;

Matches 354; Conservative 0; Mismatches 216; Indels 6; Gaps 2;

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QY 98 CAACCCCACTCGAGGCGTGGACGATGTTATTACTATTTCTGTGGAGTGAACGCTG 157
DB 142 CAGACCCGAGCTGACCGGCGGAGAAACAGCGCTTCTACTACTCTTCTGACCGAGCGG 201
QY 158 GAGCGGAGCGACGTAACCAACCTTGAGAGCGGACCTTACGAGATCAGCTGGGAGATG 217
DB 202 GTGAGAGCGTGAACCTTACCAACGAGAGATGCTGTGCTTACCTGTTGAGTCCAAAG 261
QY 218 GCGGTAACTTCGTGGTGAAGAGGCTGGAAACCCCGGCTGAAACGCAAGAGCATCACT 277
DB 262 TGGGCAACTTGTGCGGTGAAGAGGCTGGAACCCCGG---AAGTGGCGAGGACATCACT 318
QY 278 TTGAGGGTGTATTCACGACCAACGCGCAACGCTACCTGCGGTCTACGTTGAGCCGCA 337
DB 319 ACAAGGCGACCTTCAACCCCTTACGCGGCAACGCGCTTCTCGTCTATGCTGAGCACTG 378
QY 338 ACCCGCTGTGAGATTTATACATGTCGAGAACTTTGGCACTTATGATCTTCTCCGGTG 397
DB 379 ACCCTCTGATCGAGTACTACATGTCGAGTCTTACCGGCACTAACCCCGGAGTGGAG 438
QY 398 CTACCGATCTAGGAATGTCGAGTGGAGCGTGAACCTTATGCACTCGGAAACCACTC 457
DB 439 GCACTTCAAGGCGACCGTCACTCGAGCGAGATCGTTTACATCTTCAACGCGCTTACC 498
QY 458 GCGTCAACGCACTTACATGACGCGCAACCAACCTTTCGACCAATCTGCTCGGCTCGGC 517
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Db 499 GTACCAATGCTGCTTCATTCCATTCAGGGAACCCCTTCACTCACTAGTACTGCTGCTTCCGCC 558
 Qy 518 AGAACAAAGCCACACAGGCTTACCGTTCAGACGGGCTGCACTTCGACGCGTGGGCTCGCG 577
 Db 559 AGAACAAAGAGTGGGCGAAACCTTACCACTTCACCAACCTTCATTAAGCTTGGGCTTAAC 618
 Qy 578 CTGGTTGAATGTCACGCTGACCACTTACCAAGATCGTTTGGCAACGAGGCTACTTCA 637
 Db 619 TGGGAATGAA---CTGGGTAATCTACAACTACCAAGATCGTGGCTACCGAGGTTACCAAGA 675
 Qy 638 GCAGCGGCTATGCTCGCATCAACCTTGTCTGACGTGG 673
 Db 676 GCAGTGATCTTCTCTCATCATCACTGTTCGTAAAGCGG 711
 RESULT 15
 AAX90405
 ID AAX90405 standard; DNA, 1375 BP.
 XX AAX90405;
 AC
 XX 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-SEP-1999 (first entry)
 XX
 DE Actinomadura sp. DSM43186 35 kDa xylanase encoding DNA.
 XX
 KM Actinomadura sp. DSM43186; xylanase; Actinomadura flexuosa; lignin;
 KM thermostable; biobleaching; wood pulp; bleaching; hemicellulase;
 KM paper processing; hemicellulose; ss.
 XX
 OS Nonomurasea flexuosa.
 XX
 FH Key Location/Qualifiers
 FT 303..1337
 FT /*tag= a
 FT /product= "xylanase"
 XX
 PN US5935836-A.
 XX 10-AUG-1999.
 XX
 PF 06-JUN-1995; 95US-00468812.
 XX
 PR 29-JUL-1994; 94US-00282001.
 PR 31-OCT-1994; 94US-00332412.
 XX
 PA (ROHG) ROEHM ENZYME FINLAND OY.
 XX
 PI Fagerstrom R, Lantto R, Palohelmo M, Suominen P, Vehmanperae J;
 PI Maentylae A;
 XX
 DR WPI; 1996-141347/38.
 DR P-PSDB; AAY24480.
 XX
 PT Actinomadura xylan sequences and method of use.
 XX
 PS Disclosure; Fig 13; 54pp; English.
 XX
 CC The present invention describes a culture medium obtained from the
 CC culture of a recombinant host cell that is not Actinomadura flexuosa and
 CC has been transformed with a vector encoding a protein having xylanase
 CC activity, where the protein comprises an amino acid sequence from a
 CC xylanolytic fragment of the amino acid sequence in AAY24480 or AAY24481.
 CC Also described is an enzyme preparation derived from the culture medium.
 CC The enzyme composition can be used in a method for biobleaching,
 CC modifying plant biomass properties, especially the reduction of lignin
 CC content in pulp and paper processing. The xylanases are hemicellulases
 CC which partially degrade the hemicellulose and enhance the extractability
 CC of lignins by conventional chemical bleaching of wood pulp. It can be
 CC used alone or as a supplement to other treatments that reduce lignin
 CC content of wood pulp, increase its drainability or decrease its water
 CC retention. The culture medium can be used directly without the need to

CC purify the enzymes. Actinomadura flexuosa xylanases have a pH optimum and
 CC thermostability desirable for the biobleaching of wood pulp reducing the
 CC need to acidify the pulp prior to xylanase treatment. The xylanases
 CC partially degrade the hemicellulose in wood pulp which enhances the
 CC extractability of lignins by conventional bleaching chemicals and results
 CC in a lower consumption of bleaching chemicals reducing the formation of
 CC environmentally undesired organic compounds. N.B. This sequence is indexed
 CC Actinomadura sp. DSM43186 35 kDa xylanase. N.B. This sequence is indexed
 CC from US5935836 which is a treat as basic specification for F19503639.
 CC (Updated on 25-MAR-2003 to correct DR field.) (Updated on 16-OCT-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 1375 BP; 265 A; 517 C; 400 G; 193 T; 0 U; 0 Other;
 Query Match 29.1%; Score 196.2; DB 2; Length 1375;
 Best Local Similarity 59.0%; Pred. No. 2, 5e-43;
 Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;
 Qy 5 TCGGCTTTTACCCCGCTTGGCCCTTACCGGCTTACCGGACTGGAGCCCTTGGCCCTTCCCGG 64
 Db 349 TCGGCTTCCGCGCATGCTACCAAGTGCCTTCCGCTTGGCACTGCCATGCGCGGTGCGC 408
 Qy 65 CAGGGAATGCCAAGGAGCTGGAAGCAAGCAACCCCACTGSGAGGCTGGGACG 124
 Db 409 TGCTGCCGCGGACGCGCCACGCGACCAACCATCAACCGAAGCAAGCGGTACACA 468
 Qy 125 ATGATTATTACTATTCCTGCTGAGTGAAGCGTGAAGCGGACGCGACCTACCAACCTGG 184
 Db 469 ACGGCTACTTCTACTGCTTGTGACCGAGCGCGCCGGAGACCGTCTCATGACCTCCACT 528
 Qy 185 AAGGCGGACCTTACGAGATCAGCTGGGAGATGAGCGGTAACTGTGCTGTAAGAAAGGCT 244
 Db 529 CGGCGGCACTACAGCACTCGTGGGGAACCGGGAACCTTGTGCGCGGCAAGGCGT 588
 Qy 245 GGAACCCCGGCTGGAAGCGCAAGCAATCCACTTTAGGGTGTTCACAGCAAAAGGCA 304
 Db 589 GGTCCACCGG---GGAGCGCGGACGCTGACCTTACCAAGCGCTCTTCAACCCGTGGGTA 645
 Qy 305 ACAGCTTACTTGGGCTTACGCTTGAAGCGCAACCGCGCTGCTGATTAATTAATTCGTCG 364
 Db 646 ACGGCTACTTCAAGCTTACGCTGAGCAAGAACCGGCTGTGATTAATTAATTCGTCG 705
 Qy 365 AGAATTGGACCTTATGATCTTCTCGGCTGCTACCGATCTTAGAACTGTGAGTGGC 424
 Db 706 AGAGTGGGCACTTACCGGCGCACCGGCGC-----ACCTTCAAGGGGACCGTCAACCGG 759
 Qy 425 ACGGTAGCATCTTACGACTGGGCAAGCACTGCGCTCAACGCACTAGATGAGAGGCA 484
 Db 760 ACGGGGGAACGTACGACATCTACGAGACTGGCGGTACCAAGCGGCTCAATGAGGACA 819
 Qy 485 CCCAAACCTTGCACCAATATCTGTCGGTCCGCCAGACAAGCGCACAGCGGTACCGTCC 544
 Db 820 CCGGACCTTCCAGCACTTCTGAGAGCTCCGGAGCAAGAACGGAACAGCGGCACTTCA 879
 Qy 545 AGACGGGCTGCCACTTGCAGCGCTGGGCTGCGCTGTTGAATGTCAACGTTGACCACT 604
 Db 880 CCACTGGCAACCACTTGCAGCGCTGGGCGCGCGCGGCAATGAA---CCTGGGCGAGCAAG 936
 Qy 605 ACTTACGATCTGTTGCAAGGAGGCTTACCTTCAAGCAAGCGGTAGCTGATCAACCGTGG 664
 Db 937 ACTTACGATCTGTTGCAAGGAGGCTTACCTTCAAGCAAGCGGTAGCTGATCAACCGTGG 964
 Qy 665 CTGACGTGGGC 675
 Db 997 GCGAGGGTGGC 1007

Search completed: February 11, 2006, 18:30:53
 Job time : 423.587 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:13:54 ; Search time 3418.97 Seconds

(without alignments)
9237.078 Million cell updates/sec

Title: US-09-467-368-1_COPY_31_705

Perfect score: 675

Sequence: 1 ATGATCGCGCTTACCCCGT.....TCACCGTGTGACGTGGGC 675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapept 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|-------------|
| 1 | 291.2 | 43.1 | 860 | DR637934 | EST102855 |
| 2 | 291.2 | 43.1 | 883 | DR643290 | EST103391 |
| 3 | 240.2 | 35.6 | 882 | DR037502 | 49478.2 L |
| 4 | 233.4 | 34.6 | 675 | DN588726 | 49478.1 L |
| 5 | 229 | 33.9 | 744 | CP867983 | tr1c013xe |
| 6 | 229 | 33.9 | 799 | CB898036 | tr1c013xe |
| 7 | 222.6 | 33.0 | 772 | CN133022 | OX1_9_D10 |
| 8 | 220.4 | 32.7 | 639 | DR624928 | EST101505 |
| 9 | 220.4 | 32.7 | 749 | DR623097 | EST101322 |
| 10 | 219.4 | 32.5 | 686 | DR624738 | EST101486 |
| 11 | 219.4 | 32.5 | 719 | DR631520 | EST102164 |
| 12 | 219.4 | 32.5 | 733 | DR630899 | EST102102 |
| 13 | 219.4 | 32.5 | 739 | DR624376 | EST101450 |
| 14 | 219.4 | 32.5 | 741 | DR625790 | EST101591 |
| 15 | 219.4 | 32.5 | 763 | DR624330 | EST101445 |
| 16 | 219.4 | 32.5 | 784 | DR628641 | EST101876 |
| 17 | 219.4 | 32.5 | 801 | DR631291 | EST102141 |
| 18 | 219.4 | 32.5 | 807 | DR621776 | EST101190 |
| 19 | 219.4 | 32.5 | 809 | DR627394 | EST101752 |
| 20 | 219.4 | 32.5 | 842 | DR630275 | EST102040 |
| 21 | 219.4 | 32.5 | 866 | DR621753 | EST101188 |
| 22 | 219.4 | 32.5 | 891 | DR632055 | EST102218 |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | | | | | | |
|----|-------|------|-----|---|----------|----------|-----------|
| 23 | 219.4 | 32.5 | 916 | 8 | DR622008 | DR622008 | EST101213 |
| 24 | 219.2 | 32.5 | 729 | 8 | DR629975 | DR629975 | EST102010 |
| 25 | 219.2 | 32.5 | 763 | 8 | DR623625 | DR623625 | EST101375 |
| 26 | 219 | 32.4 | 734 | 8 | DR622879 | DR622879 | EST101300 |
| 27 | 219 | 32.4 | 768 | 7 | CF881056 | CF881056 | tr1c083xj |
| 28 | 219 | 32.4 | 822 | 6 | CB907827 | CB907827 | tr1c083xj |
| 29 | 215.8 | 32.0 | 711 | 8 | DR622988 | DR622988 | EST101311 |
| 30 | 215.8 | 32.0 | 770 | 8 | DR622508 | DR622508 | EST101263 |
| 31 | 214.6 | 31.8 | 708 | 8 | DR631672 | DR631672 | EST102180 |
| 32 | 211.4 | 31.3 | 921 | 6 | CD458837 | CD458837 | F908_04b1 |
| 33 | 207.2 | 30.7 | 714 | 8 | DR631518 | DR631518 | EST102164 |
| 34 | 202.8 | 30.0 | 671 | 8 | DR632323 | DR632323 | EST102245 |
| 35 | 202 | 29.9 | 697 | 8 | DR625721 | DR625721 | EST101584 |
| 36 | 201.8 | 29.9 | 673 | 8 | DR625705 | DR625705 | EST101583 |
| 37 | 199.4 | 29.5 | 655 | 8 | DR625642 | DR625642 | EST101577 |
| 38 | 199.4 | 29.5 | 677 | 8 | DR629147 | DR629147 | EST101927 |
| 39 | 198.6 | 29.4 | 871 | 8 | DR037503 | DR037503 | 49478.3 L |
| 40 | 198.4 | 29.4 | 738 | 6 | CD464145 | CD464145 | ETH1_48_B |
| 41 | 198.4 | 29.4 | 746 | 8 | DR701170 | DR701170 | Asn_00615 |
| 42 | 196.4 | 29.1 | 746 | 6 | CB901964 | CB901964 | tr1c028xi |
| 43 | 196.4 | 29.1 | 746 | 7 | CF871731 | CF871731 | tr1c028xi |
| 44 | 195 | 28.9 | 680 | 8 | DR707969 | DR707969 | Asn_08783 |
| 45 | 191.4 | 28.4 | 682 | 8 | DR702584 | DR702584 | Asn_02201 |

ALIGNMENTS

RESULT 1
LOCUS DR637934 860 bp mRNA linear EST 11-JUN-2005
DEFINITION EST1028559 FvM Gibberella moniliformis cDNA clone FvMB275, mRNA
SEQUENCE:
DR637934 DR637934.1 GI:70712768

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

AUTHORS

1 (bases 1 to 860)
Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y., Utechtack,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D., Kendra,D.F., Town,C.D. and Whitelaw,C.A.

TITLE

Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster

JOURNAL

Unpublished (2005)

COMMENT

Contact: Brown, D.W.
USDA/ARS/NCAR
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncar.usda.gov
TIGR sequence name: FvMB275TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES

Location/Qualifiers
1..860

/organism="Gibberella moniliformis"
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/clone_lib="FvMB275"
/clone_type="FvM"
/note="Vector: Bluescript II SK(+); Site 1: EcoRI; Site 2: XhoI; amorph: Fusarium verticillioides. Library FvM was prepared from pooled RNA obtained from a 48-hour and a 72 hour, liquid GYM culture from strain M-3125. Cultures were vacuum filtered and the mycelial mats were frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIzol. The cDNA was

ORIGIN

directionally ligated into the pBluescript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."

Query Match 43.1%; Score 291.2; DB 8; Length 860;
Best Local Similarity 67.4%; Pred. No. 1,1e-69;
Matches 442; Conservative 0; Mismatches 208; Indels 6; Gaps 2;

18 CGTTGCCCTTGGCGGCTTAAAGCCGAGCTGGGGCCCTGCGCCCTCCGAGGAGGAATGCGAC 77
Db CGCTGGGCTGTCACTGTAAGTGTCTTCTTGGCGGCGCCCTCCAAAGAGTCTTCTC 101
QY 78 GAGAGCTGAAAAGGAGACAGACCAACCCCACTCGAGGCTGAGCAGATGTTATTA 137
Db 102 CAAGATTACCAAGGGGGGTGGTACTCCCAAGTTCCGGTACTTAACAACGATTTCTTCTA 161
QY 138 TTCTGTGTGAGTACGCTGAGCGCAGGCAAGCTAACCACTGGAAGGCGGCACTTA 197
Db 162 CTCTGTGTGAGTACGCTGAGCGGCGGCTGCTACTTAACCAACGATGAGGAGGTTCTTA 221
QY 198 CGAATCAGCTGGGGAGATGGCGGTAACCTGTGCGTGGAAAGGAGCTGGAACCCCGGCT 257
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QY 258 GAAAGCAAGAGCCATTCACCTTTGAGGTGTTTACAGCCAAACGCAACAGCTACCTTGC 317
Db 279 AAAAGCTGAAACCAATCTCTTGAAGGAGTACAAAGCCCAACGCAACAGCTACCTTGC 338
QY 318 GGTCTAGCGTTGAGACCGGCAACCGGCTGTGAGTATTAATCTGTCCAGAACTTTGGCAC 377
Db 339 CGTCTAGCGGTGAGACCGCAACCCCTAGTGAAGTACTAATCTGTGAGTCTTCTGTTAC 398
QY 378 CTATGATCCTTCTCCCGGTGTACCGATCTAGAACTGTGAGGCGGAGCGGTAGCATCTA 437
Db 399 CTACAAACCTCTCCAGCGGTGTACCAAGAGGTTACGTTAGGCTGATGAGCAGACCTTA 458
QY 438 TCAGCTGGGCAAGACCACTGCGTCAACGCACTAGATCGACGCAACCAACCTTTCGA 497
Db 459 CGAATCTTTCAGAGTACTTGGCAACCAACGCGCTTCAATTCAGCGGTACTCAGACCTTCA 518
QY 498 CCAATATCTGTGCGTCCGCCAGACAGCGCAACGCGGTACCTTCCAGAGCGGCTGCGCA 557
Db 519 GCAGTACTGTGTCTGTCCGCAAGCATGCTCTACTGTGAGCGTTCGACTGTGCTTCA 578
QY 558 CTTGAGGCGCTGGGCTGGCGGTGTTGATGTCAAGCTGACCACTACTACAGATGCT 617
Db 579 CTTGAGCGCTGGGAGGAGGCTGTATTAAGCT---CGTACCCACGACTACAGATGCT 635
QY 618 TCGAAGCGAGGAGCTACTTCAGACGCGCTATGCTGCATCAACGTTGCTGACGTGG 673
Db 636 CGCTACTGAGGGTACTTCAGAGCGGATCTTCTACATGACCGTTTCTGAGGGGG 691

RESULT 2
DR643290 883 bp mRNA linear EST 11-JUL-2005
LOCUS ESM1033915 FvM Gibberella moniliformis cDNA clone FvMCX47, mRNA
DEFINITION
ACCESSION DR643290
VERSION DR643290.1 GI:70718124
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocnemycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 883)
AUTHORS Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,
Utecher, T., Smith, S., Feldlyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitehead, C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
JOURNAL Unpublished (2005)
COMMENT Contact: Brown, D.W.

USDA/ARS/NCAUR
USA
1815 N. University St., Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FvMCX477H
Seq primer: AAT TAA CCC TCA AAG GG.
Location/Qualifiers
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/clone_lib="FvM"
/note="Vector: pBluescript II SK(+) XR, Site 1. EcoRI.
Site 2: XhoI; amorph: Fusarium verticillioides. Library
FvM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 43.1%; Score 291.2; DB 8; Length 860;
Best Local Similarity 67.4%; Pred. No. 1,1e-69;
Matches 442; Conservative 0; Mismatches 208; Indels 6; Gaps 2;

18 CGTTGCCCTTGGCGGCTTAAAGCCGAGCTGGGGCCCTGCGCCCTCCGAGGAGGAATGCGAC 77
Db 42 CGCTGGGCTGTCACTGTAAGTGTCTTCTTGGCGGCGCCCTCCAAAGAGTCTTCTC 101
QY 78 GAGAGCTGAAAAGGAGACAGACCAACCCCACTCGAGGCTGAGCAGATGTTATTA 137
Db 102 CAAGATTACCAAGGGGGGTGGTACTCCCAAGTTCCGGTACTTAACAACGATTTCTTCTA 161
QY 138 TTCTGTGTGAGTACGCTGAGCGCAGGCAAGCTAACCACTGGAAGGCGGCACTTA 197
Db 162 CTCTGTGTGAGTACGCTGAGCGGCGGCTGCTACTTAACCAACGATGAGGAGGTTCTTA 221
QY 198 CGAATCAGCTGGGAGATGGCGGTAACCTGTGCGTGGAAAGGAGCTGGAACCCCGGCT 257
Db 222 CTCATGAGAGTGAAGAGTGTGTACGTGTGAGGTGTGTGTCTCTG--- 278
QY 258 GAAAGCAAGAGCCATTCACCTTTGAGGTGTTTACAGCCAAACGCAACAGCTACCTTGC 317
Db 279 AAAAGCTGAAACCAATCTCTTGAAGGAGTACAAAGCCCAACGCAACAGCTACCTTGC 338
QY 318 GGTCTAGCGTTGAGACCGGCAACCGGCTGTGAGTATTAATCTGTCCAGAACTTTGGCAC 377
Db 339 CGTCTAGCGGTGAGACCGCAACCCCTAGTGAAGTACTAATCTGTGAGTCTTCTGTTAC 398
QY 378 CTATGATCCTTCTCCCGGTGTACCGATCTAGAACTGTGAGTGCAGCGGTAGCATCTA 437
Db 399 CTACAAACCTCTCCAGCGGTGTACCAAGAGGTTACGTTAGGCTGATGAGCAGACCTTA 458
QY 438 TCGAAGCGAGGAGCACTGCGTCAACGCACTAGATCGACGCAACCAACCTTTCGA 497
Db 459 CGAATCTTTCAGAGTACTTGGCAACCAACGCGCTTCAATTCAGCGGTACTCAGACCTTCA 518
QY 498 CCAATATCTGTGCGTCCGCCAGACAGCGCAACGCGGTACCTTCCAGAGCGGCTGCGCA 557
Db 519 GCAGTACTGTGTCTGTCCGCAAGCATGCTCTACTGTGAGCGTTCGACTGTGCTTCA 578
QY 558 CTTGAGGCGCTGGGCTGGCGGTGTTGATGTCAACGCTGACCACTACTACAGATGCT 617
Db 579 CTTGAGCGCTGGGAGGAGGCTGTATTAAGCT---CGTACCCACGACTACAGATGCT 635

Qy 618 TGCAACGAGGAGGCTACTTACAGACGGCTATGCTGCATACCGTTGCTGACGCTG 673
Db 636 CGCTACTGAGGGTACTTACAGACGGGATCTTCTACATGACCGTTTCTGAGGGGG 691

RESULT 3
LOCUS DR037502 882 bp mRNA linear EST 31-MAY-2005
DEFINITION 49478.2 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
49478.5', mRNA sequence.
ACCESSION DR037502
VERSION DR037502.1 GI:66839397
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 882)
AUTHORS Flint, B., Roehwell, C., Sardana, R., Griffiths, R., Laque, M., De Koeijer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.
TITLE Generation of ESTs from late blight-challenged potato tubers
JOURNAL Unpublished (2005)
COMMENT Contact: Barry Flint
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflint@bioatlantech.nb.ca
Seq primer: T3.
Location/Qualifiers
1..882
/organism="Solanum tuberosum"
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/clone_idb="Late Blight-Challenged Tubers"
/note="Vector: pBluescript II SK(+); XR; Site_1: EcoRI; Site_2: XhoI; supplier: Pathogen-challenge series. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with 5 ul of Phytophthora infestans (A2-mating type), through 2 puncture wounds 3 cm apart. The tubers were incubated 1 minute to allow inoculum absorption. The infection area was outlined for future collection reference. Surface slices were sampled from the tubers at 1 day, 5 days, 7 days, 11 days and 14 days post-infection. All samples were pooled and used for RNA isolation and library construction. A normalized library was constructed following a modified protocol of Bonaldo et al. (1996). Genome Research 6: 791-806."

ORIGIN
Query Match 35.6%; Score 240.2; DB 8; Length 882;
Best Local Similarity 60.9%; Pred. No. 1,6e-55;
Matches 411; Conservative 0; Mismatches 256; Indels 6; Gaps 1;
1 ATGGTCGGCTTTACCCCGTTGCGGCGCTTACGCGAGCTGGGGCCCTGCGCTTC 60
25 ATGGTTTCCTTACTACTCTCTCATCTGCGTGTGCGGTGCTGGCGCTGA 84
Qy 61 CCGGACGAGGATGCGACGAGAGCTGAAAAGCAGACACCCCAACTCGAGGGCTG 120
Db 85 CCGGACGAGGATGCGACGAGAGCTGAAAAGCAGACACCCCAACTCGAGGGCTG 138
Qy 121 CACGATGTTATTAATCTATCTGAGTGAAGTGAAGGCGACGACCTACACCAAC 180
Db 139 AACGGCGGTAATCTACTCTCTGAGTGAAGTGAAGGCGACGACCTACACCAAC 198
Qy 181 CTGAAAGCGGACCTACGAGATGAGCTGGGAGATGCGGTAACTCTGCTGGTAAAG 240
Db 199 AAGCGCGGTGAGAGTACTCCCTGACCTGAGCGGCAACGCAACGTGCTGGTAAAG 258

Qy 241 GGTGGAACCCCGGCTGAAAGCAAGACCACTTCATTGAGGGTGTACAGCCAAAC 300
Db 259 GGATGGAACCCGGAAGTGGCCAGACATACCTACTGGGACCTTCAACCCCAATG 318
Qy 301 GGCACAGCTTACTTGGGGTCTACGGTTGACCCCGCAACCCGCTGTGAGTATTAC 360
Db 319 GGCACAGCTTACTTGGGGTCTACGGTTGACCCCGCAACCCGCTGTGAGTATTAC 378
Qy 361 GTGAGAACTTTGGGACCTTATGATCTTCTCCGGGTGCTACCGATTAGAAAGTGC 420
Db 379 GTTAAAGCTTGGTGTATATGACCCCTCTCCGGGTGCTGAGCAAGGACGTTACC 438
Qy 421 TGCGACGGTAGCATCTATTCGACCTGCGAAGCACTGCGCTCAACGACCTAGATC 480
Db 439 GTTATGCGACGACCTTACCATCTCTCAAGCTACCGGTACCAACGACCTTCAAT 498
Qy 481 GGCACCAAACTTTCGACCAATATCTGTCGCGCGCAGACAAAGCGACGAGGTACC 540
Db 499 GGCACCTGCACTTTTCAGAGTACTGCTGTTGCGCAAGAACCAACCGACGAGGATCC 558
Qy 541 GTCCAGACGGGCTCCGCTTCGACGCTGCGGCTGCGCTGTTGAATGCAAGGTAC 600
Db 559 GTTATGTCGAGCTCACTTTCGCGCTGGAAGTCAAGGAATGAACCTGGGACATG 618
Qy 601 CACTACTACGAGATCTTTCGACGAGGAGCTTCTACGACGAGGCTATGCTGCATCAC 660
Db 619 CACAATCAACGATGTTGCTTCCGAGGGTTACCAACGACGAGGCTTCCGCGATATCA 678
Qy 661 GTTGTGACGCTGGGC 675
Db 679 GTTGATCCGGGTGC 693

RESULT 4
LOCUS DN588726 675 bp mRNA linear EST 15-MAR-2005
DEFINITION 49478.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
49478.5', mRNA sequence.
ACCESSION DN588726
VERSION DN588726.1 GI:61239134
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 675)
AUTHORS Flint, B., Roehwell, C., Sardana, R., Griffiths, R., Laque, M., De Koeijer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.
TITLE Generation of ESTs from late blight-challenged potato tubers
JOURNAL Unpublished (2005)
COMMENT Contact: Barry Flint
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflint@bioatlantech.nb.ca
Seq primer: T3.
Location/Qualifiers
1..675
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="49478"
/tissue_type="Tubers"
/lab_host="X110-Gold"
/clone_idb="Late Blight-Challenged Tubers"
/note="Vector: pBluescript II SK(+); XR; Site_1: EcoRI; Site_2: XhoI; supplier: Pathogen-challenge series. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with 5 ul of Phytophthora infestans (A2-mating type), through 2 puncture wounds 3 cm apart. The tubers were incubated 1 minute to allow inoculum absorption. The infection area was outlined for future

collection reference. Surface slices were sampled from the tubers at 1 day, 5 days, 7 days, 11 days and 14 days post-infection. All samples were pooled and used for RNA isolation and library construction. A normalized library was constructed following a modified protocol of Bonaldo et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Query Match 34.6%; Score 233.4; DB 8; Length 675;
Best Local Similarity 60.9%; Pred. No. 1.2e-53;
Matches 400; Conservative 0; Mismatches 251; Indels 6; Gaps 1;

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Qy 1 ATGTCGCGCTTTACCCCGCTTGGCCGCTTACCGCGAGCTGGGCGCTTC 60
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Db 25 ATGCTTCCCTTACCTTCTCATTCCTCGTCCGCTGGGCTTCGCTGAA 84
Qy 61 CCGGACGGAATGCCAGGAGCTGAAAAGCAGACACCCTCACTGGAGGCTGG 120
    |||||
Db 85 CCCGAGCAGCCCTTACCCCGCCACA-----AGAGCCGACAGAACAGACTGGCCAG 138
Qy 121 CAGATGGTTATTCTATTCTGGTGGAGTAGACGGTAGGCGGACGATACCAAC 180
    |||||
Db 139 AACGGCGGTACTACTCTCTTGGAGTAGACAGGCGGACCACTTACCAAC 198
Qy 181 CTGGAAGCGGACCTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGAAG 240
    |||||
Db 199 AAGCCCGGTGAGAGTCTCCCTGACCTGGAGCGGCAACGGCAAGTGTGGAAG 258
Qy 241 GCGTGAACCCCGGCTGAGACGCAAGCCATCCACTTGAAGGTTTACAGCAAC 300
    |||||
Db 259 GGATGGAACCCAGAGAGTCCGACATCACTCTGGGACCTTCAACCCCAATGT 318
Qy 301 GGAACAGCTACCTTGGCGGTCTACGGTGGACCCGCAACCCGCTGTGATATTATC 360
    |||||
Db 319 GGCACGCTACCTCTGCTATGAGCTGAGACCGGAAACCGCTGATGATCTACATC 378
Qy 361 GTCGAGAACTTTGGCACTTATGATCTTCTCCGCTGCTACCGATTAGAACTGTGAG 420
    |||||
Db 379 GTTGAAAGCTTCGGTATATGACCCCTCTCCGCTGCTGAGCAAGGACGCTCAC 438
Qy 421 TGGCAGGTATGATCTATGACTGGGCAAGACACTGCGCTCAACGACCTTAGATGAC 480
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Db 439 GTTATGTCACACCTTACACATCTCTCAAGCTACCCCTTACCAACGACTTCAATCAT 498
Qy 481 GGAACCCCAACCTTGCACCAATATCTGCTGCGCTGCGGCAAGCAAGCGGAGCTTAC 540
    |||||
Db 499 GGCACCTGACCTTTTCAAGATGACTGCTGCTGCTGCGGCAAGCAAGCGGAGCTTAC 558
Qy 541 GTCGAGCGGCTGCTGACCTTGCAGCGCTGGGCTGCGCTGTTGATGATCAACGCTGAC 600
    |||||
Db 559 GTTGATGTGCGAGCTCACTTTGGCGGCTGGAGATCCAGGGAATGAACTGGGCACTGAG 618
Qy 601 CACTACTTACGAGTGTGGCAAGGAGGCTTCTTACGACAGCGGCTTATGCTGCAATC 657
    |||||
Db 619 CACAACCTACGAGATGTGTCTCCGAGGGTTACCAACAGACGCGGTTCCGCGATATTC 675

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RESULT 5
CP867983 744 bp mRNA linear EST 31-OCT-2003

LOCUS tric013xe09.b1 T.reesei mycelial culture, Version 6 October 2003

ACCESSION CP867983 Hypocrea jecorina cDNA clone tric013xe09, mRNA sequence.

VERSION CP867983.1 GI:38122635

KEYWORDS

ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)

REFERENCE 1 (bases 1 to 744) Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,

Ward, M. and Dean, R.A. Tuber infection of *Trichoderma reesei* by *Hypocrea jecorina* and *Hypocrea reesei* isolates. *Journal of General Microbiology* 147: 147-152 (2003).

TITLE

Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from *Trichoderma reesei*

JOURNAL

FEMS Microbiol. Lett. 230 (2), 275-282 (2004)

14757250

Contact: Ralph A. Dean

Fungal Genomics Laboratory

North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020

Fax: 919-513-0024

Email: ralph_dean@ncsu.edu

Seq primer: Tr-F1 primer.

Location/Qualifiers

1..744

/organism="Hypocrea jecorina"

/mol_type="mRNA"

/strain="QM6a"

/db_xref="taxon:51453"

/clone="tric013xe09"

/dev_stage="mycelia"

/clone_1lb="T.reesei mycelial culture, Version 6 October 2003"

/note="Vector: pBBP3Y, Site 1. Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

Query Match 33.9%; Score 229; DB 7; Length 744;
Best Local Similarity 61.6%; Pred. No. 2.1e-52;
Matches 400; Conservative 0; Mismatches 245; Indels 4; Gaps 2;

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Qy 5 TCGGCTTTACCCCGCTTGGCCGCTTACCGCGAGCTGGGCGCTTCGCCG 64
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Db 96 TCACCTCCCTCTCTGCGGGGTGCGGCCATCTGGCGCTTGGCGGCTCCGCCGCG 155
Qy 65 CAGGAAATGCCAGGAGCTGAAAAGCAGACACACCCCACTCGAGGCTGGCAG 124
    |||||
Db 156 AGTCGAATCCGTGCTGTGAGAGGCGCAGAGATTCAGGCGGCGGCTTACCA 215
Qy 125 ATGCTTATTCTTCTGATGAGTAGCGGTGAGGCGGCAAGCTTACCAACCTGG 184
    |||||
Db 216 ACGGCTTCTTACTCTTACTGAGAGCATGGCCAGCGGCGGTGACATCAATGCTC 275
Qy 216 ACGGCTTCTTACTCTTACTGAGAGCATGGCCAGCGGCGGTGACATCAATGCTC 275
    |||||
Db 216 ACGGCTTCTTACTCTTACTGAGAGCATGGCCAGCGGCGGTGACATCAATGCTC 275
Qy 185 AAGCGGCACTTACGAGATCAGCTGGGAGATGGGTTAACTCTGTGGAAGGCT 244
    |||||
Db 276 CCGGCGGAGCTTCTCGGTCACTGCTGCAACTGGGCACTTGTGGCGGCAAGGAT 335
Qy 245 GAAACCCCGGCTGAGACGCAAGACCATCCATTGAGGTGTTTACCAACGCA 304
    |||||
Db 336 GGCAGCCCGGCAACAGAGGTCATCAACTTCTGGGCGGCTTACCAACCCCAAGCA 395
Qy 305 ACAGCTACCTTGGCGGTCTAGCGTGGACCGGCAACCGGCTGAGATTAACATCGCG 364
    |||||
Db 396 ACAGCTACCTTCTCGGTGAGCGCTGTGCGCAACCCCTGATGAGATTAACATCGCG 455
Qy 365 AGACTTTGGCACTTATGATCTTCTCGGTGCTTACGATCTTGAAGTTCGAGTGG 424
    |||||
Db 456 AGAATTGGGCACTTACACCCGCTCAAGGCGGCAACAGCTGGGAGGTCACCTCG 515
Qy 425 ACGGTAGATCTATGACTGCGCAAGACCACTGCGCTCAACGCACTTACGAGGCA 484
    |||||
Db 516 ACGGAGCGGTCTACGATTTTACGCGACGCGCGCTTCAACACCGCTTCAATCGGCA 575
Qy 485 CCAAACTTGGCACTTATGATCTTCTCGGTGCTTACGATCTTGAAGTTCGAGTGG 544
    |||||
Db 576 CCGGCACTTTTACAGATCTGCTGCTGCGGCAACCAACGCTCGAGGCTTCGCA 635
Qy 545 AGAGGCGGTGCACTTGAAGCTGCGGCTGCTGCTGCTTGAATGTCAACGCTGCACT 604
    |||||
Db 636 ACAGGCGGAACCACTTCAAGCGCTGCGGCTTACGCAAGGCTTACCGCT---CGGACGATGG 692
Qy 605 ACTACGATGCTTG-CAACGAGGCGTACTTTCAGACGCGGCTATGCTC 652

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| | | | |
|--|---|--|-----|
| Db | | 693 ATTACAGATTCTTCCCGGAGGGTTACTTAACTCTGCCTCCTC | 741 |
| RESULT 6 | | | |
| CB898036 | | | |
| LOCUS | | | |
| DEFINITION | CB898036 | 799 bp mRNA linear EST 02-JUL-2001 | |
| tricle01x09 T. reesei mycelial culture, Version 3 april Hypocrea | | | |
| jecorina cDNA clone tricle01x09, mRNA sequence. | | | |
| Accession | CB898036 | | |
| VERSION | GI:30112694 | | |
| KEYWORDS | EST. | | |
| SOURCE | Hypocrea jecorina (anamorph: Trichoderma reesei) | | |
| ORGANISM | Hypocrea jecorina | | |
| REFERENCE | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | |
| AUTHORS | Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea. | | |
| | 1 (bases 1 to 799) | | |
| TITLE | Foreman,P.K., Brown,D.E., Dankmeyer,L., Dear,R., Diener,S., | | |
| JOURNAL | Dunn-Coleman,N.S., Goedegebuer,F., Houfek,T.D., England,G.J., | | |
| PUBMED | Kelley,A.S., Meerman,H.J., Teunissen,P.J., Yao,J. and Ward,M. | | |
| COMMENT | Olivares,H.A., transcriptional regulation of biomass-degrading enzymes in the filamentous fungus Trichoderma reesei | | |
| | J. Biol. Chem. 278 (34), 31988-31997 (2003) | | |
| | 12788920 | | |
| | Contact: Pamela K. Foreman | | |
| | Genencor Intl. | | |
| | 925 Page Mill Road, Palo Alto, CA 94304, USA | | |
| | Tel: (650) 846-7635 | | |
| | Fax: (650) 621-7817 | | |
| | Email: Pforeman@genencor.com | | |
| FEATURES | Seq primer: Lt-F1 primer. | | |
| source | Location/Qualifiers | | |
| | 1..799 | | |
| | /organism="Hypocrea jecorina" | | |
| | /mol_type="mRNA" | | |
| | /strain="QMe6" | | |
| | /db_xref="taxon:51453" | | |
| | /clone="tricle01x09" | | |
| | /dev_stage="mycelia" | | |
| | /clone_1lb="T. reesei mycelial culture, Version 3 april" | | |
| | /notes="Vector: pREP3Y, Site 1: Not I/Sal I, Mycelial | | |
| | culture grown from 24 hrs to 6 days with varying Carbon | | |
| | and Nitrogen sources and concentrations." | | |
| ORIGIN | | | |
| Query Match | 33.9%; Score 229; DB 6; Length 799; | | |
| Best Local Similarity | 61.6%; Pred. Nt. 2.1e-52; | | |
| Matches | 400; Conservative 0; Mismatches 245; Indels 4; Gaps 2 | | |
| 5 | TCGGCTTAACCCCGCTTGCCCTTGCGGGCTTAGCCGCACTGGGACCCTGAGCTTCCGG | 64 | |
| 151 | TCACCTCCCTCCTCGCCGGCGTGGCGCATTCGGGGGTCTTGGCCCTCCCGCGCGC | 210 | |
| 65 | CAGGAATGCCAAGAGCTCGAAAAGCACAAGAACCCCACTCGAGGGCTGACG | 124 | |
| 211 | AGTGCATCCGTGCTGTGAGAGCGCCAGACGATTCAGCGCGGCAAGGCTACACA | 270 | |
| 125 | ATGGTATTACATTCCTGCTGTGGAATGACGTGAGAGCGCAGCCATGACACCACTGG | 184 | |
| 271 | ACGGCTACTTCTACTCGTACGTGAACGATGGCACGGCGGCTGACGTACACCAATGGTC | 330 | |
| 185 | AAGCGGACACTACAGATTCAGCTGGGAGAATGCGGTTACTCGTGGTGAAGGGCT | 244 | |
| 331 | CCGGGGGCAATTCCTCGTCACTGTCACACTCGGGCACTTTTGTCCGGCGCAAGGAT | 390 | |
| 245 | GGAACCCGGGCTGAACGACAGAGCATTCACCTTGAAGGGTGTATACAGCAACGCA | 304 | |
| 391 | GGCAGCCCGGACCAAAGACAAAGTCATCACTTCTCGGGGACGTACAAACCCCAAGCA | 450 | |
| 305 | ACAGTACTCTTGGCTTACAGTTGGACCCCGCAACCCCGTGTGAGATTCATCTGTCG | 364 | |
| 451 | ACAGTACTCTTCCGTGATCGGCTGTGTCCCGAACCCCTTATCAAGTACTACATCTGTCG | 510 | |

| | | | |
|------------|---|---|---|
| OY | 365 | AGAACTTTGGACCACTAATGATCTTCCTCCCGGTGCATCCGATCTTAGAACTGTGAGTGC | 424 |
| Dd | 511 | AGAACTTTGGACCACTTAACAACCTGTCACAGGAGGCCAACCAACTGGGCGAGGTCACTCCG | 570 |
| OY | 425 | ACGGTAGCATCTATGCACTCCGCAAGAACACTCGCTGTCAACGACATTAGATCAGCGCA | 484 |
| Dd | 571 | ACGGCAGAGGTCTTAGACATTTACCGGCAACGACGCGGTTCACACGCGGTCAATTCGGCA | 630 |
| OY | 485 | CCCAAACCTTGACCAATATCTGTGTCGTCCGCCAGAGACAAGCGCACACGCGTACCGTCC | 544 |
| Dd | 631 | CCGCGACCTTTTACACAGTACTGTGTCGCTCCGCCCAACAACCGCTCGACGCGCTCCGCA | 690 |
| OY | 545 | AGACGGGGGTGCGACCTTGAGAGCGCTGGGGGTGCGCGCTGGTTGAATGTCAAGGTGACCACT | 604 |
| Dd | 691 | ACACGGCGGACCACTTTCAACGCGTGGGCTCAGCAAGCGCTACGCT--CGGAGCATGG | 747 |
| OY | 605 | ACTACCAAGATCGTGTG-CAACGAGAGGGCTACTTTCAGCAGCGGCTATGCTC | 652 |
| Dd | 748 | ATTACCAAGATTTGTTGCGGTGGAGGGTTACTTTAGCTGTGCTCTGCTC | 796 |
| RESULT 7 | CN133022 | 772 bp | mRNA linear EST 01-APR-2004 |
| LOCUS | CN133022 | OX1_9_D10_g1_A002 | oxidatively-stressed leaves and roots Sorghum |
| DEFINITION | CN133022 | bicolor cDNA clone OX1_9_D10_A002 5', mRNA sequence. | |
| ACCESSION | CN133022 | | |
| VERSION | CN133022.1 | GI:45963542 | |
| KEYWORDS | EST. | | |
| SOURCE | Sorghum bicolor (sorghum) | | |
| ORGANISM | Sorghum bicolor | | |
| REFERENCE | Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum. | | |
| AUTHORS | 1 (bases 1 to 772) Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Lim,S., Baerman,A. and Pratt,L.H. An EST database from Sorghum: oxidatively stressed leaves and roots unpublished (2003) | | |
| TITLE | Other_ESTs: OX1_9_D10_b1_A002 | | |
| JOURNAL | Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel.: 706 542 1860 Fax: 706 583 0210 Email: mmprratt@uga.edu | | |
| COMMENT | Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq primer: Sugs (CTTCGCTCTAAAAGCTGCG). Location/Qualifiers 1..772 /organism="Sorghum bicolor" /mol_type="mRNA" /culivar="BTx623" /db_xref="taxon:4558" /clone="OX1_9_D10_A002" /lab_host="DH10B-T1 phage-resistant E. coli" /note="Organ: Leaf and Root; Vector: pMB18s-FL3; Site: 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were mlsted with 10 uM methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all | | |
| FEATURES | | | |
| SOURCE | | | |

tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pMB18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 33.0%; Score 222.6; DB 7; Length 772;
Best Local Similarity 63.5%; Pred. No. 1.2e-50;
Matches 374; Conservative 0; Mismatches 209; Indels 6; Gaps 2;

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QY 74 CCACGAGCTCGAAAAAGGACAGACACCCCACTCGGAGGGCTGGACATGTTATT 133
Db 132 CCTGGTCTTGAGAGCCCGCCAGTCACTGGTAATCTGAGGGTTACCATATGATTA 191
QY 134 ACTATTCCTGGTGGAGTGAAGAGGCGGACGACGTAACCAACCTGGAAAGCGGCA 193
Db 192 TCTACTCTTGGTGTCTGATGCGGTGCTATGCCAATTCAGATGGGTAGGAAATC 251
QY 194 CCTACGAGATCAGCTGGGAGATGGCGGTAACTCTGTCGTGAAAGGGCTGAAACCCG 253
Db 252 ACTACAGGTTGATTTGGCGCAACTGGTAACTTTGTTGGTGAAGGGTTGAACCCG 311
QY 254 GCCTGAACGCAAGACCTCACTTTAGGGTGTTCACAGCCAAAGCGCAACGTTACC 313
Db 312 G---TACTGGCCGAACCATCACTATGCGGTTCTTTCAGCCCTCAGGGTTAACGCTAAC 368
QY 314 TTGGGGTTACGATTGAGACCCGCAACCCGCTGTCGATGATTAATCATCGTGAACCTTTG 373
Db 369 TCTGGCTTACGGCTGAGCTGAGCCCTCTCTGTTGATTAATCACTCATCGAATCAACG 428
QY 374 GCACCTATGATCTCTCTCCGGTGTCTACCATCTAGAACTGTGAGTGCAGCGGTAGCA 433
Db 429 GCACCTTACACCCCTGCTCTGCTGGCCAGCAACAGGGCACCGTCTTACACAGCGCGACA 488
QY 434 TCTATCAGCTGGGCAAGACCACTGCGCTCAACGCACTAGATGACGGCACCCAACT 493
Db 489 CCTAGATCTTACCAAGCAACCCGCTTACCAACCAAGCCCTTATCGACGGCCAAACGACT 548
QY 494 TCGACCAATATCTGGTGGTCCGCGCAGACCAAGCGACAGCGGTACCGTCCAGACGGCT 553
Db 549 TCAACCAATATCTGGGCTTCCGCGCCAGCAACAGCGAGCGCGCTTCAACATGACGA 608
QY 554 GCACCTTGACGCGCTGGGCTCGCGCTGTTGATATGTAACGCTGACCACTTACACGA 613
Db 609 CTATCTTCAATGCTTGGGCTTAACTGGTATGAGACT---TGAAACCACTACTACACGA 665
QY 614 TCGTTGCAACGAGGGCTACTTCAAGACGGCTATGCTCGCATCACTCCGT 662
Db 666 TCTGGCTTACCGAGGATACAGACAGTGAATCTTCTTATATATGT 714
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RESULT 8
DB624928 639 bp mRNA linear EST 11-JUL-2005

LOCUS EST1015056 Fv1 Gibberella moniliformis cDNA clone FV1B05, mRNA
DEFINITION Sequence.

ACCESSION DB624928
VERSION DB624928.1 GI:70699610

KEYWORDS EST.

ORGANISM Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocnemycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 639) Proctor, R.H., Butenko, A.E., Zheng, L., Lee, Y.,
Brown, D.W., Cheung, F., Town, C.D., and Whitelaw, C.A.

AUTORS Kendra, D.F., Town, C.D., and Whitelaw, C.A.

TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster

JOURNAL Unpublished (2005)
COMMENT Contact: Brown, D.W.
USDA/ARS/NCADR

USDA
1815 N. University St., Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FV1B05TH
Seq primer: ATAT TAA CCC TCA AAG GG.
Location/Qualifier

FEATURES

source

1. 639
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="3125"
/db_xref="taxon:117187"
/clone="FV1B05"
/cdate="1998-11-17"
/note="Vector: pBlueScript II SK(+); Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad, CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit, Stratagene)."

ORIGIN

Query Match 32.7%; Score 220.4; DB 8; Length 639;
Best Local Similarity 63.2%; Pred. No. 4.9e-50;
Matches 373; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

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QY 74 CCACGAGCTCGAAAAAGGACAGACACCCCACTCGGAGGGCTGGACATGTTATT 133
Db 24 CCTCTGCTCTTGGAGCCCGCCAGGTCACTGGATCTTGAAGGTTACCAACGATTA 83
QY 134 ACTATTCCTGGTGGAGTGAAGAGGCGGACGACGTAACCAACCTGGAAAGCGGCA 193
Db 84 TCTACTCTTGGTGTCTGATGCGGTGCTATGCCAATCTAGATGGGTAGGAAATC 143
QY 194 CCTACGAGATCAGCTGGGAGATGGCGGTAACTCTGTCGTGAAAGGGCTGAAACCCG 253
Db 144 ACTACAGGTTGATTTGGCGCAACACTGTAACTTTGTTGGTGAAGGGTTGAACCTCG 203
QY 254 GCCTGAACGCAAGACCACTTGAAGGTGTTTACAGCCAAAGCGCAACGTTACC 313
Db 204 G---TACTGGCCGAACATATCACTATGCGGTTCTTTCAGCCCTCAGGGTTAACGCTATC 260
QY 314 TTGGGGTTACGATTGAGACCCGCAACCCGCTGTCGATGATTAATCATCGTGAACCTTTG 373
Db 261 TCTGGCTTACGGCTGAGACCCGCGCCAGCTCTCTGTCGATTAATCATCGAATCAACG 320
QY 374 GCACCTATGATCTCTCTCCGGTGTCTACCATCTAGAACTGTGAGTGCAGCGGTAGCA 433
Db 321 GCACTTCAATCCCGGCTGCTGCTGGCCAGCAACAGGACCGTCTTACACAGCGCGACA 380
QY 434 TCTATCAGCTGGGCAAGACCACTGCGCTCAACGCACTAGATGACGGCACCCAACT 493
Db 381 CCTATGATCTGTATCAAGACCAACCGCTTACCAACAGCCCTTATGACGCGCCAAACGACT 440
QY 494 TCGACCAATATCTGGTGGTCCGCGCAGACCAAGCGGACCAAGCGGTACCGTCCAGACGGCT 553
Db 441 TCAACCAATATCTGGGCTTCCGCGCCAGCAACAGCGGAGCGGCTTCAACATGACGA 500
QY 554 GCACCTTGAAGCTTGGGCTTGGCTGCTGCTGTTGAAATGTCACAGGTGACCACTTACACGA 613
Db 501 CTATCTTCAATGCTTGGGCTTAACTGTCGCAATGAGACT---TGAAACCACTACTATACGA 557
QY 614 TCGTTGCAACGAGGGCTACTTCAAGACGGCTATGCTCGCATCACTCCGT 663
```


#1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to Trizol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml Trizol. The cDNA was directionally ligated into the pBluescript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 686;
Best Local Similarity 63.2%; Pred. No. 9.4e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Qy 74 CCACGAGCTCGAAAAGGACAGACACCCCACTCGAGGGCTGCGACGATGTTATT 133
Db CCTGTGCTTGAAGCCCGCAGGTCACCGGTAATCTGAGGGTTACCAACAGGATACT 129

Qy 134 ACTATTCCTGGTGGAGTGAAGGCGGACGCGACGTAACCAACTGGAAGCGCGCA 193
Db TCTACTCTTGGTGGTCTATGATGGTGGCTATGCAACTACCGTATGGGTAGGAAATC 189

Qy 194 CCTACGAGATGAGCTGGGAGAGTGGCGGTAACTCTGCTGTGAAAGGGCTGGAACCCG 253
Db ACTACGAGTGTGATGGGCGCAACCTGTTACTTTGTGTGGAAGGGTTGGAACCTG 249

Qy 254 GCTGGAAGCAAGAGCCATCCATTGAGGGTTTACCAAGCCAAACGCAACGCTACC 313
Db G---TACTGGCCGAACATCTCAATGCGGTTCTTTCAGCCCTCAGGGTAAACGCTATC 306

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RESULT 11
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LOCUS DR631520 Fv1 Gibberella moniliformis cDNA clone FVIEA21, mRNA
DEFINITION DR631520.1 GI:70706360
ACCESSION DR631520.1 GI:70706360
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Contact: Brown, D.W.
USDA/ARS/NCAR
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@wncar.usda.gov
TIGR sequence name: FVIEA21TH
Seq primer: AAT TAA CCC TCA AAG GG.
Location/Qualifiers

FEATURES

source

1..719
/organism="Gibberella moniliformis"
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/strain="m3125"
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/clone="FVIEA21"
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Site 2: XhoI; anemorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 719;
Best Local Similarity 63.2%; Pred. No. 9.5e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

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Db CCTGTGCTTGAAGCCCGCAGGTCACCGGTAATCTGAGGGTTACCAACAGGATACT 167

Qy 108 TCTGCTCTTGAAGCGCCGCGCAGGTCACTCGGTACTGAGGGTTACCAACAGGATACT 167
Db 134 ACTATTCCTGGTGGAGTGAAGGCGGACGCGCATCACCACTGGAAGCGCGCA 193

Qy 168 TCTACTCTTGGTGGTCTATGATGGTGGCTATGCAACTACCGTATGGGTAGGAAATC 227
Db 194 CCTACGAGATGAGCTGGGAGAGATGGCGGTAACTCTGCTGTGAAAGGGCTGGAACCCG 253

Qy 228 ACTACGAGTGTGATGGGCGCAACCTGTTACTTTGTGTGGAAGGGTTGGAACCTG 287
Db 254 GCTGGAAGCAAGAGCCATCCATTGAGGGTTTACCAAGCCAAACGCAACGCTACC 313

Qy 288 G---TACTGGCCGAACATCTCAATGACGCGTCTTTCAGCCCTCAGGGTAAACGCTATC 344
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Qy 345 TCTGGGTTACGGCTGAGACCCGACGCTCTGCTGTGATGATGTCATTCAGAACTACG 404
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Qy 585 CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT---TGGAAACCACTATATCAGA 641

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| | | | | |
| Dd | | 642 | TTCTAGCTAACGAGGAGGATACAGACGATGGATCTTTCATCATATGT | 690 |
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| RESULT 12 | | | | |
| LOCUS | DR630899 | | | |
| DEFINITION | EST1021027 Fv1 Gibberella moniliformis cDNA clone FVIDX40, mRNA | 733 bp | mRNA | linear EST 11-JUL-2005 |
| ACCESSION | DR630899 | | | |
| VERSION | DR630899.1 | | | |
| KEYWORDS | GI:70705629 | | | |
| SOURCE | EST. | | | |
| ORGANISM | Gibberella moniliformis Gibberella moniliformis Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella. 1 (bases 1 to 733) | | | |
| REFERENCE | Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,J., Lee,Y., Utterback,T., Smith,S., Feldblum,T., Glenn,A.B., Plattner,R.D., Kendra,D.F., Town,C.D. and Whitelaw,C.A. Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster unpublished (2005) | | | |
| AUTHORS | Contact: Brown, D.W. | | | |
| JOURNAL | USDA/ARS/NCAUR | | | |
| COMMENT | 1815 N. University St, Peoria, IL 61604, USA Tel.: 309 681 6230 Fax: 309 681 6689 Email: brown.d@ncaur.usda.gov TIGR sequence name: FVIDX40TH Seq primer: AAT TAA CCC TCA AAG GG. Location/Qualifiers | | | |
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| source | 1..733 | | | |
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| | /strain="mj125" | | | |
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| | /clone="FVIDX40" | | | |
| | /cfeature "FV1" | | | |
| | /clone_lib="mycelia" | | | |
| | /note="Vector: pBluescript II SK(+); XR; Site 1: EcoRI; Site 2: XhoI; amorph: Fusarium verticillioides. Library FV1 was prepared from growth on excised maize seedling roots and shoots. The roots and shoots were prepared as described above and then inoculated by dipping briefly in a suspension of 5 x 10 ⁶ conidia per ml. The inoculated roots and shoots were then incubated on moistened Whatman #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to Trizol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml Trizol. The cDNA was directionally ligated into the pBluescript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)." | | | |
| ORIGIN | | | | |
| Query Match | 32.5%; Score 219.4; DB 8; Length 733; | | | |
| Best Local Similarity | 63.2%; Pred. No. 9.5e-50; | | | |
| Matches 372; Conservative | 0; Mismatches 211; Indels 6; Gaps 2; | | | |
| OY | 74 | CCAGGAGCTGGAAAAGGACGACGAACAACCCCACCTGGAGAGGGCTGCAGATGTTATT | 133 | |
| Dd | 147 | CCTCTGTCCTTGAGGCCCGCCAGCTCACCGGTACTTGAGGGTTACCACAAAGGATCT | 206 | |
| OY | 134 | ACTATCTCGGTGAGTAGCAGGTGAGCGCAGGCCACGTACACCAACTGGAGAAGCGGCA | 193 | |
| Dd | 207 | TCTACTCTTGGTGGTGTGATGATGGTGTGGCTATGCCAATCAGTAATGGGTAGAGGAAGTC | 266 | |
| OY | 194 | CTTACGAGATCAGCTGGGGAGATGGCCGGTAACCTCTGCTGGTGAAGAAGGCTGGAAACCCG | 253 | |
| | | | | |

| Db | Accession | Version | Source | Organism | Reference Authors | Title | Journal Comment |
|------------|---|---|--------|----------|-------------------|-------|-----------------|
| Db | 267 | ACTACAGAGTTGATTGGGCAACACTGGTAACCTTTGTTGGTGGAAAGGGGTGGAAACCTTG | 326 | | | | |
| Qy | 254 | GCTGAAACGGAAGACCCATCCACTTTGAGGGTGTTTACCAAGCCAAACGGCAACAGTTAC | 313 | | | | |
| Db | 327 | G---TACTGGCCGGAACCTATCAACTATGCGGGTTCCTTTCAAGCCCTCAGGGTAAACGGCTATC | 383 | | | | |
| Qy | 314 | TTGGGGTCTACGGTTGGACCCGGCAACCCGGTGGTGGAGTAATTAACATCGTCGAACCTTGG | 373 | | | | |
| Db | 384 | TTGGGGTCTACGGCTGAGACCCGCAACCCCTCTGTGTGAAGTACTAGCTCATCGAAGACTACG | 443 | | | | |
| Qy | 374 | GCACCTATGATTCCTTCTCCGGTGTCTACCGATCTTAGGAAGTTGCGAGTGGCGAGTAGCA | 433 | | | | |
| Db | 444 | GCACTTAAATCCCGGCTCTGTGTGGCCAGCAACAAGGGACCGTCTTAACAAGACGCGGAGCA | 503 | | | | |
| Qy | 434 | TCATATGACTCGGCAAGCAACACTGCGGTCAACGCACTTAGCATGCAAGCGGCAACCAACT | 493 | | | | |
| Db | 504 | CCATATGATCTGTACCAAGACCAACCCGCTCAACCAAGCCCTCTATTCAGACGGCCAAACAGACT | 563 | | | | |
| Qy | 494 | TCGACCAATATCTGTCTGGTCTCGGCCAGACCAAGCGGATCCGTCAGACGGGCT | 553 | | | | |
| Db | 564 | TCAACCAATATCTGGGCTCAATCCGCGCGCAACAACGGAAGCGGCGCTGTCAACATGACAGA | 623 | | | | |
| Qy | 554 | GCCACTTTCGAGCGCTCGGGCTCGCGGTGGTTGATGTCAAACGGTAGCAACACTACTACAGA | 613 | | | | |
| Db | 624 | CTATCTTCAATGCTTGGGCTAATGCTGGCATGAGACT---TGGGAACCACTACTATCAGA | 680 | | | | |
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| DEFINITION | EST1014504 Fv1 Giberella moniliformis cDNA clone FVIB280, mRNA | | | | | | |
| ACCESSION | DR624376 | | | | | | |
| VERSION | DR624376.1 | | | | | | |
| KEYWORDS | EST. | | | | | | |
| SOURCE | Giberella moniliformis | | | | | | |
| ORGANISM | Giberella moniliformis | | | | | | |
| REFERENCE | Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | | | | | |
| AUTHORS | Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella. | | | | | | |
| | 1 (bases 1 to 739) | | | | | | |
| | Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y. | | | | | | |
| | Utterback, T., Smith, S., Feldblum, T., Glenn, A.E., Plattner, R.D., | | | | | | |
| | Kendra, D.F., Town, C.D. and Whitelaw, C.A. | | | | | | |
| | Analysis of 87,000 expressed sequence tags reveals alternatively | | | | | | |
| | spliced introns in multiple genes of the funomisin gene cluster | | | | | | |
| | Unpublished (2005) | | | | | | |
| | Contact: Brown, D.W. | | | | | | |
| | USDA | | | | | | |
| | 1815 N. University St, Peoria, IL 61604, USA | | | | | | |
| | Tel: 309 681 6230 | | | | | | |
| | Fax: 309 681 6689 | | | | | | |
| | Email: brown@ncaur.usda.gov | | | | | | |
| | TIGR sequence name: FVIB280TH | | | | | | |
| | Seq primer: AAT TAA CCC TCA AAG GG. | | | | | | |
| FEATURES | Location/Qualifiers | | | | | | |
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| | /strain="m125" | | | | | | |
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| | /tissue_type="mycelia" | | | | | | |
| | /clone_id="Fv1" | | | | | | |
| | /note="Vector: pBluescript II SK(+); XR; Site 1: EcoRI; | | | | | | |
| | Site 2: XhoI; anamorph: Fusarium verticillioides. Library | | | | | | |
| | Fv1 was prepared from growth on excised maize seedling | | | | | | |
| | roots and shoots. The roots and shoots were prepared as | | | | | | |
| | described above and then inoculated by dipping briefly in | | | | | | |

a suspension of 5 x 10⁶ conidia per ml. The inoculated roots and shoots were then incubated on moistened Whatman #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to Trizol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml Trizol. The cDNA was directionally ligated into the pBluescript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 739;
Best Local Similarity 63.2%; Pred. No. 9.5e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

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Qy 74 CCACGAGCTCGAAGAGGACAGACAAACCCCACTCGAGAGGGCTGACAGATGTTATT 133
Db 119 CCTGTGCTTGAAGCCCGCCAGGTCACCGGTAATCTGAAGGTTACCAACAGGATACT 178
Qy 134 ACTATTCCTGTGAGTAGACCGGTGAGGCGACGTAACCAACCTGGAAAGCGGCA 193
Db 179 TCTACTCTGTGGTGTGATGTGTGGCTATGCAACTACGATGGGTGAGGAAATC 238
Qy 194 CTTACGAGATCACTGGGAGATGCGGTAACTCTGCTGTTGAAAGGCTGAAACCCG 253
Db 239 ACTACGAGTTGATTTGGCGCAACTGTGTAATTGTTGGTGAAGAGGTTGAAACCTG 298
Qy 254 GCCTGAAGCGAAGAGCCATTCACCTTTGAGGGTGTTCACAGCAACGCGCAACGCTAC 313
Db 299 G---TACTGCGCCAACTATCAACTATGCGGTTCTTTGAGCCCTCAAGGTTACGGCTATC 355
Qy 314 TTGCGGTCTACGATTGAGACCGCAACCGCTGATGAGATTAATGCTGCAACTTTG 373
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Qy 374 GCACCTATGATCTTCTCCGGTGTACCGATCTAGAGAACTGTGAGTGCACCGTACCA 433
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Qy 554 GCCACTTGCAGCGCTGGGCTCGCGTGTGATGTCACGCTGACCACTACTACCA 613
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RESULT 14
DR625790 741 bp mRNA linear EST 11-JUN-2005
LOCUS EST1015918 Fv1 Gibberella moniliformis cDNA clone FV1BR33, mRNA
DEFINITION Sequence.
ACCESSION DR625790
VERSION DR625790.1 GI:70700504
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
REFERENCE 1 (bases 1 to 741)
AUTHORS Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively

JOURNAL
COMMENT

spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAR

1815 N. University St., Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncar.usda.gov

TIGR sequence name: FV1BR33JTH

Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES

Location/Qualifiers

1..741

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/mol_type="mRNA"

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/db_xref="taxon:117187"

/clone="FV1BR33"

/issue_type="mycelia"

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/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library

Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 741;
Best Local Similarity 63.2%; Pred. No. 9.5e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

```
Qy 74 CCAAGAGCTCGAAGAGGACAGACAAACCCCACTCGAGAGGGCTGACAGATGTTATT 133
Db 125 CCTGTGCTTGAAGCCCGCCAGGTCACCGGTAATCTGAAGGTTACCAACAGGATACT 184
Qy 134 ACTATTCCTGTGAGTAGACCGGTGAGGCGACGTAACCAACCTGGAAAGCGGCA 193
Db 185 TCTACTCTGTGGTGTGATGTGTGGCTATGCAACTACGATGGGTGAGGAAATC 244
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Db 305 G---TACTGCGCCAACTATCAACTATGCGGTTCTTCAAGCCCTCAGGGTACCGCTATC 361
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Qy 494 TCAGCAATATCTGTGCTGCTCCGCGAGCAAGCGCACAGCGTACCGTCCAGACGGGCT 553
Db 542 TCAACGATATCTGGGCGATCCGCGCAACAGCGAGCGGCGCTGTCAACATGACGA 601
Qy 554 GCCACTTGCAGCGCTGGGCTCGCGGCTGTTGAATGTCACAGGTCACCACTACTACCA 613
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Db 602 CTATCTTCATGCTGGGCTATGCTGGCATGAGACT---TGAAACACACTACTATGGA 658
Qy 614 TCGTTGCAACGAGGGGCTACTTTCAGACAGCGGCTATGCTGCATCAACGCT 662
Db 659 TTCTAGTACCGAGGATACGAGCAGAGTGGATCTTCTTCACTCATGT 707

RESULT 15

DR624330

LOCUS DR624330 763 bp mRNA linear EST 11-JUL-2005
DEFINITION EST1014458 Fv1 Gibberella moniliformis cDNA clone FVIB212, mRNA
sequence.

ACCESSION

DR624330

VERSION DR624330.1 GI:70699012
KEYWORDS EST.

SOURCE

ORGANISM

Gibberella moniliformis

Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 763)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,
Utechtack, T., Smith, S., Feldblyum, T., Glenn, A.B., Plattner, R.D.,
Kendrix, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAR

1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230

Fax: 309 681 6689
Email: brown@ncar.usda.gov

TIGR sequence name: FVIB212TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES

SOURCE

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/organism="Gibberella moniliformis"
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/note="Vector: pBluescript II SK(+); Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 33.5%; Score 219.4; DB 8; Length 763;
Best Local Similarity 63.2%; Pred. No. 9.6e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Qy 74 CCAAGAGCTCGAAGGAGCAGACCAACCCCACTCGAGGCTGGACGATGTTATT 133
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Qy 134 ACTATTCTGTGATGACGCTGAGCGCAGGCCAGCTACCAACCTGGAGCGGCA 193
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Qy 194 CTTACGAGATCAGCTGGGAGATGCGGTAACCTCGTGGTGAAGAGGCTGAAACCCG 253
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Qy 614 TCGTTGCAACGAGGGGCTACTTACAGACGCGCTATGCTGCTGCTGCTGCTGCT 662
Db 688 TTCTAGTACCGAGGATACGAGCAGAGTGGATCTTCTTCACTCATGT 736

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-467-368-1_COPY_31_705

Perfect score: 675
Sequence: 1 ATGCTGGCGTTACCCCGT.....TCACCGTGTGCGACGTGGC 675

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 675 | 100.0 | 983 | 2 | US-08-886-765-1 |
| 2 | 675 | 100.0 | 983 | 2 | US-08-115-660-1 |
| 3 | 239 | 35.4 | 1123 | 3 | US-08-458-0238-3 |
| 4 | 196.2 | 29.1 | 1375 | 2 | US-08-468-812-1 |
| 5 | 196.2 | 29.1 | 1375 | 2 | US-08-590-563-1 |
| 6 | 196.2 | 29.1 | 1375 | 3 | US-09-770-621-1 |
| 7 | 196.2 | 29.1 | 1375 | 3 | US-09-235-832-1 |
| 8 | 194.2 | 28.8 | 822 | 3 | US-07-254-733-8 |
| 9 | 190 | 28.1 | 1015 | 2 | US-08-121-436A-1 |
| 10 | 181.8 | 26.9 | 1281 | 3 | US-08-768-373-1 |
| 11 | 181.8 | 26.9 | 1281 | 3 | US-08-849-242A-1 |
| 12 | 168.4 | 24.9 | 675 | 2 | US-07-744-5708-1 |
| 13 | 164.6 | 24.4 | 927 | 2 | US-08-507-431-5 |
| 14 | 164.6 | 24.4 | 927 | 2 | US-08-902-655A-5 |
| 15 | 164.6 | 24.4 | 927 | 3 | US-09-116-622-5 |
| 16 | 164.6 | 24.4 | 927 | 3 | US-09-219-277-5 |
| 17 | 164.6 | 24.4 | 927 | 3 | US-09-599-661-5 |
| 18 | 162.4 | 24.1 | 489 | 2 | US-08-119-169A-7 |
| 19 | 159 | 23.6 | 2219 | 2 | US-08-290-979A-7 |
| 20 | 144.8 | 21.5 | 573 | 2 | US-08-709-912-18 |
| 21 | 144.8 | 21.5 | 573 | 2 | US-09-047-370-18 |
| 22 | 138 | 20.4 | 1174 | 3 | US-08-768-373-3 |
| 23 | 138 | 20.4 | 1174 | 3 | US-08-849-242A-3 |
| 24 | 129.6 | 19.2 | 2055 | 3 | US-09-367-891A-1 |

| | | | | | | |
|----|-------|------|------|---|-------------------|--------------------|
| 25 | 124 | 18.4 | 2898 | 3 | US-09-462-246-1 | Sequence 1, Appli |
| 26 | 119.2 | 17.7 | 557 | 3 | US-09-230-590-1 | Sequence 1, Appli |
| 27 | 119.2 | 17.7 | 557 | 3 | US-09-970-616-1 | Sequence 1, Appli |
| 28 | 119 | 17.6 | 744 | 3 | US-09-189-060B-11 | Sequence 11, Appli |
| 29 | 108.8 | 16.1 | 1207 | 2 | US-08-575-964-2 | Sequence 2, Appli |
| 30 | 108.8 | 16.1 | 1207 | 2 | US-08-963-500-2 | Sequence 2, Appli |
| 31 | 103.6 | 15.3 | 2054 | 3 | US-08-981-729-5 | Sequence 5, Appli |
| 32 | 103.6 | 15.3 | 2054 | 3 | US-09-613-811-5 | Sequence 5, Appli |
| 33 | 101.4 | 15.0 | 2967 | 3 | US-09-367-891A-4 | Sequence 4, Appli |
| 34 | 98.2 | 14.5 | 685 | 3 | US-07-955-726A-7 | Sequence 7, Appli |
| 35 | 98.2 | 14.5 | 2059 | 2 | US-08-244-686-1 | Sequence 1, Appli |
| 36 | 96.2 | 14.3 | 234 | 3 | US-09-189-060B-46 | Sequence 46, Appli |
| 37 | 95.6 | 14.2 | 847 | 3 | US-09-260-283-1 | Sequence 1, Appli |
| 38 | 95.6 | 14.2 | 954 | 2 | US-08-315-695-15 | Sequence 15, Appli |
| 39 | 95.6 | 14.2 | 1945 | 2 | US-09-595-344-1 | Sequence 1, Appli |
| 40 | 94 | 13.9 | 2055 | 2 | US-07-842-349-1 | Sequence 1, Appli |
| 41 | 84.6 | 12.5 | 941 | 2 | US-08-121-436A-3 | Sequence 3, Appli |
| 42 | 83 | 12.3 | 2364 | 3 | US-09-390-234-23 | Sequence 23, Appli |
| 43 | 83 | 12.3 | 2364 | 3 | US-09-603-311-23 | Sequence 23, Appli |
| 44 | 82.6 | 12.2 | 642 | 2 | US-08-104-445-2 | Sequence 2, Appli |
| 45 | 82.6 | 12.2 | 1413 | 2 | US-08-104-445-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-08-886-765-1
Sequence 1, Application US/08886765
Patent No. 5817500
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58175000 No. 5817500disk of No. 5817500th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9655
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Thermomyces lanuginosus
STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705

US-08-886-765-1

Query Match 100.0%; Score 675; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.5e-179; Indels 0; Gaps 0;
Matches 675; Conservative 0; Mismatches 0;

QY 1 ATGGTGGCTTTTACCCCGCTTGGCCCTTGGCCCTTGGCCCGGAGCTGGGGCCCTGGCCCTTC 60
DB 31 ATGGTGGCTTTTACCCCGCTTGGCCCTTGGCCCGGAGCTGGGGCCCTGGCCCTTC 90
QY 61 CCGGACGAGGATGCGACGAGCTCGAAGAGACGACGACGACGACGACGACGACGACGACGACGAC 120
DB 91 CCGGACGAGGATGCGACGAGCTCGAAGAGACGACGACGACGACGACGACGACGACGACGACGAC 150
QY 121 CAGATGGTATTATCTATCTTCTGGTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 151 CAGATGGTATTATCTATCTTCTGGTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 210
QY 181 CTGGAGGCGGACCTTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAG 240
DB 211 CTGGAGGCGGACCTTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAG 270
QY 241 GGTGGAACCCCGGCTGGAACGCAAGCCCATCTTGAAGGCTTTTACGACGCAAC 300
DB 271 GGTGGAACCCCGGCTGGAACGCAAGCCCATCTTGAAGGCTTTTACGACGCAAC 330
QY 301 GGCAGACGCTACCTTGGGCTTACGCTTGGAGCCGCAACCCGCTGCTGAGTATTATC 360
DB 331 GGCAGACGCTACCTTGGGCTTACGCTTGGAGCCGCAACCCGCTGCTGAGTATTATC 390
QY 361 GTCGAGAACTTTGGCACCTATGATCTTCTCGGCTGCTACCATCTAGGAATGTCGAG 420
DB 391 GTCGAGAACTTTGGCACCTATGATCTTCTCGGCTGCTACCATCTAGGAATGTCGAG 450
QY 421 TGGCAGCGTATGATCTTACGCTGGCAAGCACTGGCTGCAACGCACTAGATGAC 480
DB 451 TGGCAGCGTATGATCTTACGCTGGCAAGCACTGGCTGCAACGCACTAGATGAC 510
QY 481 GGCAGCCAAACCTTGCACCAATCTGGTGGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 511 GGCAGCCAAACCTTGCACCAATCTGGTGGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 570
QY 541 GTCGAGACGGGCTGCACTTGCAGCGCTGGGCTGGCTGTTGAATGTCAACGGTGAC 600
DB 571 GTCGAGACGGGCTGCACTTGCAGCGCTGGGCTGGCTGTTGAATGTCAACGGTGAC 630
QY 601 CACTACTACGATCTTGGCAAGGAGGCTACTTACGACGCGCTATGCTCGATCAC 660
DB 631 CACTACTACGATCTTGGCAAGGAGGCTACTTACGACGCGCTATGCTCGATCAC 690
QY 661 GTTGTGACGTGGG 675
DB 691 GTTGTGACGTGGG 705

RESULT 2

US-09-115-660-1

Sequence 1, Application US/09115660
Patent No. 6245546
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Muller, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No. 62455460 No. 6245546disk of No. 6245546ch America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,660
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/886,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Thermomyces lanuginosus
STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705
US-09-115-660-1

Query Match 100.0%; Score 675; DB 3; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.5e-179; Indels 0; Gaps 0;
Matches 675; Conservative 0; Mismatches 0;

QY 1 ATGGTGGCTTTTACCCCGCTTGGCCCTTGGCCCGGAGCTGGGGCCCTGGCCCTTC 60
DB 31 ATGGTGGCTTTTACCCCGCTTGGCCCGGAGCTGGGGCCCTGGCCCTTC 90
QY 61 CCGGACGAGGATGCGACGAGCTCGAAGAGACGACGACGACGACGACGACGACGACGACGACGAC 120
DB 91 CCGGACGAGGATGCGACGAGCTCGAAGAGACGACGACGACGACGACGACGACGACGACGACGAC 150
QY 121 CAGATGGTATTATCTATCTTCTGGTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 151 CAGATGGTATTATCTATCTTCTGGTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 210
QY 181 CTGGAGGCGGACCTTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAG 240
DB 211 CTGGAGGCGGACCTTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAG 270
QY 241 GGTGGAACCCCGGCTGGAACGCAAGCCCATCTTGAAGGCTTTTACGACGCAAC 300
DB 271 GGTGGAACCCCGGCTGGAACGCAAGCCCATCTTGAAGGCTTTTACGACGCAAC 330
QY 301 GGCAGACGCTACCTTGGGCTTACGCTTGGAGCCGCAACCCGCTGCTGAGTATTATC 360
DB 331 GGCAGACGCTACCTTGGGCTTACGCTTGGAGCCGCAACCCGCTGCTGAGTATTATC 390
QY 361 GTCGAGAACTTTGGCACCTATGATCTTCTCGGCTGCTACCATCTAGGAATGTCGAG 420
DB 391 GTCGAGAACTTTGGCACCTATGATCTTCTCGGCTGCTACCATCTAGGAATGTCGAG 450
QY 421 TGGCAGCGTATGATCTTACGCTGGCAAGCACTGGCTGCAACGCACTAGATGAC 480
DB 451 TGGCAGCGTATGATCTTACGCTGGCAAGCACTGGCTGCAACGCACTAGATGAC 510
QY 481 GGCAGCCAAACCTTGCACCAATCTGGTGGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 511 GGCAGCCAAACCTTGCACCAATCTGGTGGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 570

| Qy | Db | Qy | Db |
|---|---|---|---|
| 541 | 571 | 601 | 631 |
| GTCACAGCGGGCTGGCACTTCAGCGCTGGCTGGCTGGTTGAATGCAAGGAGAC | GTCACAGCGGGCTGGCACTTCAGCGCTGGCTGGCTGGTTGAATGCAAGGAGAC | CACACTACACAGATCGTTCGCAACGAGAGGAGCTACTTCAGCAGCGGCTATGTCGATCACC | CACACTACACAGATCGTTCGCAACGAGAGGAGCTACTTCAGCAGCGGCTATGTCGATCACC |
| | | | |
| 661 | 691 | 661 | 691 |
| GTTGCTGACGTGGGC | GTTGCTGACGTGGGC | GTTGCTGACGTGGGC | GTTGCTGACGTGGGC |
| | | | |
| 705 | 705 | 705 | 705 |

RESULT 3

Sequence 3 Application US/08458023B
Patent No. 5667990
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boomkathen, Karuppan C.
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 56679900diak of No. 56679900th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4066.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Humicola insolens
INDIVIDUAL ISOLATE: DSM 6995
FEATURE:
NAME/KEY: CDS
LOCATION: 126..806
US-08-458-023B-3

| | | | | |
|---------------------------|-------|-------------------|----------|-------------|
| Query Match | 35.4% | Score 239 | DB 2 | Length 1123 |
| Best Local Similarity | 64.4% | Pred. No. 3,2e-57 | | |
| Matches 391, conservative | 0 | Mismatches 210 | Indels 6 | Gaps 2 |

| | | | |
|----|-----|--|-----|
| Oy | 57 | CTTCGGGCAAGGAATGCCACGAGACTGAAAAGGACACACACCCCAACTCGAGGG | 116 |
| Db | 197 | CGTTCCTCGGAGCAACTGACGCGGCTTCCTCAGGCTGACAGGTCGATCCCAACGGGAGGG | 256 |

| | | | |
|----|-----|--|-----|
| Oy | 117 | CTGGACAATGGTATTATCTATCTCTGGTGAAGTACGGGTGAGCGCAGAGCCACGTAAC | 176 |
| Dd | 257 | CTGGCAACAACGGCTACTTCTACTCTGTGGTGTCCGACGGCGGAGGCGAGGTTCAGTACAC | 316 |
| Oy | 177 | CAACCTGGAAAGCGGCACCTACGAGATCAGCTGGGGAAGATGGCGGTAACTCTGTCGGTGG | 236 |
| Dd | 317 | CAACCTCGAAGGGCAGCCGCTACCAAGTCAAGATGGCGTAACAACCGGCAACTTCGTGGTGG | 376 |
| Oy | 237 | AAAGGGCTGGAACCCCGGCTGGAACGGAAGCCATCCACTTTAGGGTGTTCACAGCC | 296 |
| Dd | 377 | TAAAGGTTGGAACCCGGG---AACGGCGGCAAGATCACTACGGCGGCTACTTCAACCC | 433 |
| Oy | 297 | AAACGGCAACAGCTACTCTTGCGGTCTACGGTGTGAACCGGCAACCGCTGGTGCAGATTA | 356 |
| Dd | 434 | CAAGGCAACCGGCTACTCGGCCGCTTACGGCTGGAACCGGCAACCGCTGTGAGATCTA | 493 |
| Oy | 357 | CATCGTCAGAACTTTGGCACTTATGATCTCTTCCTCGGTGCTAACGATCTAGAACTGT | 416 |
| Dd | 494 | TGTATGAGTGTGTAACGGCAAGTAACTCCGGCAGACCAAGCTCAGTAAACAGGGCAGATT | 553 |
| Oy | 417 | CGAGTGCAGCGGTACATCTATCGACTGGGCAAGACCACTCGCGTCAACGCCTTAGCAT | 476 |
| Dd | 554 | CTATATCCACGGCGATCAGTATGACATCTTTGTGAGCAACCCCTCAACCAAGCCCGCAT | 613 |
| Oy | 477 | CGAGCGGCAACCCAACTTCGACCAATACGTGTGCGGTCCGCGCAGGCAACAGCGCACAGCGG | 536 |
| Dd | 614 | CGACGGCACCCGGAGCTTCAGACGATCTCGGTCTATTCGCAAGAACCAACCGTGTCCGAAG | 673 |
| Oy | 537 | TACGGTCAGACGGGCTGCCACTTTCGACGCTCGGGCTCGCGCTGGTTGAATGTCAACGG | 596 |
| Dd | 674 | CTCGGTCAACATGCAGAACCACTTCAACGCGTGGGAGGACGACACGGAAATCCCGCT--- | 730 |
| Oy | 597 | TGACCACTACTACAGATCGTTTGCACGAGAGGCTACTTCAGACAGCGCTATGTCTGCAT | 656 |
| Dd | 731 | CCAGGACTACTACAGGTCTGTGCGCACGAGGGCTTACAGACAGATGGCGAGTCCGACAT | 790 |
| Oy | 657 | CACCGTT 663 | |
| Dd | 791 | CTATGTT 797 | |

RESULT 4

Sequence 1, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmaanger, Jari
APPLICANT: M ntyl, Arja
APPLICANT: Pegeretrm, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Maria
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,812
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-08-468-812-1

Query Match 29.1%; Score 196.2; DB 2; Length 1375;
Best Local Similarity 59.0%; Pred. No. 3.5e-45;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;
QY 5 TCGGCTTTACCCCGGTTGCGCTTACGCGGACCTGCGGCGCTTCCCGG 64
DB 349 TCGGCTTCCGCGCATCTCAACAGTGTCTTCCGCTGCGCTGCGCATGCGCGTGGC 408
QY 65 CAGGAATGCCACGAGCTCGAATAAGCAGACAGACACCCCACTCGAGGGCTGGACG 124
DB 409 TCGTCCCGCGGACGCGCCAGCCGACACACATCACCAGAACAGACGCGGTACGACA 468
QY 125 ATGCTTATTACTTCTCTGTTGAGTGTGAGCGGTGAGCGCCAGCACTGACCACTGG 184
DB 469 ACGGCTACTTCTACTCTGTTCTGACCGACGCGCCGCGGACCGTCTCCATGACCTTCACT 528
QY 185 AAGCGGACCTAGACAGATGACGCTGGGAGATGGCGGTAACTCGTGGTGAAGAGGCT 244
DB 529 CGGGCGGACGCTACGACCTCTGCGCGAACCAGGGAATTGTCGCGCGCAAGGCT 588
QY 245 GGAACCCCGGCTGAAACGCAAGACCATCACTTGAAGGTGTTTACCAAGCCAAACGCA 304
DB 589 GGTCCACCGG---GGACGCGGGAACCGTGAACCTAACGCTCTTCAACCGTCCGGTA 645
QY 305 ACAGCTACCTTGGCGGTCTACGCTTGAACCCGCAACCGCTGTGAGTATTAATCTGCG 364
DB 646 ACGGCTACTCAGCTCTACGCTGAGACAGAAACCCCTGTGAGTACTACATCTGCG 705
QY 365 AGAATTGGACACCTATGATCTTCTCGCGGTGCTACCGATCTAGAACTGTGAGTGGC 424
DB 706 AGAGCTGGGGACCTTACCGGCGCACCGC-----ACCTTCAAGGGCACCGTACACACCG 759
QY 425 ACGGTAGCATCTATGACTCGGACAGACCACTCGGCTCAAGCACTAGACATGACGCGCA 484
DB 760 ACGGGGGAACGTAAGACATCTACGAGACTGCGGTACAAAGCGCGCTCATTCAGGGCA 819
QY 485 CCGAACTTTCAGCAATACTGTGTCGCGCAGAGCAAGCGCACCGCGTACCGTCC 544
DB 820 CCGGACCTTCAGAGTTCGAGCGTCCGCGCAGCAAGCGGACGCGCACCATCA 879
QY 545 AGAGGGGCTGCACTTTCAGCGCTGGGCTCGGCTGCTGTTGAATGCAACGGTACCACT 604
DB 880 CCATCGGGAACCACTTCGACGCTGGGGCCGCGCGCATGA---CTGGGACAGCCACG 936
QY 605 ACTACCAATGCTTGCAACGAGGGGCTACTTCAGACAGCGGCTATGCTGCACTACCGTTG 664

DB 937 ACTACCAATGCTTGCAACGAGGGGCTACTTCAGACAGCGGCTATGCTGCACTAC 996
QY 665 CTGACGTGGCG 675
DB 997 GCGAGGTGGC 1007

RESULT 5
US-08-590-563-1

Sequence 1, Application US/08590563
Patent No. 630014
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmaaper, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-08-590-563-1

Query Match 29.1%; Score 196.2; DB 3; Length 1375;
Best Local Similarity 59.0%; Pred. No. 3.5e-45;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

QY 5 TCAGCTTAAACCCCGGCTGCGGCTTAAAGCCGACCTGAGGCCCTTGCCG 64
DB 349 TCAGCTTAAACCCCGGCTGCGGCTTAAAGCCGACCTGAGGCCCTTGCCG 408
QY 65 CAGGGAATGCCAGGAGCTCGAAAACGACAGACACCCCACTCGAGGGCTGGACG 124
DB 409 TGCTGCCCCGCGACCGCCACGCGACACCATCACAGAACCGGGTACGACA 468
QY 125 ATGGTTATTAATCTCTGAGGAGTGAAGGTGAGCCGACGACGACCACTGG 184
DB 469 ACAGCTACTTCTACTGCTTCTGAGACGACGCGCCGAGCCGCTTCATGACCTTCACT 528
QY 185 AAGCGGACCTTACAGAGATCAAGCTGGGAGATGGCGTAACTCGTGGGAAAAGGCT 244
DB 529 CGGGGCGACGTAAGACACTCTGTGGCGGAACACCGGAACTTCTCCCGGCAAGGCT 588
QY 245 GGAACCCCGGCTGAAAGCAAGAGCATTCATTGAGGGTGTTCACAGCCAAAGGCA 304
DB 589 GGTCCACCGG---GGAGCGCGGACCGTGAACCTTCAACGCTCTTCAACCGTGGGTA 645
QY 305 ACAGCTACTTCTGAGGCTTACGCTTGAAGACCGGACCGGCTGAGTAACTTCACTGCG 364
DB 646 ACAGCTACTTCTGAGGCTTACGCTTGAAGACCGGACCGGCTGAGTAACTTCACTGCG 705
QY 365 AGAATTGAGCACTATGATCTCTCTCGGCTGCTACGATCTAGAACTGTGAGTGG 424
DB 706 AGAGCTGGGGCACTTACCGGCGCCACCGG-----ACCTTCAAGGGGACCGTACCAACG 759
QY 425 ACAGTATCTATGATCTGAGCTGCGGACGACCACTGCGGTCAAGCAGCTAGCATGACGCA 484
DB 760 ACAGGGAAGATGACGATCTTACGAGACCTGAGCGGTACACGCGCGTTCATCGAGGCA 819
QY 485 CCCAACTTGGACCAATATCTGTGTGCTGCGGACGAGACAGGCGACCGGTAACGCTCC 544
DB 820 CCGGACCTTTCAGAGATCTTGAAGCTGCGGACGAGACAGGCGACCGGCAACATCA 879
QY 545 AGACGGGCTGCACTTTCAGCGCTGCGGCTGCTGTTGAATGTCAACGGTACGACT 604
DB 880 CCAATCGGACCACTTTCAGCGCTGCGGCTGCGGCGCGGATGAA---CTGGGACGCGACG 936
QY 605 ACTACCAATGCTTTCAGGACGAGGGCTTTCAGGACGCGGCTTTCAGTCCGATCAACGCTTG 664
DB 937 ACTACCAATGCTTTCAGGACGAGGGCTTTCAGGACGCGGCTTTCAGTCCGATCAACGCTTG 996
QY 665 CTGAGTGGGC 675
DB 997 GCGAGGCTGGC 1007

RESULT 6

US-09-770-621-1
Sequence 1, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M neyl, Arja
APPLICANT: Vehmaepp, Jari
APPLICANT: Pegerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Laitinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. 6506593 Relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-09-770-621-1
Query Match 29.1%; Score 196.2; DB 3; Length 1375;
Best Local Similarity 59.0%; Pred. No. 3.5e-45;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;
QY 5 TCAGCTTAAACCCCGGCTGCGGCTTAAAGCCGACCTGAGGCCCTTGCCG 64
DB 349 TCAGCTTAAACCCCGGCTGCGGCTTAAAGCCGACCTGAGGCCCTTGCCG 408
QY 65 CAGGGAATGCCAGGAGCTCGAAAACGACAGACACCCCACTCGAGGGCTGGACG 124
DB 409 TGCTGCCCCGCGACCGCCACGCGACACCATCACAGAACCGGGTACGACA 468
QY 125 ATGGTTATTAATCTCTGAGGAGTGAAGGTGAGCCGACGACGACCACTGG 184
DB 469 ACAGCTACTTCTACTGCTTCTGAGACGACGCGCCGAGCCGCTTCATGACCTTCACT 528
QY 185 AAGCGGACCTTACAGAGATCAAGCTGGGAGATGGCGTAACTCGTGGGAAAAGGCT 244
DB 529 CGGGGCGACGTAAGACACTCTGTGGCGGAACACCGGAACTTCTCCCGGCAAGGCT 588
QY 245 GGAACCCCGGCTGAAAGCAAGAGCATTCATTGAGGGTGTTCACAGCCAAAGGCA 304
DB 589 GGTCCACCGG---GGAGCGCGGACCGTGAACCTTCAACGCTCTTCAACCGTGGGTA 645
QY 305 ACAGCTACTTCTGAGGCTTACGCTTGAAGACCGGACCGGCTGAGTAACTTCACTGCG 364
DB 646 ACAGCTACTTCTGAGGCTTACGCTTGAAGACCGGACCGGCTGAGTAACTTCACTGCG 705
QY 365 AGAATTGAGCACTATGATCTCTCTCGGCTGCTACGATCTAGAACTGTGAGTGG 424
DB 706 AGAGCTGGGGCACTTACCGGCGCCACCGG-----ACCTTCAAGGGGACCGTACCAACG 759
QY 425 ACAGTATCTATGATCTGAGCTGCGGACGACCACTGCGGTCAAGCAGCTAGCATGACGCA 484
DB 760 ACAGGGAAGATGACGATCTTACGAGACCTGAGCGGTACACGCGCGTTCATCGAGGCA 819

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Yy 485 CCCAAACCTTCGACCAATCTGTCGCGTCCGCGCAGAGAACGCGACCGGTACCGTCC 5444
Db 820 CCGGAGACTTTCAGCGACTTCTGGAGGCTCCGCGACAGAAAGCGACCGACCGACCATCA 8799
Qy 545 AGACGGGCTGCGCACTTCGACGCGCTGGGCTCGCGCTGTTTGAATGTCAACGGTGACCACT 6044
Db 880 CCATCGGCAACCACTTCGACGCGCTGGGCGCGGCGCGGATGAAA--CCTGGGAGCGCACG 9366
Qy 665 CTGACGTGGGC 675
Db 997 GCGAGGCTGGC 1007

RESULT 7
US-09-235-832-1
Sequence 1, Application US/09235832
Patent No. 6667170
GENERAL INFORMATION:
APPLICANT: M neyl, Arja
APPLICANT: Vehmaender, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235, 832
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. 6667170 Relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
/
/
/

```

```

; NAME/KEY: CDS
; LOCATION: 303..1334
US-09-235-832-1

Query Match      29.1%; Score 196.2; DB 3; Length 1375;
Best Local Similarity 59.0%; Pred. No. 3.5e-45;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3

QY      5  TCGGCTTTACCCCGGTTGCCCTTACGCGCTTACAGCCGAGCACTGGGGGCCGCGGCTTCCGCG 64
DB      349 TCGGCTCTTCGGCGCATCTGCACCAAGTGGCTTTGGCCCTTGGCACTCGCCATCGCCGGTGC 408
QY      65  CAGGAAATGCGACCGAGAGCTCGAAAAAGCAGACAGAACACCCTCGAGAGGGCTGACAG 124
DB      409 TGTCTGCCCGGACCGGCCCAACCCGACACACCAATATCCAGAACAGAACCGGGTACAGCA 468
QY      125 ATGGTATTATCTATTCTCTGTGAGTGAAGGTGAGCGGTGAGCGCAGCAGTACACCAACTGG 184
DB      469 ACGGCTACTTCTACTCTGTTCTGTGAACCGGACCGGCCCGGGAGCGGTCTCATATGACCTTCACT 528
QY      185 AAGCGCGGACCTTAGAATTCAGCTGGGGAGATGCGGATTAAGTGGTGGTGGTGAAGGGCT 244
DB      529 CGGGCGGAGGTACAGCACTCTGTGGCGAAACACCGGGAACCTTCTGTGCGCGGCAAGGCT 588
QY      245 GGAACCCCGGCTGAAACGACAGAGCATTCACCTTTGAGGGTGTATTACAGCCAAACGCA 304
DB      589 GGTCAACCGG--GGAGCGGGGACCGGTGACTTACACGCTCTTCAACCCGTGGGGTGA 645
QY      305 ACAGCTACTTTCGGGTCTACGGTTTGAACCCGCAACCCGCTGGTGAATTAATCATCTGTCG 364
DB      646 ACGGCTACTCAGCGCTTACCGGTGGAACAGAAACCCGCTGTCGATTACTATCTGTCG 705
QY      365 AGAATTGTGCACTTATATCTCTTCTCGGTGCTACCGATTTAGAACTGTGCACTGG 424
DB      706 AGAGTGGGGGACCTTACCGGGCCACCGGAC-----ACCTTACAAAGGACCGTACCAACCG 759
QY      425 ACGGTAGCATCTATGCACTTCGAGCAAGACCACTCGGCTGACAGCACTTAGCATGACAGCA 484
DB      760 ACGGGGGAAGGTAAGCACTTACAGACCTTGGCGGTACACGCGCGCTTCACTGAGGGCA 819
QY      485 CCGAAACCTTTCGACCAATATCTGTGCGTTCGCGCAGAGAACGCGACCAAGGGTACCGTTC 544
DB      820 CCGGACCTTTCAGAGCATTTCTGAGCGTTCGCGCAGAGAACGCGACCAACATCA 879
QY      545 AGACGGGCTGCCACTTTCAGCGCTTGGGCTCGCGCTGTGTTGAATGTCAACGGTGAACCAT 604
DB      880 CCATCGGCAACCACTTTCAGCGCTTGGGCGCCGCGCGGACATGAA---CTGGGCAAGCAAG 936
QY      605 ACTACCAATCGTTTTCGACGAGGAGGCTCTTTCAGACGCGGCTATGCTGCATCACCGTTG 664
DB      937 ACTACCAATCATGCGGACCGAGGGCTTACAGAGCAAGCGGTAGCTTCACCGCTTCATCATCA 996
QY      665 CTGACGTGGGC 675
DB      997 GCGAGGCTGGC 1007

RESULT 8
US-09-254-733-8
; Sequence 8, Application US/09254733
; Patent No. 6277596
GENERAL INFORMATION:
APPLICANT: WATANABE, MANABU
APPLICANT: MORIYA, TATSUKI
APPLICANT: AOYAGI, KAORI
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cbh1 GENES ORIGINATING
FROM THE GENES OF TRICHOCHODERA VIRIDE AND SYSTEM FOR MASS-PRODUCING
CELLULOSE
FILE REFERENCE: 99-0266*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07

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| | | | | |
|---------------------------|-------|-------------------|-----------|------------|
| Query Match | 28.8% | Score 194.2 | DB 3 | Length 822 |
| Best Local Similarity | 69.0% | Pred. No. 1.1e-44 | | |
| Matches 281, Conservative | 0 | Mismatches 123, | Indels 3, | Gaps 1 |

RESULT 9
US-08-121-436A-1

Patent No. 5837515
GENERAL INFORMATION:
APPLICANT: Suominen, Pirkko
APPLICANT: Nevalainen, Helena
APPLICANT: Saarelainen, Ritva
APPLICANT: Paloheimo, Marja
APPLICANT: Lahninen, Tarja
APPLICANT: Fagerström, Richard
TITLE OF INVENTION: No. 5837515a1 Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15

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|-----------------------|--------------|--------------------|----------------|--------------|
| Query Match | 28.1% | Score 190; | DB 2; | Length 1015; |
| Best Local Similarity | 68.5% | Pred. No. 1.7e-43; | | |
| Matches 278; | Conservative | 0; | Mismatches 15; | Indels 3; |
| | | | | Gaps 1; |

| | | | |
|----|-----|--|-----|
| Qy | 257 | TGAACGAAAGGCATCATCTTTGAGGGGTGTTTACGAGCCAAACGGCAACGATCACTTG | 316 |
| Db | 546 | TAAATAAAAGGGTCATCACTTTCGGAAAGCTTCAACCCCAACGGCAACAGCTACTCT | 605 |
| Qy | 317 | CGGCTACCGGTGGACCCGGCAACCCGGCTGTGAGATTTTACATGTCGAGAACTTTTGCA | 376 |
| Db | 606 | CCGGTACCGGTGGTCCCGCAACCCCTGTATCGATCTCAATGTCGAAACTTTTGCA | 665 |
| Qy | 377 | CCATATGATCCGTCCTCCGGTGTCTACGATCTAGAAATGTACGATGCGACGGTATGACT | 436 |
| Db | 666 | CTTCAACCCGTCACACGGGGCCACCAAGCTGGGCGAGGTTCCTCCGACGGACGCTCT | 725 |
| Qy | 437 | ATCGACTCGGAGAGCACTCGGCTCAAGCACTTAGCATGACGCGCAACCCAAACCTTTCG | 496 |
| Db | 726 | ACGACATTTTACCGCACCGACCGGCGCTCAACAGCGCTCATCATTCGGACCGCCACTTTT | 785 |
| Qy | 497 | ACCAATCTAGTCCGATCCGCGCAAGGACAAAGCGTACCGTCCAGACGGGCTGCC | 556 |
| Db | 786 | ACCAAGTACTGTCCGTCGCGCGCAACACCGGCTCGGATCAACACCGCGAAC | 845 |
| Qy | 557 | ACTTTCAGCGCTGGGCTCGCGCTGGTTTGAATGTCAACGGTACCACTACTACCAATTCG | 616 |
| Db | 846 | ACTTCAACCGGTGGCTCAACAAAGGCTTACGCT--CGGACGATGATTTACCAATTTG | 902 |

ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chactomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION: /product= "XLNA"
NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /product= "XLNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-469-242A-1

Query Match 26.9%; Score 181.8; DB 3; Length 1281;
Best Local Similarity 65.4%; Pred. No. 3.8e-41;
Matches 283; Conservative 0; Mismatches 147; Indels 3; Gaps 1;
QY 237 AAAGGCTGGAACCCGGCCGGAAGCAAGAGCCATCATTGAGGCTTTTCCAGCC 296
DB 478 AACGGCTGGAACCCGGGTAACCGGTGATCACTACACCGGCTACAGACC 537
QY 297 AAAGGCAAGACTACCTTGGCTCTACGTTGACCGCAACCGGCTGTCAGATTAA 356
DB 538 CAACGGCACTCTACCTCGCCGTCTACGCTGACCGCAACCGGCTGATCGATCTA 597
QY 357 CATGCTGAGAACCTTTGGACCTTATGATCTTCTCGGTGCTAACGATCTAGAACTGT 416
DB 598 CGTGTGAGAGCTTCGGCACTTACGACCCGTCGACGGGCGCCACCGGACGACGT 657
QY 417 CGAGTGGAGCGGTGATCTTATGACCTCGGCAACCACTGCGCTCAACGCACTAGAT 476
DB 658 GACCAACGAGCGGCGCACTTACCAATCTACCGCAAGCGGCTCAACCGGCTTCAT 717
QY 477 CGAGCGACCAAACTTGCACAACTAGTGGTCCGTCGCGGAGGAGGACGACGAGCGG 536
DB 718 CGAGGCAACGACCTTCTACCAATCTAGTCTGTGCGACCTCCAAAGGCGACCGGCGG 777
QY 537 TACCGTCAAGCGGCTGCGCACTTTCAGCGCTGGGCTCGCGTGGTTGAATGCAAGG 596
DB 778 TACTGTATACATGCGCAACGCTTCAATGCTTGAAGGAGGCTGTGAGAGCT---GGG 834
QY 597 TGACCACTACTACCAAGATCGTTGCAAGGAGGCTACTTCAAGCGGCTATGCTCCAT 656
DB 835 TTCCCAATGATTTATGATGATGCTACTGAGGAGTTACTACTGCTCGGCTCGGCACTGT 894
QY 657 CACGTTGCTGAC 669
DB 895 CAATGTTGGGCGC 907

RESULT 12
US-07-744-570B-1
Sequence 1, Application US/07744570B
Patent No. 5202249
GENERAL INFORMATION:
APPLICANT: Kluepfel, D.
APPLICANT: Morosoff, R.
APPLICANT: Shareck, F.

TITLE OF INVENTION: Xylanase for Biobleaching
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Michael J. Bradley
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
COUNTRY: United States
ZIP: 94804-0023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44MB storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,570B
FILING DATE: 19910813
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single strand
TOPOLOGY: Circular
US-07-744-570B-1

Query Match 24.9%; Score 168.4; DB 2; Length 675;
Best Local Similarity 60.0%; Pred. No. 1.7e-37;
Matches 343; Conservative 0; Mismatches 211; Indels 18; Gaps 3;
QY 97 ACAACCCCAACTCGAGGCTGGCAAGATGTTATTACTATTCCTGAGAGGAGGT 156
DB 34 ACCATCAACCAACCAACGACCGGACCGAGGATGATCTACTGTTCTGACCGAGCGC 93
QY 157 GAGCGGAGGCAAGTACCAACCAACCTGGAAGGGGCGCACTTACGAGATCACTGGGAGAT 216
DB 94 GGGGGCTCGTTCATGACGCTCAACGATGGGGGAGATATAGACACCGAGTGAACAAC 153
QY 217 GGGGTAACCTCGTGGTGAAGAGGCTGGAACCCCGGCTGAACGCAAGCCATCCAC 276
DB 154 TGGCGCAACTTGTGCGCGGCAAGGGCTGAGGACCGG-----CGACGGCAACGTCGCG 207
QY 277 TTTGAGGGTATTACCAAGCCAAACGCAACGCTACCTCGGCTTACGTTGAGACCGC 336
DB 208 TACAAGGCTACTTCAACCCCGTGGCAAGGCTACGCGCTGCTACGCTGAGACCTCG 267
QY 337 AACCGGCTGATGATTTATCATCTGTCAGAACTTTGGCACTATGATCTTCTCGGT 336
DB 268 AACCGGCTGATGATTTATCATCTGTCAGAACTTTGGCACTATGATCTTCTCGGT 336
QY 397 GCTACGATCTAGAACTGTGAGTGGAGCGGTAGACCTTATGACTCGGCAAGACCACT 456
DB 322 GGTACGTAAGAGGACCGCTCTCAAGGAGGAGCACTTACGACATCTACGAGACGACC 381
QY 457 CGGCTCAAGCACTTACATGACGAGGACCAAACTTTCACCAATATGTTGGTCCG 516
DB 382 CGGTACAAAGCCCTCTCGGTAAGGACCAAACTTTCAGAGATGAGATGTCGCG 441
QY 517 CAGAACAGGCGACAG-----CGGTACCGTCAAGCGGCTGCGCACTTCAAGCGCTGG 570
DB 442 CAGTGAAGGTGACAGTGGCTCGGACCATATCAACACCGGCAACCACTTCAAGCGCTGG 501
QY 571 GCTCGCGCTGTTGAATGTCAAAGGTGACCACTTACCAAGATCGTTGCAAGGAGGC 630
DB 502 GCGCGCGCGGAGTGAACATGGGCGCAGTTCAAGGTACTATGATGATGAGCAGGAGGC 561
QY 631 TACTTCAAGAGCGGCTATGCTGCATCAACCGT 662
DB 562 TATCAAGCAAGTGAAGCTGAACTCAACCGT 593

RESULT 13

US-08-507-431-5
Sequence 5, Application US/08507431
Patent No. 5693518
GENERAL INFORMATION:
APPLICANT: Kofod, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan Q.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 56935180 No. 5693518disk of No. 5693518th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,431
FILING DATE: 15-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,800
FILING DATE: 25-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3954.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-08-507-431-5
Query Match 24.4%; Score 164.6; DB 2; Length 927;
Best Local Similarity 58.3%; Pred. NO.2.3e-36;
Matches 346; Conservative 0; Mismatches 239; Indels 8; Gaps 3;
QY 77 CGAGCTCGAAGGAGCAAGCAACCCCACTCGAGAGGCTGGCAGATGTTTAACT 136
DB 134 CTGCCCTTGCTGGGCGCTGCACTGGCAAGCTCACTGGCTACTGCAACGGCTATTACTATA 193
QY 137 ATTCTGTGAGAGGAGCGGTGAGAGCGCAGGCACTACCAACTGGAAGCGGCACCT 196
DB 194 GCTTCTGAGACCGATGGCGCAAGCGCGATGTTGAATACAGCAACGGCGCCCGGGGGGTCTT 253
QY 197 ACAGATGATGCTGGGAGATGGCGGTAACTGTCGTGAGTGAAGAGGCTGAACCCCGGCC 256
DB 254 ACAGCGTACCTGTGATCTGGCGCTGCAACTTCTGCTGGTGAAGAGGCTGGAACCTTGG-A 312
QY 257 TGAACGCAAGAGCATTCATTGAGGGTGTTTACAGCC---AAACGGCAACAGCTAC 312

DB 313 AGTCTCATGACATTACGTAATCTCCGGCTCTCTGAGCACAGCAAGAAATAGCAACAGCTAC 372
QY 313 CTTCGGCTCTACCGTTGACCCCGCAACCGCGTGTGATGATTACATCTGTGAGAACTTT 372
DB 373 CTCTCCGTCTACGGCTGAGACCAACCGGTCTCTGTGAGATGATATCTCTGAGAGACTAC 432
QY 373 GGCACTGATGATCTTCTCTCCGGTGTACCGATCTTGAACTGTCCAGTCCGACGTTAGC 432
DB 433 GGGAGATACAAACCCCGCTCAGCTGACATTAACAAAGGCTCGGTCTCACTCCGACGATTCG 492
QY 433 ATCTATGACTGGGCAAGCACTCGCGTCAAGCACTAGATTCGACGCGCACCAACC 492
DB 493 ACATACATATTTCTACACGGGACCCGACCAACGCCCTCTTCATTCAGGACGCGCACT 552
QY 493 TTGCACCAATATCTGTCGTGCTCCGCGCAGAGCAACGCGACACCGGTACCGTCCAGCGGCG 552
DB 553 TTACAGCAGTACTGTGCTCATTTCCGCGACAAACCGCGTCCGCGGTACCGTACGACGCTGCC 612
QY 553 TGCCTCTGACGCTCGGGCTCGCGCTGTTGAATGTCAACGCTGACCACTACTACAG 612
DB 613 AACCATTTCAATGCTGGGGCAAGCTGGGATGATCT---GGGACGCAACACTATACAG 669
QY 613 ATCGTTCGAACGAGGCTTACTTACAGAGCGGCTATGCTGCATCAACCGTTGC 665
DB 670 ATCGTCTACTAAGGCTACTACTGCTGTGGGTCTGCGTCCATACGAGTTGC 722
RESULT 14
US-08-902-655A-5
Sequence 5, Application US/08902655A
Patent No. 5885819
GENERAL INFORMATION:
APPLICANT: Kofod, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Christgau, Stephan P.
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan Q.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 58858190 No. 5885819disk of No. 5885819th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,655A
FILING DATE: 30-July-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agriis, Cheryl T.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-08-902-655A-5

Query Match 24.4%; Score 164.6; DB 2; Length 927;
Best Local Similarity 58.3%; Pred. No. 2.3e-36;
Matches 346; Conservative 0; Mismatches 239; Indels 8; Gaps 3;

77 CGAGCTCGAAAAGCGACAGCAACCCCACTCGAGAGGCTGGCAGCATGTTATTACT 136
134 CTGCGCTTGCTGGCGCTCGACTGCGACGCTCACTGGCTACTGAAAGGCTATTACTATA 193
137 ATTCTGTGAGAGTACGCTGAGAGCGCAGGACAGTACCAACCACTGGAAGCGGCACT 196
194 GCTTCTGAGCCGATGGCGCAAGCGCGATGTTGAATACAGCAACGCGCGCGGGGCTCT 253
197 ACAGATCAGCTGGGAGATGCGGTAACCTGTCGTGTAAGAAAGGCTGAAACCCGCGCC 256
254 ACAGCGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
257 TGAACGAGAGCCATCTTGAAGGCTGTTACAGCC---AAACGCGACAGCTAC 312
313 AGTCTCATGACATTACGTACTCGGCTCTGACACAGCAAGAAATAGCAACAGCTAC 372
313 CTTCGGCTTACGCTGTAAGACCCGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
373 CTTCGGCTTACGCTGTAAGACCCGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
373 GGCACATGATCTCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
433 GGGAGATGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492
433 ATCTATGACTCGGCAAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492
493 ACATATCATATCTACAGCGGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
493 TTGCAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
553 TTGCAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
553 TGCCACTTTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
613 AACCATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669
613 ATCGTTGCAACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
670 ATCGTCTGTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722

RESULT 15
US-09-116-622-5
Sequence 5, Application US/09116622
Patent No. 6080567
GENERAL INFORMATION:
APPLICANT: Kofod, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: St, Joan O.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 60805670 No. 6080567disk of No. 6080567th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor

CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,622
FILING DATE: 16-July-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954, 224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-09-116-622-5

Query Match 24.4%; Score 164.6; DB 3; Length 927;
Best Local Similarity 58.3%; Pred. No. 2.3e-36;
Matches 346; Conservative 0; Mismatches 239; Indels 8; Gaps 3;

77 CGAGCTCGAAAAGCGACAGCAACCCCACTCGAGAGGCTGGCAGCATGTTATTACT 136
134 CTGCGCTTGCTGGCGCTCGACTGCGACGCTCACTGGCTACTGAAAGGCTATTACTATA 193
137 ATTCTGTGAGAGTACGCTGAGAGCGCAGGACAGTACCAACCACTGGAAGCGGCACT 196
194 GCTTCTGAGCCGATGGCGCAAGCGCGATGTTGAATACAGCAACGCGCGGGGCTCT 253
197 ACAGATCAGCTGGGAGATGCGGTAACCTGTCGTGTAAGAAAGGCTGGAACCCGCGCC 256
254 ACAGCGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
257 TGAACGAGAGCCATCTTGAAGGCTGTTACAGCC---AAACGCGACAGCTAC 312
313 AGTCTCATGACATTACGTACTCGGCTCTGACACAGCAAGAAATAGCAACAGCTAC 372
313 CTTCGGCTTACGCTGTAAGACCCGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
433 GGGAGATGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492
433 ATCTATGACTCGGCAAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492
493 ACATATCATATCTACAGCGGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
493 TTGCAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
553 TTGCAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
553 TGCCACTTTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
613 AACCATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669
613 ATCGTTGCAACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665

Db 670 ATCGTCGCTACTGAAAGGCTACTCGTGGCTGGCTGGCCATTACGTTGC 722

Search completed: February 11, 2006, 20:45:51
Job time : 149.191 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollateral Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:35:33 ; Search time 702.684 Seconds
(without alignments)
7943.586 Million cell updates/sec

Title: US-09-467-368-1_COPY_31_705

Perfect score: 675
Sequence: 1 ATGATCGGCTTACCCCGT.....TCACCGTGTGACGTGGC 675

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_Main:*

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1 | 675 | 100.0 | 983 | US-09-467-368-1 | Sequence 1, Appli |
| 2 | 582 | 86.2 | 588 | US-10-237-386-9 | Sequence 9, Appli |
| 3 | 371.6 | 55.1 | 678 | US-09-803-454-3 | Sequence 3, Appli |
| 4 | 257.2 | 38.1 | 850 | US-10-425-115-17283 | Sequence 17283, |
| 5 | 246.6 | 36.5 | 749 | US-10-425-115-82922 | Sequence 82922, A |
| 6 | 240.4 | 35.6 | 818 | US-10-425-115-37173 | Sequence 37173, A |
| 7 | 224.6 | 33.3 | 666 | US-10-213-990-65 | Sequence 65, Appli |
| 8 | 221.6 | 32.8 | 705 | US-10-213-990-68 | Sequence 68, Appli |
| 9 | 196.2 | 29.1 | 1375 | US-09-770-621-1 | Sequence 1, Appli |
| 10 | 189.2 | 28.0 | 739 | US-10-286-993-1 | Sequence 67, Appli |
| 11 | 186.2 | 26.8 | 712 | US-10-213-990-67 | Sequence 64, Appli |
| 12 | 181.2 | 26.8 | 942 | US-10-213-990-64 | Sequence 21, Appli |
| 13 | 185.4 | 24.5 | 978 | US-11-018-645-21 | Sequence 39, Appli |
| 14 | 155.2 | 23.0 | 1002 | US-10-213-990-70 | Sequence 8, Appli |
| 15 | 147.2 | 21.8 | 596 | US-10-307-441-39 | Sequence 1, Appli |
| 16 | 146.4 | 21.7 | 2225 | US-09-790-070A-8 | Sequence 1, Appli |
| 17 | 134.6 | 19.9 | 2898 | US-10-299-393-1 | Sequence 1, Appli |
| 18 | 124 | 18.4 | 2898 | US-11-154-793-1 | Sequence 1, Appli |
| 19 | 124 | 18.4 | 2898 | US-11-154-793-1 | Sequence 1, Appli |
| 20 | 119.2 | 17.7 | 557 | US-09-970-616-1 | Sequence 1, Appli |
| 21 | 119.2 | 17.7 | 557 | US-10-765-716-1 | Sequence 31, Appli |
| 22 | 119.2 | 17.7 | 642 | US-09-149-310-31 | Sequence 17, Appli |
| 23 | 118 | 17.5 | 594 | US-11-018-645-17 | |

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| 24 | 103.6 | 15.3 | 2054 | 6 | US-10-419-969-5 | Sequence 5, Appli |
| 25 | 101.8 | 15.1 | 643 | 6 | US-10-340-860A-39 | Sequence 13, Appli |
| 26 | 94.2 | 14.0 | 561 | 10 | US-11-018-645-13 | Sequence 15, Appli |
| 27 | 90.2 | 13.4 | 561 | 10 | US-11-018-645-15 | Sequence 19, Appli |
| 28 | 89.4 | 13.2 | 972 | 10 | US-11-018-645-19 | Sequence 48309, A |
| 29 | 83.6 | 12.4 | 394 | 8 | US-10-425-115-48309 | Sequence 4, Appli |
| 30 | 82.6 | 12.2 | 642 | 9 | US-10-626-583-4 | Sequence 4, Appli |
| 31 | 82.6 | 12.2 | 642 | 9 | US-10-626-724-4 | Sequence 15625, A |
| 32 | 80.8 | 12.0 | 539 | 7 | US-10-437-963-15625 | Sequence 10, Appli |
| 33 | 78.4 | 11.6 | 591 | 10 | US-11-018-645-3 | Sequence 1, Appli |
| 34 | 78.4 | 11.6 | 628 | 10 | US-11-018-645-10 | Sequence 2, Appli |
| 35 | 72.4 | 10.7 | 663 | 3 | US-09-909-207-1 | Sequence 5, Appli |
| 36 | 72.4 | 10.7 | 663 | 3 | US-09-909-207-2 | Sequence 11, Appli |
| 37 | 72.4 | 10.7 | 744 | 3 | US-09-909-207-4 | Sequence 12, Appli |
| 38 | 72.4 | 10.7 | 744 | 3 | US-09-909-207-5 | Sequence 10, Appli |
| 39 | 72.4 | 10.7 | 1513 | 3 | US-09-909-207-10 | Sequence 11, Appli |
| 40 | 72.4 | 10.7 | 1513 | 3 | US-09-909-207-11 | Sequence 12, Appli |
| 41 | 71.8 | 10.6 | 642 | 8 | US-10-626-583-6 | Sequence 6, Appli |
| 42 | 71.8 | 10.6 | 642 | 8 | US-10-626-583-12 | Sequence 12, Appli |
| 43 | 71.8 | 10.6 | 642 | 9 | US-10-626-724-6 | Sequence 12, Appli |
| 44 | 71.8 | 10.6 | 642 | 9 | US-10-626-724-12 | Sequence 10, Appli |
| 45 | 71.8 | 10.6 | 645 | 6 | US-10-237-386-10 | |

ALIGNMENTS

RESULT 1
US-09-467-368-1
Sequence 1, Application US/09467368
Patent No. US20020160080A1
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
Wagner, Peter
Mullertz, Anette
Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020160080A10 No. US20020160080A1disk of No. US200201600
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,368
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Thermomyces lanuginosus

LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-803-454-3

Query Match 55.1%; Score 371.6; DB 3; Length 678;
Best Local Similarity 72.0%; Pred. No. 4,1e-107;
Matches 485; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

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QY 1 ATGGTCGGCTTTACCCCGGTTGCCCTTACCGCGAGCTGGGCGCCCTGCGCTTC 60
DB 1 ATGGTGGTTTACTCCAGTTGCTTACCTGCTTACCTGCTGCTGCTGCTTACCTTTC 60
QY 61 CCGGACGGGAAATGCGACGAGCTGAAAAGACAGACACCCCACTCCGAGGCTGG 120
DB 61 CCACACAGGTAAATGCTACGAAATGAAAAAAGACAAACCTCCAAATTCGAAAGTTGG 120
QY 121 CACGATGGTTATTAATTCCTGCTGAGTGAAGCGGTGAGCGGACGCTACCAAC 180
DB 121 CATATGTTATTTATTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 CTGGAAGCGGACCTACGAGATCAGCTGGGAGATGCGGTTAACTGCTGCTGAAAG 240
DB 181 TTGAAGGTGCTACCTAGAAATTTCTGGGGTGAATGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GCGCTGAACCCCGCTGACGCAAGACCACTTCACTTGAAGGCTTTTACAGCCAAAC 300
DB 241 GGTGGATCCAGGTTTAAAGCAAGACTATTCATTTTGAAGGCTTTTACCAACAAAT 300
QY 301 GGCAACAGCTACCTTGGGCTGAGCGTTGACCGGCAACCGGCTGCTGCTGCTGCTGCT 360
DB 301 GGTATTTCTTATTTAGCTGTTATGCTGTTAGCTGTTAGCTGTTAGCTGTTAGCTGTT 360
QY 361 GTCCGAACTTTGCAACCTATGATCTTCTCGGCTGCTACCACTGAGAACTGCTGAG 420
DB 361 GTTGAATTTTGGTACTTATGATGATCATCTTGGTGTCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 TGGCAGGTGATCTATGCACTGGGCAAGACCACTCGGCTGCAAGCACTGATGATGAC 480
DB 421 TGTATGTTCTATTTATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 GGCAACCCAACTTGCACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 GGTATCTCAACTTTCGATCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GTCCGACGCGCTGCACTTGCAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 GTTCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CACTACTACAGATGCTTGGCAACGAGGCTACTTCAAGCGGCTATGCTGCTGCTGCTGCT 660
DB 601 CATATTTATCAAAATGTTGCAACTGAAAGTATTTCTCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GTTGTGACGCTGG 674
DB 661 GTTGTGATGTTGG 674
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RESULT 4

US-10-425-115-177283
Sequence 177283, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 177283
LENGTH: 850
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_93271C.1
US-10-425-115-177283

Query Match 38.1%; Score 257.2; DB 8; Length 850;
Best Local Similarity 64.2%; Pred. No. 7.6e-71;
Matches 420; Conservative 0; Mismatches 228; Indels 6; Gaps 2;

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QY 14 CCCCCTGTCCTGCGGCTTACCCGCACTGGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 73
DB 139 CCACCGGTGCTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 198
QY 74 CCACGAGCTGAAACGACAGCAACCCCACTCGAGGCTGGCAGATGTTATT 133
DB 199 TCAATGATTTGATGCTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258
QY 134 ACTATTCCTGCTGAGTGAAGCTGAGCGAGCGACGCTACCAACCTGAGAGCGGCA 193
DB 259 TCTACTCTGCTGCTGAGCGAGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
QY 194 CTTACGAGATGATGCTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
DB 319 AGTACAGCGCTACCTGAGAGACCGGTGCTAACATGTTGGTGAAGAGGCTGGAACCTG 378
QY 254 GCTGAAGCGAAGACCATCACTTGAAGGCTGTTTACAGCCAAACGCAACAGTACC 313
DB 379 GTGCG--GCCGACCATCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
QY 314 TTGCGGTCTACGCTTGAACCGGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
DB 436 TTGCGATCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
QY 374 GCACCTATGATCTTCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
DB 496 GTACTCTGACACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
QY 434 TCTATGACTCGGCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
DB 556 CTTACAAAGATTTGCGCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
QY 494 TCGACCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
DB 616 TCAACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
QY 554 GCCACTTGAAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
DB 676 CCCACTTGAAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
QY 614 TCGTTGAACGAGAGGCTACTTGAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
DB 733 TCGTGCACCGAGGCTTACTTCTCTCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
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RESULT 5

US-10-425-115-82922
Sequence 82922, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28

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? NUMBER OF SEQ ID NOS: 369326
? SEQ ID NO 82922
? LENGTH: 749
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (1)..(749)
? OTHER INFORMATION: unsure at all n locations
? FEATURE:
? OTHER INFORMATION: Clone ID: MRT4577_175642C.1
? US-10-425-115-82922

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|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 36.5% | Score 246.6; | DB 8; | Length 749; |
| Best Local Similarity | 63.9% | Pred. No. 1.7e-67; | | |
| Matches 423; Conservative | 0; | Mismatches 220; | Indels 9; | Gaps 3; |

| | | | |
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| Oy | 1 | ATGGCGGCTTTAAACCCCGTTCGCCCTTGGGCGCTTAAAGCGGCATCTGGGCGCTTC | 60 |
| Db | 80 | ATGGTTTCTTTCACCTTCATCATCAACCGTGCCTTTGGCGGCTACCGGCGCTCTTGGCGGC | 139 |
| Oy | 61 | CCGGCAGGGAATGCCACGAGCTCGAAGGAGCAGACACACCCCACTCGAGGGGCTGG | 120 |
| Db | 140 | CCCCG---CACTGATGTGTCTCTCGTTGCCGCTCAGAACACCCCCCAACCGGCAGGGTACC | 196 |
| Oy | 121 | CACGATGGTTATTAATTCTCCGTGGAGGTGAACGGTGGAGCGCACGGCCACGGTAAACACAC | 180 |
| Db | 197 | CACACGGCTGCTTCTGGCTTTGGTGGTCTGAATGGGGGGTCCCGGCTACCTACACCAAC | 256 |
| Oy | 181 | CTGGAAAGCGGCACCTACGAGATCAAGCTGGGGAGATGGCGGTAACTCTGTCGGTGGAAAG | 240 |
| Db | 257 | GGTCCGGGTGGATAGCTACACGGCTAAAGCTGGGGAAGGGTGGCACTCTCGGCTGGAAAG | 316 |
| Oy | 241 | GGCTGGAAACCCCGGCTGTAAGCGCAAGAGCATTCACATTGGAGGTGTTTACACGCCAAC | 300 |
| Db | 317 | GGATGGAAACCCAG--AACTGCCGTAACATCACTACTCTGTGTACTTACAACTACAC | 373 |
| Oy | 301 | GGCAACAGCTACTTGGCGGTCTACGGTGTGAACCCGCAACCCGCTGGTCGAGTATTCATC | 360 |
| Db | 374 | GGCAACTCTACTTGGCGGTCTACGGCTGGACCCGCAACCCCTTGTGAGTACTACGTC | 433 |
| Oy | 361 | GTGGAACCTTGGCACTTATGATCTCTTCGCGGTACCGAGTTAGAACTGTGAG | 420 |
| Db | 434 | GTTGGAACTTCGGGACCTACACACCCCTCTCCACAGTCCAGAACAAAGGTACCCGTACC | 493 |
| Oy | 421 | TGGCAGGGATGATCTATGACATCGGCAAGACACACTCGGCTCAAGCCTGATCATGAC | 480 |
| Db | 494 | TCTGATGGATCTTCTCTCAAGATCGCTCAGTGGACCCGTAACCAACAGCCCTTCATCGAT | 553 |
| Oy | 481 | GGCACCCAAACCTTCGACCAATAGTGGTTCGCTCCGACAGACAAAGGCAACAGGGTACC | 540 |
| Db | 554 | GGCACCAAGACCTTTCAGCAGTATTTGTCTGTTTGGTCAAGAACAGGGCTTTCGGGCTCC | 613 |
| Oy | 541 | GTCGAGACGGGCTGCACATTTCGACCGCTGGGGCTCGGCGCTGTGTAATGTCAACGGTGAC | 600 |
| Db | 614 | GTCATATATGAAGACTACATTGACCGCTGGGCGCAGCAAGGGCAATGAA---CTTGGCCAG | 670 |
| Oy | 601 | CACCTACTACAGATCGTTGCAACGAGGGCTACTTTCAGACAGCGGCTATGCTCGATCAC | 660 |
| Db | 671 | CACCTACTACAGATTTGTGCCACCGAGGTACTTCTCCACTGTGTAACGGCCAGATCAC | 730 |
| Oy | 661 | GT 662 | |
| Db | 731 | GT 732 | |

RESULT 6
US-10-425-115-37173
; Sequence 37173, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.

```

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 37173
LENGTH: 818
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_133906C.1
US-10-425-115-37173

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|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 35.6% | Score 240.4; | DB 8; | Length 818; |
| Best Local Similarity | 62.5% | Pred. No. 1.6e-65; | | |
| Matches 411; Conservative | 0; | Mismatches 241; | Indels 6; | Gaps 2; |

| | | | |
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| Db | 96 | TCATACACTGCTGCTGTTGTCGACGACTGGTGCCTTTCGCTGCTCCGCGCACTGATGTAGCTG | 155 |
| OY | 65 | CAGGGAATGCCAGGAGCTCGAAAAAGCAGACAAACCCCACTCGAGGGCTGGCAG | 124 |
| Db | 156 | CTCGTTCTCCGGCGACTCGTCGCTCGCCAGAGACACCCCAACCCGAAAGAAACACACA | 215 |
| OY | 125 | ATGTTATTACTATTTCCTGTTGAGTAGACGTTGAGGCGCAGGCCACGTACACCAACTG | 184 |
| Db | 216 | ACGGTGTCTTACTCTTGTGTGAGTAGTATGGTGCTCCAAAGTTACTTACACCAAGGTTG | 275 |
| OY | 185 | AAGCGGCACCTAGAGATCAGCTGGGGAGATGCGGTTAACTCGTCGGTGGAAAAAGGCT | 244 |
| Db | 276 | CAGGTGGAGGTACAGGCTCAACTGGGAAAGGGGGCAACTTTGTGTGGTAAGGGCT | 335 |
| OY | 245 | GGAACCCCGCCTGGAAGCAAGAGCCATTCACCTTTGAGGGTGTTTACAGCCAAACGCA | 304 |
| Db | 336 | GGAACCCCTGGATGCG--GCCCGCACCGTTACTCTACCTACCTGCGGCTCTTACAACCCCAAGGCA | 392 |
| OY | 305 | ACAGTACCTTACGGGTCTACGGTTGGACCCCGCAACCGGTGGTTCGATTTACATCGTGG | 364 |
| Db | 393 | ACTCTTACTTTCCTCATCTATGGGTGGAACGTAAACCTTCTCGTCGATATCTATGTGCTTG | 452 |
| OY | 365 | AGAACTTTGGCACCATTGATCTCTTCCCTCGGTGCTAACGATCTAGAACTGTGCACTGCG | 424 |
| Db | 453 | AGAACTTGGAAACGTATGACCCGAACTTCCAGGCTTAGCAACAAGGGTACCGTAGCTGCGG | 512 |
| OY | 425 | ACGGTAGATCTATGACTCGGCAAGACCACTCGCGTCAAGGCACCTAGCATCTGACGGCA | 484 |
| Db | 513 | ACGGCTCTTCTTACMAAGATCGCTCAGTGCACCCGTAACTAAACAGGCATCATCTGATGGAA | 572 |
| OY | 485 | CCCAAACCTTGGACCAATACGTGATGGTCCGCGCAGGACCAAGGCGCACAGCGTACCGTCC | 544 |
| Db | 573 | CAGGACCTTTTCAGCAGATCTGCTGTTCTTCCGCAAGAACAGGGCTTCAAGCGATCCGTGA | 632 |
| OY | 545 | AGACGGGCTGCCACTTCGACGGCTTGGGCTCGCGCTGCTTGAATGTCAAACGCTGACACT | 604 |
| Db | 633 | ACATGAACATCACTTCGATGCTTGGGCCAGCAAGGCGATGACTCT--TGTAGACCACT | 689 |
| OY | 605 | ACTACCAATGTTGTCACACGAGGGGCTACTTACAGACGGCGCTATGCTCCGATCAACGT | 662 |
| Db | 690 | ACTACCAATGTGCTTACCGAGGGATATCTTTCACACGGGTTCTGCGTATACACTGT | 747 |

RESULT7
US-10-213-990-65
; Sequence 65, Application US/102139900
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg

APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
FILE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213.990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 666
TYPE: DNA
ORGANISM: Aspergillus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(666)
US-10-213-990-65

Query Match 33.3%; Score 224.6; DB 5; Length 666;
Best Local Similarity 61.5%; Pred. No. 1.5e-60;
Matches 413; Conservative 0; Mismatches 249; Indels 9; Gaps 3;

QY 1 ATGTCGAGCTTACCCCGTGGCTTGGCGCTTACCGCGACTGGGCGCTTGCCTTC 60
DB 1 ATGTCGATCA 60
QY 61 CCGG---CAGGGAATGCCAGGAGCTGAAAAGGAGAGAGAACCCCACTCGGAGGCG 117
DB 61 CCGGCTCGAGCAATGAGTGAAGTACCAAGCGGCGCTCAAGCTTCAGACTGCGC 120
QY 118 TGGCAGATGATTTACTATCTCTGTGAGTGAAGCGTGGAGCGAGCCACGTAACC 177
DB 121 ACGAATAGCGCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 180
QY 178 AACCTGGAAGCGGCACTAGAGATCACTGGGGAGATGGCGGTAACTCTGTGGTGA 237
DB 181 AACCGCAATGCGCGCAGATCAAGTCACTGGAACAACCTCGGCACTTTGTGCTGGG 240
QY 238 AAGGCTGGAACCCCGGCTGAAGCGCAAGCACTTGAAGGGGTTTACCAAGCA 297
DB 241 AAGGCTGGAACCCCGGCT---AGCGAAGAGCGGTCACTACAGCGGCTCTCGGAGACC 297
QY 298 AACGCAACAGCTACTTGGCGGTCTACCGGTGGAACCGCAACCGCTGGTGAATTAAC 357
DB 298 ACGGGAACGCGCTACTCTCGGTGTAAGCGCTGGAAGCACTCCGCTGTGGAATTTAC 357
QY 358 ATCTGGAATCTTTGGCACTTATGATCTTCTCGGTGTACCGATCTAGAACTGTC 417
DB 358 ATCTGGAATCTTTGGCACTTATGATCTTCTCGGTGTACCGATCTAGAACTGTC 417
QY 418 GAGTGGCAAGGATGATCTAGACTCGGCAAGCACTCGCGTCAAGCACTAGCATC 477
DB 418 GAGTGGCAAGGATGATCTAGACTCGGCAAGCACTCGCGTCAAGCACTAGCATC 477
QY 478 GAGGCAACCAACCTTGAACCAATATGATCGGTGCGGCAAGCAAGCGAGCGGT 537
DB 478 GAGGCAACCAACCTTGAACCAATATGATCGGTGCGGCAAGCAAGCGAGCGGT 537
QY 538 ACGTCAAGAGCGGCTGCACTTGAAGCGCTGGGCTGCGGTGTTGAATGTCAAGCGT 597
DB 538 ACGTCAAGAGCGGCTGCACTTGAAGCGCTGGGCTGCGGTGTTGAATGTCAAGCGT 597
QY 598 GACCACTACTACAGATGTTGCAAGCGAGGCGTACTTACAGACGGGTATGCTGCGATC 657
DB 598 GACCACTACTACAGATGTTGCAAGCGAGGCGTACTTACAGACGGGTATGCTGCGATC 657
QY 658 ACGTGTGCTGA 668
DB 658 ACGTGTGCTGA 668

RESULT 8
US-10-213-990-68
Sequence 68, Application US/10213990

Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
FILE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213.990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 68
LENGTH: 705
TYPE: DNA
ORGANISM: Aspergillus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(705)
US-10-213-990-68

Query Match 32.8%; Score 221.6; DB 5; Length 705;
Best Local Similarity 60.5%; Pred. No. 1.4e-59;
Matches 409; Conservative 0; Mismatches 249; Indels 18; Gaps 2;

QY 2 TGTGCGCTTACCCCGTGGCTTGGCGCTTACCGCGACTGGGCGCTTGCCTTC 61
DB 2 TGTGCGCTTACCCCGTGGCTTGGCGCTTACCGCGACTGGGCGCTTGCCTTC 61
QY 62 CCGGAGGAATGCCAGGAGCTGAAAAGGAGAGAGAACCCCACTCGGAGGCTGGC 121
DB 62 CCGGAGGATGCTCTTCAATGATGCTGAGAGCGCGGCGGAGCCCAAGCTCACCGGCTGGA 145
QY 86 ATGAGATGCTCTTCAATGATGCTGAGAGCGCGGCGGAGCCCAAGCTCACCGATG 205
DB 122 ACGATGATTTACTATCTCTGTGAGTGAAGCGTGGAGCGGCAAGCTCAACCAACC 181
QY 146 ACAAGGCTACTACTCA 205
DB 182 TGAAGCGGCACTAGAGATCACTGGGAGATGGCGGTAACTGTGTGGTGAAGG 241
QY 206 GCGCGGCTGCTCA 265
DB 242 GCTGGAACCC-----CGGCTGAAGCGAAGGCACTTGAAGGCTG 286
QY 266 GCTGGAACCTTGAAGGCTGAGTACCGAGCTTTAATGAACTCACTACGAGGCA 325
DB 287 TTACCAAGCAACGGAAGCAAGTACCTTGGGTCTACCGGTGGAACCGGCAACCGGCTGG 346
QY 326 GCTTCAACCCGAGGCAATGGGTACTGCTGTCTACCGGTGGAACCGGCAACCGGCTTGA 385
DB 347 TCGAGTATTAATGATGTAAGTCTTGGCACTTATGATCTTCTCGGTGTACCGATC 406
QY 386 TTGAGTACTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 445
DB 407 TAGGAATGTCAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 466
QY 446 GGGGCACTGCAACCAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 505
DB 467 CACCTACATGACGAGCAACCAACCTTGAACCAATATGATCGGTGCGGCAAGCAAGC 526
QY 506 CTCCCTCATGAGAGGCAACCAACCTTGAACCAAGTACTGCTGTGTGCGGCACTCGCAAGC 565
DB 527 GCACCAAGCGGTACCGTCAAGCGGCTGCACTTGAAGCGCTTGGGCTGCGGCTGTTGA 586
QY 566 GTACCGGCGGCACTGATCAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 625
DB 587 ATGCAAGGTCACCACTACTACCAATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 646
QY 626 A---CTGGGAATCAACCACTACTACCAATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 682
DB 647 ATGCTGCACTACCGGT 662
QY 683 CTGCTTCACTACCGGT 698

/ NAME/KEY: CDS
/ LOCATION: (303)..(1337)
/ OTHER INFORMATION: Product= AM35 xylanase
US-10-286-993-1

Query Match 29.1%; Score 196.2; DB 6; Length 1375;
Best Local Similarity 59.0%; Pred. No. 1.8e-51;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

```
QY 5 TCGGTTTAAACCCCGTTCCTTGGGCTTAAAGCCGCACTGGGGCCCTTGCCCTTCCGG 64
DB 349 TCGGCTCCGGGGCACTGTCACAGTGCCTTCGCTCGACACTCGCACTCGCGGTGGC 408
QY 65 CAGGAGATGCCAGGAGCTCGAAAGCAGACAAACCCCACTCGAGGGCTGGCAG 124
DB 409 TCGTCCCGGCAAGCCGCAACCGGACACACCATCAACCAAGACAGCGGTACGA 468
QY 125 ATGTTATTACTATTCTGTGTGAGTGAACGCTGAGCGCAAGCCACGTACCAACTGG 184
DB 469 ACGGCTACTTCTACTGTTCTTGACCGACGCGCCGGGACCGTCTCATAGACCTTCACT 528
QY 185 AAGGGGCACTTACAGATCAAGTGGGAGATGGCGGTAACTCGTGGTGGAAAGGCT 244
DB 529 CGGGGAGAGCTACGACACTTCGTGGCGAAACCGGAACTTCGTGCGCGCAAGGCT 588
QY 245 GAAACCCGCGCTGAAACGCAAGAGCCATCACTTTGAGGGGTGTTACAGCGCAAGGCA 304
DB 589 GGTCCACCGG---GGAGCGGCGAACCTGATCTTAAACGCTCTTCAACCGCTGGGTA 645
QY 305 ACAAGTACTTTCGCTTACAGGTGGAACCCGCAACCGCTGGTGCAGTATTACATCGTCG 364
DB 646 ACGGCTACTTCAAGCTTACGAGTGAACAGGAACCGCTGTGAGTACTACATCGTCG 705
QY 365 AGAATTGGCACTTATGATCTTCTCGGTGCTACCGATCTAGAACTGTCCAGTCCG 424
DB 706 AGAGTGGGAGCACTTACCGGCGCACCGGC-----ACCTAAGGCGCACCGTCAACACG 759
QY 425 ACGGTAGCATATGATGATCTCGGCAAGACACTCGGCTGATCAAGCACTTACAGCGCA 484
DB 760 ACGGGGAAAGCTACGACATCTACAGACCTTGGCGTACAGCGCTTCACTCGAGGCA 819
QY 485 CCCAAACCTTGCAGCAATATCTGTGCTCGCCAGAGCAAGCGCAACGCGTACCGTCC 544
DB 820 CCCGAGCTTCCAGAGTTCGTGAGCGTCCGGAGCAAGAGCGGACCAAGCGGACATCA 879
QY 545 AGAGGGGCTGCCACTTTCAGCGCTGAGCTCGCGCTGTTGAATGTAACGTTCAACT 604
DB 880 CCATCGGCAACCACTTTCAGCGCTGAGCGCGCGCGCATGAA---CCTGGGCAAGCCAG 936
QY 605 ACTACCAAGATGTTGCAAGGAGGCTACTTCAAGAGCGGCTATGCTGCAATCCGTTG 664
DB 937 ACTACCAATATAGCGAGCGAGGCTTACAGAGCAGCGTATCCACCGTTCATCA 996
QY 665 CTGACGTGGC 675
DB 997 GCGAGGTGGC 1007
```

RESULT 11
US-10-213-990-67
/ Sequence 67, Application US/10213990
/ Publication No. US20030082595A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Bo
/ APPLICANT: Bussey, Howard
/ APPLICANT: Storme, Reg
/ APPLICANT: Roemer, Terry
/ TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
/ FILE REFERENCE: 10182-019-999
/ CURRENT APPLICATION NUMBER: US/10/213,990
/ NUMBER OF SEQ ID NOS: 72

/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 67
/ LENGTH: 739
/ TYPE: DNA
/ ORGANISM: Aspergillus
US-10-213-990-67

Query Match 28.0%; Score 189.2; DB 5; Length 739;
Best Local Similarity 57.7%; Pred. No. 2.6e-49;
Matches 410; Conservative 0; Mismatches 248; Indels 52; Gaps 2;

```
QY 2 TGTGCGCTTAAACCCCGTTCCTTGGGCTTAAAGCCGCACTGGGGCCCTTGCCCTTCC 61
DB 26 TGGGCTGTCCGCAATGAGACTCTGGGTGCCCCGTCGAACCGAGACCACTCGTTCA 85
QY 62 CGGAGGAATGCCAGGAGCTGAAAAGCAGACAAACCCCACTCGAGGGCTGGC 121
DB 86 ATGAGACTGCTCTTCAATGATTCCTGAGCGCGCGGCAACCCCAAGCTCCACCGCTGGA 145
QY 122 ACGATGTTATTACTATTCTGTGTGAGTGAACGCTGAGAGGCGACAGCCACGTACCAACC 181
DB 146 ACAAGGCTACTTACTTCTTCTGACTGATGGCGGCGAGGTGACTTACCAATG 205
QY 182 TGAAGCGGCACTTACAGATCAAGTGGGAGATGGCGGTAACTCGTGGTGGAAAG 241
DB 206 GCGCGGAGGTGCTGATCTCGGTCAACTGAGGAACGTGGGAATTGTGTGGTGAAG 265
QY 242 GCTGAAACCCCGGCTG----- 258
DB 266 GCTGAAACCCCGGAGGCTAGTACCGAGCTTGTCAAGTGGATGTCAGACTGTG 325
QY 259 -----AACGAAAGCATCCACTTGAAGGTGTTTACAGCAACCGCAAGAGCTAC 312
DB 326 GCTGACAAAGTAAACATTAATCAAGAGGAGCTTCAACCCCAAGGATGGCTAC 385
QY 313 CTTCGCTTACAGGTGGAACCCGCAACCGCTGGTGCAGTATTACATCGTCAAGACTTT 372
DB 386 CTGCTGTCTACGCTGAGCAACCAACCCCTTAATTAAGTACTGTTGAGTGTAT 445
QY 373 GGCACCTATGATCTTCTCGGTGCTACCGATTAAGAACTGTGAGTGGAGCGTAC 432
DB 446 GTTACATTAACCCCGGAGCGGCTACTTCAAGGGGCACTGTCAACCGAGGTGGC 505
QY 433 ATCTATGACTCGGCAAGACACTCGGCTCAACGCACTGACATCGAGCAACCAACC 492
DB 506 ACTTACAACTTACAGCGCGGTTCGTACATGCTCTTCATCGAAGGACCAAGACC 565
QY 493 TTGACCAATATCTGTGCTCGCCAGAGCAAGCGCAACGCGTACCGTCAAGCGGC 552
DB 566 TTGACCAAGTACTGTGTCGCACTCCAGAGGTACCGGCGCACTGTACATAGGCC 625
QY 553 TGCACCTTACAGCGCTGGGCTCGGCTGTTGAATGTAACGTTCAACGTACTACAG 612
DB 626 AACCACTTCAACGCTGAGAGCAAGCTGGGATGAA---CCTGGGAATCAACACTACAG 682
QY 613 ATGTTGCAACGAGAGGCTACTTCAAGAGCGGCTATGCTGCAATCCGT 662
DB 683 ATGTGCGCACTGAGGGTTACAGAGCAGCGGATGCTTCACTCACTGT 732
```

RESULT 12
US-10-213-990-64
/ Sequence 64, Application US/10213990
/ Publication No. US20030082595A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Bo
/ APPLICANT: Bussey, Howard
/ APPLICANT: Storme, Reg
/ APPLICANT: Roemer, Terry
/ TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
/ FILE REFERENCE: 10182-019-999
/ CURRENT APPLICATION NUMBER: US/10/213,990

;; CURRENT FILING DATE: 2002-08-05
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 64
;; LENGTH: 712
;; TYPE: DNA
;; ORGANISM: Aspergillus
US-10-213-990-64

Query Match 26.8%; Score 181.2; DB 5; Length 712;
Best Local Similarity 57.7%; Pred. No. 8.7e-47;
Matches 412; Conservative 0; Mismatches 253; Indels 49; Gaps 3;

```
QY 1 ATGGTCGAGCTTTACCCCGCTGCGCTTGGCGCTTACCGCGAGCTGGGGCCCTGGCCCTTC 60
DB 1 ATGGTCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 60
QY 61 CCGG---CAGGGAATGCCACGAGAGCTGAAAAGGACAGACACCCCACTCCGAGGGC 117
DB 61 CCGGCTCGGAGCAATAGTGTAGCTACCAAGCGGCGCTCAACAGCTCTCAAGCTGGC 120
QY 118 TGGCAGATGGTTATTAATCTCTGATGATGAGCGGTGAGGCGGACGACGTAAC 177
DB 121 ACGAATACGCTCTACTACTCTCTCTGACCGAGCGGCGGCGGAGGTACCTACACC 180
QY 178 AACCTGGAAGCGGACCTACGAGATCAGCTGGGGAGATGGCGTAACTTCGCTGGA 237
DB 181 AACGCAATGCGGCGGAGATCAGGTGAGTGAACAACCTGGGCACTTTGCTGGG 240
QY 238 AAGGCTGGAACCCCGGCTGAAGCA----- 264
DB 241 AAGGCTGGAACCCCGGCGGAGAGATGATGCTCTCCCTGCTTGTAGTTCAAGC 300
QY 265 -----AGAGCATCACTTTAGGGGTGTTTACAGGCAAAAGGCAAGCTACT 314
DB 301 TAAATGATTCAGAGCGGTACCTACAGCGGCTCTGAGACAGCGGAAACGGCTACT 360
QY 315 TGGCGTCAAGCTTGAACCCGCAACCGCTGCTGAGTATTAATCTCTGAGAACTTTGG 374
DB 361 CTCGGTGAAGCGGTGAGACAGACGTCGCTGCTGAGTATTAATCTCTGAGAACTTTGG 420
QY 375 CACCTATGATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 434
DB 421 CTCCTATGATCTCTCTCTGAGGAGCCATCTCGGCAACGCTGAGACGAGCGGCGAC 480
QY 435 CTATGATCTCGGCAAGCACTCGCTGCAAGCACTGAGCACTGAGCGGCAACCAACT 494
DB 481 GTACAACTCTTACAGAGAGAGCGGAGCAATGCGCTCATTCAGGCGAGGCTACTTT 540
QY 495 CGACCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 554
DB 541 TGACCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 555 CCACTTGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 614
DB 601 CCACTTGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
QY 615 GGTGCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668
DB 658 TGTTCGAGCGGAGGAGTACAGAGCGGCTCTCTACTATCACTGTTTCTTA 711
```

RESULT 13
US-10-213-990-71

;; Sequence 71, Application US/10213990
;; Publication No. US20030082595A1
;; GENERAL INFORMATION:
;; APPLICANT: Jiang, Bo
;; APPLICANT: Bussey, Howard
;; APPLICANT: Storms, Reg
;; APPLICANT: Roemer, Terry
;; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
;; ENZYMES AND METHODS OF USE

;; FILE REFERENCE: 10182-019-999
;; CURRENT APPLICATION NUMBER: US/10/213, 990
;; CURRENT FILING DATE: 2002-08-05
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 71
;; LENGTH: 942
;; TYPE: DNA
;; ORGANISM: Aspergillus
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(942)
US-10-213-990-71

Query Match 24.5%; Score 165.4; DB 5; Length 942;
Best Local Similarity 59.3%; Pred. No. 9.4e-42;
Matches 340; Conservative 0; Mismatches 221; Indels 12; Gaps 3;

```
QY 96 GACAAACCCCACTCGAGAGGCTGGCAGATGTTATTAATCTCTCTGAGATGACGG 155
DB 99 GATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 158
QY 156 TGGAGCGCAGGCGACGATACCAACCTGGAAGCGGCGCACTTACGATCAGCTGGG--- 211
DB 159 TGCCGATCAGTGCATATTAATTAATGCTCTGCTGCGGAATATATGATGACGTGGCGAA 218
QY 212 --GAGATGGCGATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 269
DB 219 CAGAAAGGATGATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 275
QY 270 CATCACTTTGAGGATGTTTACAGCCAAACGCAACAGCTTCTGCGGTCTACAGTTG 329
DB 276 CATCACTTCTGCGAGCTTCAATCTTCCGAAAGCTTACCTGCTGCTGCTGCTGCTGCTG 335
QY 330 GACCCGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 389
DB 336 GACTACCAACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 395
QY 390 CTCCTGCTTACCGATCTGAGTGAATCTGAGTGCAGCGTGAATCTGATGATCTGCGCA 449
DB 396 CTCCTGCTTACCGATCTGAGTGAATCTGAGTGCAGCGTGAATCTGATGATCTGCGCA 455
QY 450 GACCACTGCGGTCAAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 509
DB 456 GCACCAACAGGTCAACAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 515
QY 510 GGTCCGACAGGACAAAGCGACAGCGGTACCGTCCAGCGGCGTCCGACTTGAAGCGCTG 569
DB 516 CATCCGCAAAACAGGATCTGAGCGGACAGTACCAACCGGATCACTTCAAGGCTG 575
QY 570 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
DB 576 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 632
QY 630 CTACTTGAAGCGGCTGATGCTGCAATCACTG 662
DB 633 ATATGAGGACGCGTACTCTGCAACATCACTGT 665
```

RESULT 14
US-11-018-645-21

;; Sequence 21, Application US/11018645
;; Publication No. US20050208178A1
;; GENERAL INFORMATION:
;; APPLICANT: Bauer, Michael
;; APPLICANT: Bedford, Michael
;; APPLICANT: Pulliam, Derrick
;; TITLE OF INVENTION: Microbially Expressed Xylanases and Their Use as Feed Additives a
;; FILE REFERENCE: 70357WOPT
;; CURRENT APPLICATION NUMBER: US/11/018, 645
;; CURRENT FILING DATE: 2004-12-20
;; PRIOR APPLICATION NUMBER: 60/531,404

; PRIOR FILING DATE: 2003-12-19
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 21
 ; LENGTH: 978
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: XyIALE
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(978)
 ; US-11-018-645-21

Query Match 23.0%; Score 155.2; DB 10; Length 978;
 Best Local Similarity 56.8%; Pred. No. 1.6e-36;
 Matches 327; Conservative 0; Mismatches 243; Indels 6; Gaps 2;

Qy 100 ACCCCCACTCGAGGGCTGGCAGATGTTATTCTTCTGGTGGAGTGA 159
 Db 19 ACCTGAGCCAGAGGGGACCAACAGGCAATTCTTTCTGGAAGAAGCTCG 78
 Qy 160 GCGCAGGCGACGTACCAACCTGGAGGCGGACCTACGATCAGCTGGAGATGC 219
 Db 79 GGCACGGTGAATCTTGTGATGTATGCCAATGGCCGCTATACCTCCAACTGGAGGCGCATC 138
 Qy 220 GGTAACTCTGCTGGTGGAGGAGGCTGGAAACCCCGGCTCGAAGCAAGAGCATCTT 279
 Db 139 AACAACTGGGCGGCGGAGGAGGCTGGGCTACCGGCTCCACACAGCATGCTACTCC 198
 Qy 280 GAGGGTGTTCACAGCCAAACGCAACAGTACCTTGGGCTTACGGTGGACCCGCAAC 339
 Db 199 GGCACGTTCAATTGGCCG--GGCAACGTTACTGTGGCCCTGTATGGCTGGAACACCAAT 255
 Qy 340 CCGCTGTGAGTATTCATGCTGAGAACTTTGACCTATGATCTCTCTCGGTCT 399
 Db 256 CCATTGGTGTGAGTATTCATGCTGAGCAGCTGGGGTACTTCCCTCGCGCGGCGGCGCAG 315
 Qy 400 ACCGATCTAGGAATCTGTCAGATGCGAGCGGTAGCATCTATGCACTCGGAAGACCACTGCC 459
 Db 316 GGTTCATGGGCGAGGTTAGTGAACGAGGCGGACGTACGAGCTGTACCGGACCAACGC 375
 Qy 460 GTCAAGCACCCTTACATGACGAGCAACCACTTTCGACAAATCTGGTGGTCCGCGAG 519
 Db 376 GTGAACGAGCATCATCATATGGGCAACGCCGCTTCAACGATCTGAGAGCTGGCGAG 435
 Qy 520 GACAAGCGCACAGCGGTCAGTCAGAGCGGCTGCCACTTTCGACGCTGGGCTCGCGCT 579
 Db 436 TCGAAGCGCGTGGCGGACCATCATCGCAACCATTTCAACGCTGGGCGACGCTG 495
 Qy 580 GGTTCATGTCACGCTGACCACTTACCAAGATCTTGGCAAGAGGCTTACTTCAAGC 639
 Db 496 GGCATGAA--CTGGGCGAGCACTACCAAGGTCAATGGCCACGAGGTTTACAGAGC 552
 Qy 640 AGCGGCTATGCTCGCATCACCGTTGTCAGCTGGGAC 675
 Db 553 AGCGGCAAGCTTCGACATCACCTGTACCGAAGGTGGC 588

RESULT 15
 US-10-213-990-70
 ; Sequence 70, Application US/10213990
 ; Publication No. US20030082595A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Buesey, Howard
 ; APPLICANT: Storms, Reg
 ; APPLICANT: Roemer, Terry
 ; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
 ; FILE REFERENCE: 10182-019-999
 ; CURRENT APPLICATION NUMBER: US/10/213, 990
 ; CURRENT FILING DATE: 2002-08-05

; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 70
 ; LENGTH: 1002
 ; TYPE: DNA
 ; ORGANISM: Aspergillus
 ; US-10-213-990-70

Query Match 21.8%; Score 147.2; DB 5; Length 1002;
 Best Local Similarity 62.2%; Pred. No. 5.6e-36;
 Matches 249; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

Qy 263 CAAGAGCCATCACTTTGAGGAGTGTATACAGCCAAACGCAACAGCTTACCTTGGGTCT 322
 Db 329 CTATGATCACTTACTTCTCTGGCAGCTTCAATCTTCGGAAATGCTTACTGTCCGTGT 388
 Qy 323 ACGGTTGACCCGCAACCCGCTGTGAGTATTCATGCTGAGAACTTTGGACCTTATG 382
 Db 389 ATGGATGACTACCAACCCCTAGTCGAATTAATCAATCTTCGAACTATGGCAGTTACA 448
 Qy 383 ATCTTCTCTCGGCTACCGATCTAGAACTGTGAGTGGAGACGGTATGATCTATGAC 442
 Db 449 ATCTGCTCTGGGATGACGACAAAGGCAACCGTACACGAGATGATCACTTACGACA 508
 Qy 443 TCGCAAGACCACTCGGCTCAACGCACTTACATGACAGGCAACCAACCTTGCACCAAT 502
 Db 509 TCTATGAGCAACCAAGTCAACAGCTTCAATCTGTGGCAAGGCACTTCAACCAAT 568
 Qy 503 ACTGTCGTCTCGGCAAGGCAACGAGCAACCGGTACCGTTCAGACGAGGCTGCACTTGC 562
 Db 569 ACTGTCATCTCGGCAAAACAAAGGATCCAGCGGCAAGTACCAACCGCAATCACTTCA 628
 Qy 563 ACGCTGGGCTCGGCTGTGTTGAATGTCAACGCTGACACTTACAGATGCTTGCAG 622
 Db 629 AGGCTGGGCTAGTCTGGGAGTGA--CTGGGTACCATTAATCAATGATGTTTCA 685
 Qy 623 CGAGGCTACTTTCAGCAGCGGCTATGCTGCATCACCGT 662
 Db 686 CTGAGGGATATGAGAGGAGGCTTACCTTCGACATCACTGT 725

Search completed: February 11, 2006, 23:51:28
 Job time : 703.684 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:37:15 ; Search time 215.772 Seconds
(without alignments)
2812.856 Million cell updates/sec

Title: US-09-467-368-1_COPY_31_705

Perfect score: 675

Sequence: 1 ATGCTCGCTTACCCCGT.....TCACCGTGTGACGTGGC 675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications NA_New:

1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US12_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US13_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US14_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US15_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US16_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US17_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------------|
| 1 | 582 | 86.2 | 588 | 11 | US-11-170-653-9 |
| 2 | 201.2 | 29.8 | 1008 | 7 | US-10-517-939-231 |
| 3 | 196.2 | 29.1 | 1375 | 11 | US-11-108-1638-1 |
| 4 | 189.2 | 28.0 | 663 | 11 | US-11-108-1638-5 |
| 5 | 189.2 | 28.0 | 906 | 11 | US-11-108-1638-4 |
| 6 | 186.2 | 27.6 | 1059 | 7 | US-10-517-939-225 |
| 7 | 186 | 27.6 | 663 | 11 | US-11-108-1638-3 |
| 8 | 185 | 27.4 | 906 | 11 | US-11-108-1638-2 |
| 9 | 185 | 27.4 | 1047 | 7 | US-10-517-939-165 |
| 10 | 170 | 25.2 | 1074 | 7 | US-10-517-939-199 |
| 11 | 170 | 25.2 | 1137 | 7 | US-10-517-939-255 |
| 12 | 165.8 | 24.6 | 1041 | 7 | US-10-517-939-169 |
| 13 | 165.6 | 24.5 | 1044 | 7 | US-10-517-939-221 |
| 14 | 165.4 | 24.5 | 1299 | 7 | US-10-517-939-177 |
| 15 | 160.8 | 23.8 | 1044 | 7 | US-10-517-939-195 |
| 16 | 160.8 | 23.8 | 1083 | 7 | US-10-517-939-183 |
| 17 | 159.8 | 23.7 | 1083 | 7 | US-10-517-939-217 |
| 18 | 156.2 | 23.1 | 1047 | 7 | US-10-517-939-253 |
| 19 | 150.8 | 22.3 | 1065 | 7 | US-10-517-939-215 |
| 20 | 150.6 | 22.3 | 1071 | 7 | US-10-517-939-233 |
| 21 | 150.2 | 22.3 | 1041 | 7 | US-10-517-939-159 |

| | | | | | | |
|----|-------|------|------|----|-------------------|-------------------|
| 22 | 146.4 | 21.7 | 1047 | 7 | US-10-517-939-299 | Sequence 299, App |
| 23 | 141.8 | 21.0 | 1077 | 7 | US-10-517-939-181 | Sequence 181, App |
| 24 | 131.2 | 19.4 | 1047 | 7 | US-10-517-939-161 | Sequence 161, App |
| 25 | 128 | 19.0 | 1029 | 7 | US-10-517-939-219 | Sequence 219, App |
| 26 | 127.8 | 18.9 | 747 | 7 | US-10-517-939-227 | Sequence 227, App |
| 27 | 124 | 18.4 | 1695 | 7 | US-10-517-939-317 | Sequence 317, App |
| 28 | 119.2 | 17.7 | 642 | 11 | US-11-214-413-31 | Sequence 31, App |
| 29 | 118 | 17.5 | 669 | 7 | US-10-517-939-167 | Sequence 167, App |
| 30 | 116.4 | 17.2 | 1066 | 7 | US-10-517-939-205 | Sequence 205, App |
| 31 | 114.8 | 17.0 | 1068 | 7 | US-10-517-939-153 | Sequence 153, App |
| 32 | 109.2 | 16.2 | 1020 | 7 | US-10-517-939-197 | Sequence 197, App |
| 33 | 108.4 | 16.1 | 633 | 7 | US-10-517-939-207 | Sequence 207, App |
| 34 | 107.2 | 15.9 | 636 | 7 | US-10-517-939-197 | Sequence 197, App |
| 35 | 106.8 | 15.8 | 555 | 7 | US-10-517-939-251 | Sequence 251, App |
| 36 | 94.2 | 14.0 | 570 | 7 | US-10-517-939-189 | Sequence 189, App |
| 37 | 93.4 | 13.8 | 1068 | 7 | US-10-517-939-163 | Sequence 163, App |
| 38 | 91.8 | 13.6 | 570 | 7 | US-10-517-939-377 | Sequence 377, App |
| 39 | 91.6 | 13.6 | 1338 | 7 | US-10-517-939-367 | Sequence 367, App |
| 40 | 91.4 | 13.5 | 678 | 7 | US-10-517-939-171 | Sequence 171, App |
| 41 | 91.4 | 13.5 | 1983 | 7 | US-10-517-939-353 | Sequence 353, App |
| 42 | 91 | 13.5 | 645 | 7 | US-10-517-939-157 | Sequence 157, App |
| 43 | 91 | 13.5 | 1053 | 7 | US-10-517-939-191 | Sequence 191, App |
| 44 | 90.2 | 13.4 | 570 | 7 | US-10-517-939-375 | Sequence 375, App |
| 45 | 89.8 | 13.3 | 1077 | 7 | US-10-517-939-369 | Sequence 369, App |

ALIGNMENTS

RESULT 1
US-11-170-653-9
Sequence 9, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 588
TYPE: DNA
ORGANISM: Thermomyces lanuginosus
US-11-170-653-9

Query Match 86.2%; Score 582; DB 11; Length 588;
Best Local Similarity 100.0%; Pred. No. 4,7e-156;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 94 | CACACACACCCCACTCGGAGGCTGACGAGTATTAATTCCTGAGTGAAGAC | 153 |
| DB | 4 | CACACACACCCCACTCGGAGGCTGACGAGTATTAATTCCTGAGTGAAGAC | 63 |
| QY | 154 | GGTGAAGCGAGGACGACGACCACTGGAAGCGGACCTGACGATCACTGGGGA | 213 |
| DB | 64 | GGTGAAGCGAGGACGACGACCACTGGAAGCGGACCTGACGATCACTGGGGA | 123 |
| QY | 214 | GATGGCGTAACTCTGCTGAGAAAGGCTGGAACCCGCGCTGAACGCAAGCCATC | 273 |
| DB | 124 | GATGGCGTAACTCTGCTGAGAAAGGCTGGAACCCGCGCTGAACGCAAGCCATC | 183 |

[illegible]

RESULT 2
US-10-517-939-231
; Sequence 231, Application US/10517939
; Publication No. US20060003433A1

```

APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Etesghallian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517, 939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389, 299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 231
LENGTH: 1008
TYPE: DNA
ORGANISM: Bacteria
US-10-517-939-231

```

| | | | | |
|-----------------------|-----------------|--------------------|-----------|--------------|
| Query Match | 29.8% | Score 201.2; | DB 7; | Length 1008; |
| Best Local Similarity | 59.9% | Pred. No. 1.1e-47; | | |
| Matches 376; | Conservative 0; | Mismatches 243; | Indels 9; | Gaps 2; |

QY 37 GCGGACATCGGGGCTTGGCTTCCGCGAGGATCGGAGGATCGGAGGACACAG 38
Db 73 GTGCGCTGCGCGCGCTCGCCGCGCTGATGCTCCGGGCAACCGCCAGGCGCGACAGCTC 132
QY 97 ACAACCCCAACTCGGAGGCGTGGCAAGATGTTATTACTTCTGATGAGATGACGGT 156
Db 133 GTCAACGACCAACGAGGAGGGACCAACACGCTACTACTCTCTGTTCTGGAACCGACAGC 192
QY 157 GGAGCGCAGCGCACGTAACCAACTCTGGAAGCGCGCACCTTACGAGATCAAGCTGGGAGAT 216
Db 193 CAGGGCACCGTCTCCATGAACTGGGGCTCGCGGTCAGTACGCACTTCGTGGCCCAAC 252

| | | | |
|----|-----|--|-----|
| Oy | 217 | GGCGGTAACTCCGTCGCTGGTGAAGGAGCGGTGAACCCCGGCTGTGAACGCAAGACATCCAC | 276 |
| Db | 253 | ACCGGCAACTTCGTGCGGGGCAAGGAGCTGGGCAACGGCGGCCCGA--CCGTGAG | 309 |
| Oy | 277 | TTTGAAGGTGTATTCCACGCCAAACGGCAACAGTACCTTTCGGTCTACGGTGTGACCCGC | 336 |
| Db | 310 | TACTCGGCACTTCAACCCCTCCGGCAACGGGTACCTGGCGCTCTACGGATGGAAGTGC | 369 |
| Oy | 337 | AAACCGCTGCTGAGTATTATCATGCTGAGAACTTTGGCACTTAAGTATCTTCTCCGGT | 396 |
| Db | 370 | AAACCGCTGCTGAGTACTTACATCTGTGACAACTGGGGCACTTACCGGCTCAACGGGCG-- | 427 |
| Oy | 397 | GCTACCGATCTAGGAATCTGAGTGGACGCGTACATCTATGCACTCGGCAAGACACT | 456 |
| Db | 428 | ----AGTCAAGGGGACCGTCAACGACGACGGCGGCACTTAAGATCTCAAGAGACGAC | 483 |
| Oy | 457 | CGCGTCAACGCACTTAGATGAGCGGCAACCCAAACCTTTCGACCAATCTGTGCTGGTCCG | 516 |
| Db | 484 | CGCGTCAACAGCCCTTCGTGAGGGGCAACCGCACCTTTCGACAGTACTGAGAGCGTCCG | 543 |
| Oy | 517 | CAGGCAAGGCAACGAGGGGTACCGTCCAGACGGGCTGCACTTTCGACGCTGGGCTCG | 576 |
| Db | 544 | CAGGCGAAGCGGACCGGCGGCACTACAGACCGGCAACCACTTTCGACCGCTGGGCGCG | 603 |
| Oy | 577 | GCTGATTGGAATGTCAACGCTGACCACTACTACAGATGTTGCAACGGAGGGCTTACTTC | 636 |
| Db | 604 | GCCGGGATGCGCGCTCGGCAACTTCAGCTACTCATGATCATGTGGCAACGAGGGCTTACAG | 663 |
| Oy | 637 | AGCAACGGCTATGCTCGATCAACGTTG | 664 |
| Db | 664 | AGCAACGGGACGCTCAGATCAACTCG | 691 |

RESULT 3
US-11-108-163B-1

```

/ Sequence 1, Application 05/11/2005
/ Publication No. US20060014247A1
/
/ GENERAL INFORMATION:
/ APPLICANT: Palohelmo, Marja
/ APPLICANT: Mantyla, Arja
/ APPLICANT: Leakinen, Sanna
/ APPLICANT: Fagerstrom, Richard
/ APPLICANT: Kallio, Jarno
/ APPLICANT: Puranen, Terhi
/ APPLICANT: Iantto, Ralf
/ APPLICANT: Suominen, Pirkko
/
/ TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
/ TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
/
/ FILE REFERENCE: 1716.034000B/MAC/DJN
/
/ CURRENT APPLICATION NUMBER: US/11/108.163B
/
/ CURRENT FILING DATE: 2005-04-18
/
/ PRIOR APPLICATION NUMBER: US 60/562,692
/
/ PRIOR FILING DATE: 2004-04-16
/
/ NUMBER OF SEQ ID NOS: 25
/
/ SOFTWARE: PatentIn version 3.3
/
/ SEQ ID NO 1
/
/ LENGTH: 1375
/
/ TYPE: DNA
/
/ ORGANISM: Nonomuraea flexuosa
/
/ FEATURE:
/
/ OTHER INFORMATION: NE xyIIA nucleotide sequence (A508952), the coding region is
/ OTHER INFORMATION: from nt 303 to nt 1337
/
/ US-11-108-163B-1

```

| | | | | |
|-----------------------|-----------------|--------------------|------------|--------------|
| Query Match | 29.1%; | Score 196.2; | DB 11; | Length 1375; |
| Best Local Similarity | 59.0%; | Pred. No. 3.1e-46; | | |
| Matches 396; | Conservative 0; | Mismatches 263; | Indels 12; | Gaps 3. |

QY 5 TCGGCTTACCCCGCTGGCCCTTACGCGGACTGGGGCCCTGGACTTCCCG 64

Db 349 TCGGCTCCGAGCATGTATACCAAGTCTTCGCGCTGGCACTGGCATCGCGTGC 408

QY 65 CAGGAAATGCCACGAGCTCGAAAAAGCAGACAGACCCCACTCGGAGGGCTGGACG 124
DB 409 TGCTGCGCGGACGCGCCACGACCGACACCACTACCCAGAACCAACCGGGTACGACA 468
QY 125 ATGTTATTACTATTCTCTGTGAGTGAAGGTGAGCGGACGACCGTACCAACCTGG 184
DB 469 ACGGCTACTTCTACTCTGTTCTGACCGACGCGCCGGGACCGTCTCAATGACCTCCACT 528
QY 185 AAGGCGCACTAGAGATGACGTGGGGAGATGCGGTAACTCGTGGTGGAAAGGCT 244
DB 529 CGGGCGGAGCTAGACGACCTCGTGGGAAACACCGGAACTTGTCGCGCGCAAGGCT 588
QY 245 GAACCCCGGCGCTGAGCAGACAGACCACTTTCAGAGGTGTTTACAGCCCAAGGCA 304
DB 589 GGTCTACCGGC---GACGCGGAGACCTGACCTTCAACGCTCTTCAACCCGTCGGGTA 645
QY 305 ACAGCTTCTTGGGCTTACGAGTGAACCGGCAACCGGCTGGTGAATTAATCACTGTCG 364
DB 646 ACGCTTACTCACCGCTTACGCGCTGACGAGAACCGGCTGTCGAGTACTACATCGTTCG 705
QY 365 AGAATTTGGACCTATGATATCTTCTCCGGTGTCTACCGATCTAGAACTGTGAGTGGC 424
DB 706 AGACTGCGGACCTTACCGGCGCACCGGC-----ACCTCAAGGGGACCGTCAACCG 759
QY 425 ACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACTAGATCGACGCA 484
DB 760 ACGGCGGACGTAAGACATCTACAGACCTGCGGTACAGACCGCGCTCATCGAGGCA 819
QY 485 CCCAACTTTCGACCAATATCTGTGCGTCCGCGACGACAGACGCAACGCGTACCGTCC 544
DB 820 CCGGACCTTTCACAGATGTTCTGAGGCGTCCGGGACGAGAACGAGACCGGCGGCACTCA 879
QY 545 AGAGCGGCTGCACTTGAAGCGCTGGGCTCGCGCTGTTTGAATGTCAACGTGACACT 604
DB 880 CCAATCGGCAACACTTTCGACCGCTGGGCGCGCGCATGAA---CCTGGGCGAGCGACG 936
QY 605 ACTACGAGATGTTGCAACGAGGAGCTACTTACAGAGCGGTATGCTGCACTACCGTGG 664
DB 937 ACTACGAGATGATGCGGACGAGGAGCTACAGAGCAGGAGTCTTCAACGCTTCTCATCA 996
QY 665 CTGACGTGGC 675
DB 997 GCGAGGTGGC 1007

RESULT 4
US-11-108-163B-5
; Sequence 5, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Palohelimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
; FILE REFERENCE: 1716.034000B/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; PRIOR FILING DATE: 2004-04-16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Nonomuraea flexuosa
; FEATURE:
; OTHER INFORMATION: am24*, like am24 but 9 codons are changed in the sequence like in

OTHER INFORMATION: am3* (See Example 10)
US-11-108-163B-5
Query Match 28.0%; Score 189.2; DB 11; Length 663;
Best Local Similarity 61.8%; Pred. No. 2,4e-44;
Matches 356; Conservative 0; Mismatches 208; Indels 12; Gaps 3;
QY 100 ACCCCGAACCTGAGAGGCTGGCAAGATGTTATCTACTTCTGATGAGTGAACGGTGA 159
DB 13 ACCAGAACAGACCGGCTGACAGACGCTTCTTACTGTTCTGAGACGAGCCCC 72
QY 160 GCGGAGGCACTGACACCAACCTGAGAGCGGCACTTACGAGATCACTGAGGATGAGC 219
DB 73 GGCACGCTTCATGACCTTCACTGCGGGGAGAGCTACAGACACTGTGGCGACAC 132
QY 220 GTTAACTTCTGCTGGTGAAGAGGCTGGAACCCGCGCTGAACGCAAGACCACTTCTT 279
DB 133 GGCMACTTCTGCTGCGCGGCAAGAGGCTGTCCACCGGC---GGCGCGCACCGTCACTAC 189
QY 280 GAGGATTTTACAGAGCCAAAGGCAAGCTACCTTGGGCTTACGAGTGAACCGGCAAC 339
DB 190 AACGCTCTTCAACCGGTGGGTACGCTTACTTCAAGCTTACGAGCTGAGACGAGAAC 249
QY 340 CCGCTGTGAGTATTAATCTGTCGAGAACTTTGGCACTTATGATCTTCTCGGTGCT 399
DB 250 CCGCTGTGAGTATTAATCTGTCGAGAACTTTGGCACTTATGATCTTCTCGGTGCT 399
QY 400 ACCGATCTAGAACTGTGAGTGAACGAGTGAACATCTATGACTCGGCAACCACTGCG 459
DB 304 ACTTACAGAGGACCGGTCACACCGAGCGGCAAGTACGATCTTACGAGACTTGGCGG 363
QY 460 GTCAAGCACTTATGATGACGAGCAACCACTTGAACCAATGAGTGGTCCGCGAG 519
DB 364 TACAAAGCGGCTGTCATGAGGAGGACCGGACCTTTCAGAGATTTGGAAGCTCCGAG 423
QY 520 GACAAAGGCAACAGGAGTCCGTCAGACGAGGCTGCCACTTTCAGAGGCTGGGCT 579
DB 424 CAGAGGAGGACAGCGGACCACTACATCGGCAACCACTTTCAGAGGCTGGGCTGGGCGC 483
QY 580 GGTGTAATGTCAAGGTGACACTTACCAATCGTTCGCAAGGAGCTTCTGAGC 639
DB 484 GGCATGAA---CCTGGGCGACGACGACTTACAGATGAGCGAGGCTTACAGAGC 540
QY 640 AGCGGTATGCTGCAACCGTTCATCAAGGAGGTGGC 675
DB 541 AGCGGTATGCTGCAACCGTTCATCAAGGAGGTGGC 576

RESULT 5
US-11-108-163B-4
; Sequence 4, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Palohelimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
; FILE REFERENCE: 1716.034000B/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; PRIOR FILING DATE: 2004-04-16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 906
; TYPE: DNA

ORGANISM: *Nonomuraea flexuosa*
FEATURE:
OTHER INFORMATION: am35*, like am35 but 9 codons are changed in the sequence. See
OTHER INFORMATION: Example 10 (the changes do not alter the encoded amino acid
OTHER INFORMATION: sequence)
US-11-108-163B-4

Query Match 28.0%; Score 189.2; DB 11; Length 906;
Best Local Similarity 61.8%; Pred. No. 2,76-44;
Matches 356; Conservative 0; Mismatches 208; Indels 12; Gaps 3;

QY 100 ACCCCCACTCGAGGGCTGGACAGATGTTATTACTATTCTGTTGAGTGA 159
DB 13 ACCAGAACAGACCGGCTACGACACGCTACTTCTGTTGAGTGA 72
QY 160 GCGCAGGCGACGATACCAACCTGGAAGGCGGACCTACGAGATCTGGGAGATGC 219
DB 73 GGCACCGCTTCATGATGCTTCACTCGGGCGGACGACACCTGCGGCAACACC 132
QY 220 GGTAACTCGTGGTGAAGGGCTGGAAACCCGGCTGAAAGCAAGACCATCTTT 279
DB 133 GGCACCTTCGTCGGCGGCAAGGCTGTCCACCGG---GGCGCGGCACTTCACCTTAC 189
QY 280 GAGGGTGTTCACGACCAACGCAACGCTACCTTGGGCTTACGCTTGAACCGCAAC 339
DB 190 AACGCTCTTCAACCGCTCGGTTAAGCCTACCTCAAGCTCAAGCTGGACAGGAAAC 249
QY 340 CCGGTGTCAGATTTATCATGTCGAGAACCTTGGCACTTATGATCTTCTCGGTC 399
DB 250 CCGCTCTGCACTACATGTCGAGAGCTGGGCACTTACCGGCAAC---GGC 303
QY 400 ACCGATCAGGAAGTGTGAGTGCAGCGGTAGCATCTATCGACTGGCAAGACCATCTGC 459
DB 304 ACCTTCAAGGGCACTGTACCAACGACGCGGCACTGACGATCTTACGAGACCTGGGCG 363
QY 460 GTCAAGCGACCTAGCATGACGAGACCCAACTTTGACCAATCTGGTCTGCGCAG 519
DB 364 TACAACGCGCGTCCATGAGGGGACCGGACCTTCCAGAGTCTGGAGCTCGGCGAG 423
QY 520 GACAAAGGCAACACCGGTACCGTCCAGACGCGGCTGCCATCTTGGAGCTCGGCT 579
DB 424 CAGAAAGGCAACACCGGACCATCAACCTTGGCAACCTTGGAGCTCGGCGCGC 483
QY 580 GATTGAATGTCAACGATGACCACTACTACGATCTGTTGCAAGGAGGCTACTTACG 639
DB 484 GGCATGAA---CTGGGAGGCAAGCATCAAGATCAAGGAGGCTTACAGAGC 540
QY 640 AGCGCTATGCTCGCATCACCGTTGCTGACGCTGGC 675
DB 541 AGCGTAGCTCCACCGTCTCATCAGGAGGTGGC 576

RESULT 6
US-10-517-939-225

Sequence 225, Application US/10517939
Publication No. US20060003433A1

GENERAL INFORMATION:

APPLICANT: Steer, Brian

APPLICANT: Callen, Walter

APPLICANT: Healey, Shaun

APPLICANT: Hazlewood, Geoff

APPLICANT: Wu, Di

APPLICANT: Blum, David

APPLICANT: Beesehajian, Alireza

TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM

FILE REFERENCE: 564462007901

CURRENT APPLICATION NUMBER: US/10/517,939

PRIOR FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/US03/19153

PRIOR FILING DATE: 2003-06-16

PRIOR APPLICATION NUMBER: 60/389,299

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 225
LENGTH: 1059
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-225

Query Match 27.6%; Score 186.2; DB 7; Length 1059;
Best Local Similarity 60.2%; Pred. No. 26-43;
Matches 346; Conservative 0; Mismatches 223; Indels 6; Gaps 2;

QY 100 ACCCCCACTCGAGGGCTGGACAGATGTTATTACTATTCTGTTGAGTGA 159
DB 88 ACCTTCAAGGCGGACGCGGCAACCAACGCGCATCTATCTTCTTGGAGGACATGGC 147
QY 160 GCGCAGGCGACGTAACCAACCTGGAAGGCGGACCTACGAGATCACTGGGAGATGC 219
DB 148 GGCACGTCAACTTGCATGTACGCGAAACGCGGCTACACTTCACTGAGGCGCATC 207
QY 220 GGTAACTCGTGGTGAAGGGCTGGAAACCCGGCTGAAAGCAAGACCATCTTT 279
DB 208 AACAACTGGGTGGGCGGCAAGGCTGGACAGCGGCTCACGCGGA---GATACCTTAC 264
QY 280 GAGGGTGTTCACGACCAACGCGCAACGCTACCTTGGGCTTACGCTTGAACCGGCAAC 339
DB 265 TCGGGCTCGTTCAACTACCGCGCAATGTTATCTCACTGATCGGTTGACCAACAT 324
QY 340 CCGGTGTCAGATTTATCATGTCGAGAACTTTGGCACTTATGATCTTCTCGGTC 399
DB 325 CCAATGTCAGATTAATCATGTCGAGCAACTGGGCGGCACTGACCGGCGCGGAGGCTCG 384
QY 400 ACCGATCAGGAAGTGTGAGTGCAGCGGTAGCATCTATGATCTGCGCAAGACCATCTGC 459
DB 385 GGTACATGCGGCAACGAGTGCAGGAGGAGCGGCACTTACAGATCTTATCGACCAACGCGC 444
QY 460 GTCAAGCGACCTAGCATGACGCGACCCAACTTTCAGCAATATGATGCTGGCTCGGCGAG 519
DB 445 GTAAACAGGCTTTCATCATGCGGACCGGACGCTTCTATCAATCTGAGAGGTGGCGAG 504
QY 520 GACAAAGGCAACACCGGTACCGTCCAGACGCGGCTGCCATCTTGGAGCTCGGCT 579
DB 505 CAGAAAGGCAACCGGCGGACCATCACCGGCAATCACTTTCAGCGCTGGCGGCAATAC 564
QY 580 GATTGAATGTCAACGATGACCACTACTACGATCTGTTGCAAGGAGGCTACTTACG 639
DB 565 GGAATGAA---CTGGGACCGCAACACTACAGATCAAGGAGGCTTACAGAGC 621
QY 640 AGCGCTATGCTCGCATCACCGTTGCTGACGCTGG 674
DB 622 AGCGGAGTTTCGACATCAAGTGAAGGAGGCGG 656

RESULT 7
US-11-108-163B-3

Sequence 3, Application US/11108163B
Publication No. US20060014247A1

GENERAL INFORMATION:

APPLICANT: Paloneimo, Marja

APPLICANT: Mantyla, Arja

APPLICANT: Leekinen, Sanna

APPLICANT: Pajerstrom, Richard

APPLICANT: Kallio, Jarno

APPLICANT: Puranen, Terhi

APPLICANT: Lantto, Ralf

APPLICANT: Suominen, Pirkko

TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of

TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi

FILE REFERENCE: 1716.034000B/MAC/DYN

CURRENT APPLICATION NUMBER: US/11/108,163B

PRIOR FILING DATE: 2005-04-18

| | | | | |
|-----------------------|--------------|------------------|-----------------|-------------|
| Query Match | 27.6% | Score 186; | DB 11; | Length 663; |
| Best Local Similarity | 61.5%; | Pred. No. 2e-43; | | |
| Matches 354; | Conservative | 0; | Mismatches 210; | Indels 12; |
| | | | | Gaps 3 |

RESULT 8
US-11-108-163B-2

FILE REFERENCE: 1716.034000B/MAC/DJN

| | | | | |
|-----------------------|-----------------|--------------------|------------|-------------|
| Query Match | 27.6%; | Score 186; | DB 11; | Length 906; |
| Best Local Similarity | 61.5%; | Pred. No. 2.2e-43; | | |
| Matches 354; | Conservative 0; | Mismatches 210; | Indels 12; | Gaps 31; |

RESULT 9
US-10-517-939-165

TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

```

; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-165

```

```

Query Match      27.4%; Score 185; DB 7; Length 1047;
Best Local Similarity 60.6%; Pred. No. 4,4e-43;
Matches 340; Conservative 0; Mismatches 215; Indels 6; Gaps 2;

```

```

Qy 115 GGTGGGCAAGATGATTAATCTTCTGTTGAGTGAAGCGGTGAGCGGCAAGCTTAC 174
Db 97 GGCACCAACAGCGCTTCTACTATTCGTTGGAACCGCGGTGGCTCCGTGCAAGTTC 156
Qy 175 ACCAACCTGGAAGCGGCACTAGATCAAGATCGAGTGGGAGATGGGGGTTACCTGCGGT 234
Db 157 TGCCGCAATCCGCGGCGGTGACACCTTCAGCTGGAACATATGGAATCGGAGTGGT 216
Qy 235 GGAAGAGGCTGGAACCCCGGCTGGAACGCAAGCATCACTTTGAGGGTGTATTCAG 294
Db 217 GGAAGAGGCTGGAACCCCGGCGGTGACACCTTCAGCTGGAACATATGGAATCGGAGTGGT 273
Qy 295 CCAAGCGGCAACGCTTACCTGCGGTGATGAGTGGTGAACCCGCTGGTGAATAT 354
Db 274 CCGTGGGTGAACGCGGTACCTGCGGTGATGAGTGGTGAACCCGCTGGTGAATAT 333
Qy 355 TACATCGTGAAGATTTGGACCTATGATCTTCTCGGTGGTGAACCATCTAGGAAT 414
Db 334 TACATCGTGAAGATTTGGAGGCTATGATCTTCTCGGTGGTGAACCATCTAGGAAT 393
Qy 415 GTGAGTGAAGATTTGGAGGCTATGATCTTCTCGGTGGTGAACCATCTAGGAAT 474
Db 394 GTTGTGAGGATTTGGAGGCTATGATCTTCTCGGTGGTGAACCATCTAGGAAT 453
Qy 475 ATGACGCGCAACCTTGAACCAATATGAGTGGTGAACCCGCTGGTGAATAT 534
Db 454 ATGACGCGCAACCTTGAACCAATATGAGTGGTGAACCCGCTGGTGAATAT 513
Qy 535 GGTACCGTGAAGATTTGGAGGCTATGATCTTCTCGGTGGTGAACCATCTAGGAAT 594
Db 514 GGTACCGTGAAGATTTGGAGGCTATGATCTTCTCGGTGGTGAACCATCTAGGAAT 570
Qy 595 GGTGACCACTATCAAGATGTTGCAACGAGGAGCTATCTTCAAGAGCGGCTATGCTGC 654
Db 571 GGAACCTTCAATTAACCAATGTTGCAACGAGGAGCTATCTTCAAGAGCGGCTATGCTGC 630
Qy 655 ATCAACGTTGCTGACGTGGC 675
Db 631 ATCAACGTTGAGGATGGCGC 651

```

```

RESULT 10
; US-10-517-939-199
; Sequence 199, Application US/10517939
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di

```

```

; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-199

```

```

Query Match      25.2%; Score 170; DB 7; Length 1074;
Best Local Similarity 57.5%; Pred. No. 8.1e-39;
Matches 368; Conservative 0; Mismatches 260; Indels 12; Gaps 3;

```

```

Qy 29 CGGCTTAGCCGCGACTGAGGCGCTGAGCTTCCCGGAGGAGATGCCAGAGCTCGAAA 88
Db 26 CGGCGAGCGCGCGCGCGCGCGCTGAGCTGCGCTGCGCGCGCTGACATGAGCGCGGGA 85
Qy 89 AGCGACGAC-----AACCCCACTCGAGAGGCTGACAGATGTTATTAATTCCT 142
Db 86 ATGCGCAACCTGATCATCGTGAACGAGGCAACGAGGCAACGAGGCAACCTATTTCT 145
Qy 143 GGTGAGTGAAGGAGGAGCGGCGGACGTAACCAACCTGGAAGGCGGCACTAGAGA 202
Db 146 TGTGGAAGAGAGCGGCGGCAAGTGAATCTTGTGATGATCTCGGCGGCGGCTACAGT 205
Qy 203 TCAAGTGGAGATGAGGAGGATTAATCTGAGTGAAGAGGCTGGAACCCCGGCTGAA 262
Db 206 CCAAGTGAAGGAGGATTAACCAACGAGTGAAGGAGGCGGCGGCGGCTGAGCGCTCC 265
Qy 263 CAAAGCCATTCATTTGAGGAGTGTTCACAGCCCAACGAGCAACGTAATCTTGGCT 322
Db 266 GCAACGCTCTCTACTCCGAGGCTTCAATTCGCGG---GGTAAAGGCTACCTGACGCT 322
Qy 323 ACGGTTGAACCCGCAACCGGTGAGTGAATTAATGATGAGAACTTGGCACTATG 382
Db 323 ACGGTTGAACCCGCAACCGGTGAGTGAATTAATGATGAGAACTTGGCACTATG 382
Qy 383 ATCTTCTCGGAGTGAACGATCTAGAACTGTGAGTGAACGAGTGAACCTATCGAC 442
Db 383 GTCCGCGGAGTGAACGAGGCTTATGAGGCAAGTGAACGAGGAGGCGGCACTAGACA 442
Qy 443 TCGGCAAGACCACTCGGCTCAAGCACTTGAATGAGCGGCAACCAACTTTCAGCAAT 502
Db 443 TCTATCGGCAACCGGCTCAAGCACTTGAATGAGCGGCAACCAACTTTCAGCAAT 502
Qy 503 ACTGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 562
Db 503 ACTGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 562
Qy 563 ACGCTGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 622
Db 563 ATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 619
Qy 623 CGAGAGGCTACTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 662
Db 620 CGAGAGGCTACTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659

```

```

RESULT 11
; US-10-517-939-255
; Sequence 255, Application US/10517939

```

```
/ Publication No. US20060003433A1
/ GENERAL INFORMATION:
/ APPLICANT: Steer, Brian
/ APPLICANT: Callen, Walter
/ APPLICANT: Healey, Shaun
/ APPLICANT: Hazlewood, Geoff
/ APPLICANT: Wu, Di
/ APPLICANT: Blum, David
/ APPLICANT: Eteghalian, Alireza
/ TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
/ TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
/ FILE REFERENCE: 564462007901
/ CURRENT FILING DATE: 2004-12-13
/ PRIOR FILING DATE: 2003-06-16
/ PRIOR APPLICATION NUMBER: PCT/US03/19153
/ PRIOR FILING DATE: 2003-06-16
/ PRIOR APPLICATION NUMBER: 60/389,299
/ NUMBER OF SEQ ID NOS: 380
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 255
/ LENGTH: 1137
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-255
```

```
Query Match      25.2%; Score 170; DB 7; Length 1137;
Best Local Similarity 57.5%; Pred. No. 8.2e-39;
Matches 368; Conservative 0; Mismatches 260; Indels 12; Gaps 3;
```

```
Qy 29 CGGCGTTAGCCGCGCACTGGGGCCCTTCCCGCGAGGAATCCCGAGCTCCGAAA 88
Db 89 CGGGAGGCGCGCGCTCGCGCGCTGCGCTTGCCTTGCCTTCACTGACGCGCGGA 148
Qy 89 AGCGACAGAC-----AACCCCAACTCGAGAGGCTGCGAGATGATTACTATTCT 142
Db 149 ATGGCGAAACCTGCACTACGTGAGCCAGAGCGGCAACAAACGCGCACTTCTTTCGT 208
Qy 143 GGTGAGTACGCTGAGAGCGGACGACGTAACCAACCTGAAAGCGCGCACTTACGAGA 202
Db 209 TCTGAAAGACAGCCCGGCGAGGTGAACTTCTGATGATCTCGGCGCGCTACACAGT 268
Qy 203 TCAGCTGGGAGATGAGCGGCTTAACCTCGTGGTGAAGAGGCTGAAACCCCGGCTGAACG 262
Db 269 CCAACTGAGCGGCACTCAACAACCTGGGTGGCGGCAAGCGCTGGGAGACGCGGCTGTCCTC 328
Qy 263 CAAGAGCCATCATCTTTGAGGGGTGTTTACAGCCAAACGCGAACAGCTAACCTGGCGGTCT 322
Db 329 GCACCGTCTCTTACTCCGCGAGCTTCAATTGCGCG--GGTAAAGGCTTAACTTGAAGCTCT 385
Qy 323 ACGGTTGAGCCCGCAACCCGCTGCTGAGATTAACATGTCGAGAACTTTGGCACTTATG 382
Db 386 ACGGCTGAGCAACCAATCCGCTCATGAGTACTATGTCGACAACTGGGCGAGCTATC 445
Qy 383 ATCTTCTCTCGGTGCTACCGATCTAGGAATGTGAGTGGAGGATGATCTATGAC 442
Db 446 GTCCGCGGCGGTGGCGAGGGCTTTCATGCGCACGCTGAAACACCGCGCGCGCTGATGACA 505
Qy 443 TCGGCAAGACCACTCGGCTCAACGCAACCTAGCATGAGCGGCAACCAACCTTTCAGCAAT 502
Db 506 TCTATTCGACGCAACGGGTCAACAGCCGTGATATATGGCAACGCGAGCTTTCACAGT 565
Qy 503 ACTGGTCGCTCGCGAGGACAAAGCGCACAGCGATACCGTCAAGCGGCTGGCACTTTCG 562
Db 566 ACTGAGAGGTGCGGAGTGAAGGCGCACCGGCGGACATCAACACGCGCAACCACTTCA 625
Qy 563 ACGGCTGGGCTCGCGCTGTTGAATGTCAACGCTGACCACTTACCAATGTCGTTGCA 622
Db 626 ATGCTTGGGCGAGCTTCGGCATGAA---CTGGGACAGCAACATTCACAGGTGATGGCA 682
Qy 623 CGAGGGGCTACTTTCAGACGCGGCTATGCTCGCATCACCGT 662
```

```
Db 683 CCGAGGGCTACAGAGCGGCGAGCTCCGACATCACCGT 722
```

```
RESULT 12
US-10-517-939-169
/ Sequence 169, Application US/10517939
/ Publication No. US20060003433A1
/ GENERAL INFORMATION:
/ APPLICANT: Steer, Brian
/ APPLICANT: Callen, Walter
/ APPLICANT: Healey, Shaun
/ APPLICANT: Hazlewood, Geoff
/ APPLICANT: Wu, Di
/ APPLICANT: Blum, David
/ APPLICANT: Eteghalian, Alireza
/ TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
/ TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
/ FILE REFERENCE: 564462007901
/ CURRENT FILING DATE: 2004-12-13
/ PRIOR FILING DATE: 2003-06-16
/ PRIOR APPLICATION NUMBER: PCT/US03/19153
/ PRIOR FILING DATE: 2003-06-16
/ PRIOR APPLICATION NUMBER: 60/389,299
/ NUMBER OF SEQ ID NOS: 380
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 169
/ LENGTH: 1041
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-169
```

```
Query Match      24.6%; Score 165.8; DB 7; Length 1041;
Best Local Similarity 56.8%; Pred. No. 1.3e-37;
Matches 346; Conservative 0; Mismatches 257; Indels 6; Gaps 2;
```

```
Qy 67 GGGATGCGACGAGCTCGAAAGCAAGAACACCCCAACCTTGGAGGCTGGACGAT 126
Db 52 GGCATTACCGCGCGCGAGCGCAACCTGCATCACTTTCAGCCAGACCGGTACCAAC 111
Qy 127 GGTATTACTATTCTGAGTGAAGTGAAGTGAAGCGGAGCGCAAGTCAACCACTGGA 186
Db 112 GGCACACTACTTCTTCTTGAAGAGACAGCCCGGTACCGTCACTTGTGATGATGCC 171
Qy 187 GCGCGACCTACGAGATCAGCTGGGAGATGCGGTAACTCGTGGTGAAGGCGCTGG 246
Db 172 AATGGGCGCTACACTCCACTGAAGCGGATCAACAATGGGTGGCGGCAAGGCTGG 231
Qy 247 AACCCGCGCTGAAGCGAAGAGCATCACTTGAAGGTGTTTACAGCCAAACGCGAAC 306
Db 232 CAGACGGGCTCAACCCGACGAGTCACTTCC---GGTTCGTTCAATTGCGCGGCAAT 288
Qy 307 AGCTACCTTGGGCTTACGCTTGAAGTGAAGCCGCAACCCGCTGCTGAGTATTAATGTCGAG 366
Db 289 GGTATCTCACTTGTGAGTGAAGCAACGAAATCAATTGATGAGTACTATCATGTGAC 348
Qy 367 AACTTGGACCTTATGATTCCTTCTCGGTCCTACCGATCTAGAACTGTGAGTGGAC 426
Db 349 AGCTGGGACCTTATGACAGCGCGGCGGCGCAAGGCTTTCATGGGCAACCGTCAAGAGAT 408
Qy 427 GGTAGATCTATGACTTCGCGAAGACCACTCGCGTCAACGCACTTACATGACGCGAC 486
Db 409 GCGCGACCTATGACATCTACCGGACGAGCGGTGAACGACTTTCATCATGAGGAC 468
Qy 487 CAACCTTTCAGCAATCTGCTGCTCGGCAAGAACAGGCGACCAACGATACCGTCCAG 546
Db 469 GCGAGTTTTCACGATCTGAGGCGGTGAGGCGGCGGTGAGGCGGCGGACATCAAC 528
Qy 547 ACGGCTGCACTTTCAGAGCGCTGGGCTCGGCTGTTGATGATCAACGATCACTAC 606
```

Dh 529 AGCGCCACCACTTCAACGCGCTGGGCAACGCTGGGCAATGAA--CTGGGCGCACACAC 585
Qy 607 TACCAAGTCTGTGACGAGAGGGCTACTTCAGACGCGCTATGTCTGCATACCGTGTCT 666
Dh 586 TACCAAGTCTGTGACGAGAGGGCTTACCAAGACAGTGGCAGCTCCGACATCACCGTACC 645
Qy 667 GACGTGGGC 675
Dh 646 GAGGCGGC 654

RESULT 13
US-10-517-939-221

; Sequence 221, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-221

Query Match 24.5%; Score 165.6; DB 7; Length 1044;
Best Local Similarity 58.0%; Pred. No. 1.4e-37;
Matches 332; Conservative 0; Mismatches 234; Indels 6; Gaps 2;
Qy 104 CCAACTCGAGAGGCTGGACAGATGTTATTTACTTCTGTGAGAGTGAACGTGAGGCC 163
Dh 89 CCAGCCACACCGGCACCAACACGGCAATTTATTTCTGAAAGACAAACCGGGCA 148
Qy 164 AGGCCACGTACACCACTGGAAGGCGCACCTACAGATCAGCTGGGAGATGGCGGTA 223
Dh 149 CCGTGACCTTCTGATGATGATGCAACGCGCGGTACACCTCCATCTGGAGCGGATCAACA 208
Qy 224 ACTCTGCTGTTGAAAGGGCTGGAAACCCGCGCTGGAACGCAAGCCATCCATTTGAGG 283
Dh 209 ACTGGTGGTGGGCAAGGGCTGGACAGCGGCTCGAATCGCACGGTGAATCTCCGGTT 268
Qy 284 GTGTTTACCAACGCAACGGGCAACAGCTACTTTCGGCTTACAGTTGGACCCGCAACCGC 343
Dh 269 GCTTCAACTTGGC--CGGCAACGGCTTACTTCACTTACCGGTGAGACAGAAATCGC 325
Qy 344 TGTGCAAGTATTAATCTGTCGGAACCTTGGCACTTATGATCTTCTCCGGTGTACCG 403
Dh 326 TGAATGAGTACTACATCTCTGACAGTGGGCAAGTTATCGAACGCGCGCGGCCAGGGCT 385
Qy 404 ATCTGAAGACTGTGCGAGTGCACGGGTAGCATCTATCGACTCGGCAAGACCACTGGCTCA 463
Dh 386 TCATGGGACCGGTGACGACCGGCGGCACTTACAGATCTATCGACGAGCGCGTGA 445
Qy 464 ACGCCTTAGATGACGAGCGGCAACCCAAACCTTGCAGCAATATCGTGTGGTCCGCGAGACA 523
Dh 446 ACCAGCTTTCATCATTCGGACCGGACGTTCTACAGTACGTGAGCGGTGGCGAGTCA 505

Qy 524 AGCGCACACGCGTACCGTTCAGACGCGCTGCCATTTGACGCTTGGCTCGCGTGTCT 583
Dh 506 AGCGCGTGGGGGACCATCATCACCGCCCAACCACTTCAATGCTGGGCGACCGTGGGCA 565
Qy 584 TGAATGTCAACGCTGACCACTACTTACCAATCTGTGCAAGGAGGCTACTTCAGCAGCG 643
Dh 566 TGA--CTTGGGCGACGACCACTTACCAAGGTCAATGGCACCGAGGTTTACCAAGCAGCG 622
Qy 644 GCTATGCTGCATCACCGTGTGTGAGTGGGC 675
Dh 623 GCAGCTCCGACATCACCGTGAACGAGCGGC 654

RESULT 14
US-10-517-939-177

; Sequence 177, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-177

Query Match 24.5%; Score 165.4; DB 7; Length 1299;
Best Local Similarity 56.3%; Pred. No. 1.7e-37;
Matches 351; Conservative 0; Mismatches 266; Indels 6; Gaps 2;
Qy 40 GCGACTGGGCGCTTCCGCGCAGGAGATGCCAGAGCTCGAAAAGCGACAGACA 99
Dh 28 GCGATTCCTCCGACAGACTAGCGGTGGCACTTCTCAATCGCTCATGCGCAACGCTT 87
Qy 100 ACCCCCACTCGAGAGGCTGGCACGATGTTATTAATTCCTGTTGAGTGAAGTGGGA 159
Dh 88 AGCTCAATGCGCACTGGAACCCAGAAATGTTACTTACTTATTTGTTGAGAGATTCGGT 147
Qy 160 GCGCAGGCCAGTACCAACCTTGAAGGCGGCACTACAGATCAGCTGGGAGATGGC 219
Dh 148 AAGCCACACATGACACTCGGTGGCGGTGGAACATATTTCTTATCTGTGAACAGACGACT 207
Qy 220 GGTAACTCTGCTGGTGAAGAGGCTGGAACCCGCGCTGAACGCAAGCCATTCATCTT 279
Dh 208 AACCACTGGGTGGGTGAAGGCTGATGCGGG--TACTCGGCGCACAGTCACTAT 264
Qy 280 GAGGTGTTTACAGCCCAACGCAACAGCTTACCTTCCGCTTACAGTTGGAACCGGCAAC 339
Dh 265 TCGGGAGTTTATAGCGGAGTGAACAGACTTACCTTACGCTTGAACCTCGGAAC 324
Qy 340 CCGCTGTGAGTATTAATCTGTCGGAACCTTGGCACTTATGATCTTCTCCGGTGTCT 399
Dh 325 CCGCTGATCAATTTATCTGTGAAAACTGGGTCAATTTCAATCTCTCGGTCCGGCGCA 384

QY 400 ACCGATCTAGGAACCTGTCAGAGTCGACCGGTAGCATCTATCGACCTCGCAAGACCACTGCG 459
DB 385 ACGAATTATGGGACCTGTCATATTTGAACGGACCACTTACAGCTGGGCGGACCAACGG 444
QY 460 GTCAACGCACTAGCATGACGACCAAACTTTGACCAATCTGCTGGTCCGACG 519
DB 445 GTTATTCAGCCATCTATTTGAAGGCAAGGCGCACGTTCTACCAATCTGAGTGTGGCCAA 504
QY 520 GACAAAGGCGACGACGAGTACCGTCCGAGCGGCTGCCCTTGCAGCGCTGGGCTCGCGCT 579
DB 505 AACCAAGCCGACGACGGAACGATTAATTTGAGCGCATTTTCGATGCAATGGGCTGCTG 564
QY 580 GATTGAATGTCAACGCTGACCACTACTACAGATCGTTGCAACGGAAGGCTACTTCAGC 639
DB 565 GCGTTGAA---CTGGGAGCTACAGATTATTCAGATTATGGCGACCGAGGGCTTACCAAGGC 621
QY 640 AGCGGCTATGCTCGCATACCGT 662
DB 622 AGCGCCAGTCCCAATATCACGGT 644

RESULT 15

US-10-517-939-195
; Sequence 195, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Beseighlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Unknown
; FEATURES:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-195

Query Match 23.8%; Score 160.8; DB 7; Length 1044;
Best Local Similarity 59.0%; Pred. No. 3.3e-36;
Matches 333; Conservative 0; Mismatches 222; Indels 9; Gaps 3;

QY 115 GCGTGGCACGATGTTATTAATTCCTGTCGAGTACGCTGAGCGGACCGCAAGCTTAC 174
DB 97 GGCACCAACCAACGCGTTCTATTAATTCCTTCTGAAAGACAGTCCGGGTTCAATGATTTTC 156
QY 175 ACCAAGCTGAAAGGCGGACCTTACGATGACGTCGGGAGATGGCGGTAACTCTGTCGGT 234
DB 157 TGCATGTACTCGGCGGCTGCTACAGTCGAGCTGAGAGCGGATCAACACTTGGGTCGCGC 216
QY 235 GGAAGAGGCTGGAACCCCGGCTGAAACGCAAGCCATCACTTTGAGGGTGTTCACGAG 294
DB 217 GCGAAGGAGCTGCAAAACCGATCGGCGCGGACCATCACTACTCGGCAAGCTTCAACTCG 276
QY 295 CCAAGCGCAACAGTACTTGGCGGTCTACGCTTGGACCCGCAACCCGCTGTGAGTAT 354
DB 277 CCG---GGCAATGGCTTACCTGCGCTTACGAGATGACCAACCAATCCACTGTGAGTAC 333
QY 355 TACATCGTCGAGAACTTTGGCACTATGATCTTCTCGGTCGTAACGATCTAGAACT 414

DB 334 TACATCGTCGAGAACTTGGCACTATGATCTTCTCGGTCGTAACGATCTAGGAGACG 393
QY 415 GTCAAGTGGCGAGGCTAGCATTTATGACTCGGCAAGACCACTCGGCTCAAGCAC---CT 471
DB 394 GTCAAGAGCGACGCGCGCACGATGATATGAAACGCAACGATGATGATGCGCCGTCG 453
QY 472 AGCATGACGCGACCCAAACCTTGCACCAATATCTGTGTGCGCGCACGACCAAGCGCAC 531
DB 454 ATCATGTGTATCAACGACCTTTATCATATCTGAGACGCTGCTCATGTCAGAGAGAC 513
QY 532 AGCGGTACCGTCCAGACGCGGCTGCACTTGCACCGCTGGGCTCGGCTGTTGATATGTC 591
DB 514 GCGGAAACATCAACCAACCGGCAACCACTTGTGATGCTGGGAGAGCTACGGCATGAA---C 570
QY 592 AACGTGACACTTACTTACAGATCTTGGCAACGGAAGGCTACTTACGACGCGCTATGCT 651
DB 571 CTGGGAACTCAACACTACAGATCTGCGGACCGAGGGTTATCAAAAGCAGCGGACGCTCG 630
QY 652 CGCATCAACCGTTGCTGACGTGGGC 675
DB 631 GACCTCACCGTAGAGCAAGGACG 654

Search completed: February 11, 2006, 22:06:17
Job time : 217.772 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 14:49:18 ; Search time 151.432 Seconds
(without alignment)
652.836 Million cell updates/sec

Title: US-09-467-368-2

Perfect score: 1238
Sequence: 1 MVGFTPVVALMAATGALAF.....VATEGYRSGVARTTADVG 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1238 | 100.0 | 225 | 2 | AAW01112 Xylanase. |
| 2 | 1238 | 100.0 | 225 | 2 | AAW05187 Endo-1,4- |
| 3 | 1238 | 100.0 | 225 | 2 | ABR63119 Thermomyc |
| 4 | 1238 | 100.0 | 225 | 9 | ABE00305 Xylanase |
| 5 | 1088 | 87.9 | 194 | 5 | AAE18456 Thermomyc |
| 6 | 1083 | 87.5 | 194 | 3 | ABAB48543 Thermomyc |
| 7 | 1083 | 87.5 | 194 | 5 | AAO18649 T lanugin |
| 8 | 1083 | 87.5 | 194 | 8 | AD166751 T. lanugi |
| 9 | 965 | 77.9 | 194 | 3 | AAO18648 P. varioti |
| 10 | 965 | 77.9 | 194 | 8 | AD166750 P. varioti |
| 11 | 806.5 | 65.1 | 221 | 2 | ABAB48548 Cochlioba |
| 12 | 806.5 | 65.1 | 221 | 8 | AAO18654 C. carbonu |
| 13 | 806.5 | 65.1 | 221 | 8 | AD166756 C. carbonu |
| 14 | 806.5 | 65.1 | 221 | 9 | ABE00301 Xylanase |
| 15 | 689.5 | 55.6 | 227 | 2 | AAE18421 Humicola |
| 16 | 688.5 | 55.6 | 227 | 2 | AAE18421 Humicola |
| 17 | 688.5 | 55.6 | 227 | 2 | AAE18421 Humicola |
| 18 | 684.5 | 55.3 | 223 | 2 | AAW57422 Amino aci |
| 19 | 684.5 | 55.3 | 223 | 2 | AAE18422 PI 9.0 en |
| 20 | 684.5 | 55.3 | 223 | 2 | AAE18422 PI 9.0 en |
| 21 | 681.5 | 55.0 | 221 | 6 | ABE18421 Humicola |
| 22 | 678.5 | 54.8 | 221 | 6 | AAW18115 Chaetomiu |
| 23 | 671 | 54.2 | 234 | 6 | ABE18421 Humicola |
| 24 | 663 | 53.6 | 197 | 2 | AAW60736 Xylanase |

| | | | | | | |
|----|-------|------|-----|---|----------|---------------------|
| 25 | 663 | 53.6 | 197 | 3 | AAE18406 | AAE18406 S. commune |
| 26 | 663 | 53.6 | 197 | 3 | AAE18437 | AAE18437 Schizopy |
| 27 | 663 | 53.6 | 197 | 5 | AAE18443 | AAE18443 S. commune |
| 28 | 663 | 53.6 | 197 | 5 | AAE18445 | AAE18445 Schizopy |
| 29 | 663 | 53.6 | 197 | 8 | AD166745 | AD166745 S. commune |
| 30 | 662.5 | 53.5 | 230 | 2 | AAW18116 | AAW18116 Chaetomiu |
| 31 | 647.5 | 52.3 | 190 | 7 | AAO30298 | AAO30298 Trichoder |
| 32 | 647.5 | 52.3 | 190 | 7 | AAO30297 | AAO30297 Trichoder |
| 33 | 646.5 | 52.2 | 190 | 5 | AAE18492 | AAE18492 Trichoder |
| 34 | 646.5 | 52.2 | 190 | 5 | ABE47005 | ABE47005 Thermophi |
| 35 | 644.5 | 52.1 | 190 | 5 | AAE18496 | AAE18496 Trichoder |
| 36 | 644.5 | 52.1 | 190 | 5 | AAE18494 | AAE18494 Trichoder |
| 37 | 644.5 | 52.1 | 190 | 5 | ABE47006 | ABE47006 Thermophi |
| 38 | 643.5 | 52.0 | 190 | 7 | AAO30285 | AAO30285 Trichoder |
| 39 | 643.5 | 52.0 | 190 | 7 | AAO30284 | AAO30284 Trichoder |
| 40 | 643.5 | 52.0 | 190 | 7 | AAO30286 | AAO30286 Trichoder |
| 41 | 643.5 | 52.0 | 190 | 7 | AAO30283 | AAO30283 Trichoder |
| 42 | 643.5 | 52.0 | 190 | 7 | AAO30293 | AAO30293 Trichoder |
| 43 | 643.5 | 52.0 | 190 | 7 | AAO30294 | AAO30294 Trichoder |
| 44 | 640.5 | 51.7 | 190 | 5 | ABE47004 | ABE47004 Thermophi |
| 45 | 640.5 | 51.7 | 190 | 5 | ABE47001 | ABE47001 Thermophi |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | AAW01112 standard; protein; 225 AA. |
| ID | AAW01112 |
| AC | AAW01112; |
| XX | |
| DT | 21-MAY-1997 (first entry) |
| XX | |
| DE | Xylanase. |
| XX | |
| KW | Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermosacculus; Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia; Byssoschlamus; Paecilomyces; animal feed additive; in-vivo breakdown; |
| KW | plant cell wall; growth rate; feed conversion. |
| KW | |
| XX | |
| OS | Thermomyces lanuginosus. |
| XX | |
| PN | W09623062-A1. |
| XX | |
| PD | 01-AUG-1996. |
| XX | |
| PF | 26-JAN-1996; 96MO-DK000046. |
| XX | |
| PR | 26-JAN-1995; 95DK-00000094. |
| XX | |
| PA | (NOVO) NOVO-NORDISK AS. |
| PI | Hansen PK, Wagner P, Muelleritz A, Knap IH; |
| XX | |
| DR | WPI, 1996-454790/45. |
| PT | N-PSDB; AAT40742. |
| XX | |
| PS | Fungal xylanase prepns. for use as animal feed additives - and DNA construct for producing recombinant Thermomyces xylanase. |
| XX | |
| XX | Claim 5; Page 45-46; 69pp; English. |
| XX | |
| CC | This sequence represents the xylanase from Thermomyces lanuginosus strain DSM 4109. This xylanase, and xylanases derived from Humicola, Thermosacculus, Chaetomium, Mucor, Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssoschlamus or Paecilomyces strains can be used in the monocomponent xylanase preparations of the invention. The xylanase preparations and the recombinant Thermomyces xylanase are useful as animal feed additives, which promote in-vivo breakdown of plant cell wall material and thus improve digestibility, growth rate and/or feed conversion |
| CC | |
| CC | |
| CC | |

SQ Sequence 225 AA;

Query Match 100.0%; Score 1238; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.3e-108;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFTPALAALATGALAPFAGNATELEKQTPNSEGWHIDGYYSWSDGGAQATYTN 60
 DB 1 MVGFTPALAALATGALAPFAGNATELEKQTPNSEGWHIDGYYSWSDGGAQATYTN 60

QY 61 LEGGTYSISWGDGNNLVGKGMPGLNARAIHEGVTYQPNNSYLAAYGWRPLVEYYI 120
 DB 61 LEGGTYSISWGDGNNLVGKGMPGLNARAIHEGVTYQPNNSYLAAYGWRPLVEYYI 120

QY 121 VENFGTYDPSGATDGTVECDGSIYRLGKTRVNAPSIDGTQTFPDQYMSVRQDKRTSGT 180
 DB 121 VENFGTYDPSGATDGTVECDGSIYRLGKTRVNAPSIDGTQTFPDQYMSVRQDKRTSGT 180

QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225
 DB 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225

RESULT 2
 AAM05187
 ID AAM05187 standard; protein; 225 AA.
 AC AAM05187;
 XX 16-OCT-2003 (revised)
 DT 22-FEB-1997 (first entry)
 XX
 DE Endo-1,4-beta-D-xylanase.
 XX
 KM Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;
 KM Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;
 KM flour; baking; dough.
 OS Thermomyces lanuginosus; (strain DSM 4109).
 XX
 PN MO9632472-A1.
 PD 17-OCT-1996.
 XX
 PF 11-APR-1996; 96WO-DK000171.
 XX
 PR 11-APR-1995; 95DK-00000435.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Jorgensen OB, SI JQ, Jakobsen TS;
 DR WPI; 1996-477123/47.
 DR N-PSDB; AAT43010.
 XX
 PT Bread improving additive contg. xylanase from Thermomyces - and opt.
 PT alpha-amylase, increases volume, improves anti-staling properties etc.
 XX
 XX Claim 4; Page 31-32; 41pp; English.

The sequence represents an endo-1,4-beta-D-xylanase from Thermomyces lanuginosus (Humicola lanuginosa), which may be used as a bread-improving additive. The enzyme may be expressed recombinantly from a plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed), and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour, optionally along with other enzymes (amylase, maltogenase, lipase, cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase, protease and/or peroxidase). The enzyme combines particularly well with amylolytic enzymes, and may be used to improve baking properties of flour and/or dough, by increasing volume and improving texture, flavour, crumb softness, freshness and anti-staling properties, while improving dough machinability and stability. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 225 AA;

Query Match 100.0%; Score 1238; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.3e-108;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFTPALAALATGALAPFAGNATELEKQTPNSEGWHIDGYYSWSDGGAQATYTN 60
 DB 1 MVGFTPALAALATGALAPFAGNATELEKQTPNSEGWHIDGYYSWSDGGAQATYTN 60

QY 61 LEGGTYSISWGDGNNLVGKGMPGLNARAIHEGVTYQPNNSYLAAYGWRPLVEYYI 120
 DB 61 LEGGTYSISWGDGNNLVGKGMPGLNARAIHEGVTYQPNNSYLAAYGWRPLVEYYI 120

QY 121 VENFGTYDPSGATDGTVECDGSIYRLGKTRVNAPSIDGTQTFPDQYMSVRQDKRTSGT 180
 DB 121 VENFGTYDPSGATDGTVECDGSIYRLGKTRVNAPSIDGTQTFPDQYMSVRQDKRTSGT 180

QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225
 DB 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225

RESULT 3
 ABR63119
 ID ABR63119 standard; protein; 225 AA.
 XX
 AC ABR63119;
 XX 18-DEC-2003 (first entry)
 DT
 XX
 DE Thermomyces lanuginosus xylanase.
 XX
 KM Xylanase; thermostable; enzyme; feed additive.
 OS Thermomyces lanuginosus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..30
 FT /label= signal_peptide
 FT Protein 31..225
 FT /label= Mature_protein
 PN MO2003062409-A2.
 PD 31-JUL-2003.
 XX
 PF 23-JAN-2003; 2003WO-DK000039.
 XX
 PR 25-JAN-2002; 2002DK-00000130.
 XX
 PA (HOF) ROCHE VITAMINS AG.
 XX
 PI Wu W, Pettersson D, Fuglsang CC;
 DR WPI; 2003-731382/69.
 XX
 PT Composition useful as an animal feed additive comprises at least two
 PT thermostable enzymes selected from endoglucanase, xylanase, phytase,
 PT protease, galactanase, mannanase, dextranase and alpha-galactosidase.
 XX
 XX Disclosure; Page 60-61; 0pp; English.

The present sequence is the protein sequence of a thermostable xylanase of Thermomyces lanuginosus. The xylanase has a melting temperature (Tm) of 75.0 degrees C at pH 7.0. It is preferred for use in a claimed composition of the invention, which comprises at least 2 thermostable enzymes selected from an endoglucanase, xylanase, phytase, protease, galactanase, mannanase, dextranase and alpha-galactosidase. The composition is useful for improving the nutritional value of animal feeds, especially those containing soya, wheat, barley, oats and/or rye

SQ Sequence 225 AA;
Query Match 100.0%; Score 1238; DB 7; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3e-108;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFTPVALLAALAAATGALAPAGNATELEKQQTTPNSEGWHIDGYYSWMSDGAQATYTN 60
DB 1 MVGFTPVALLAALAAATGALAPAGNATELEKQQTTPNSEGWHIDGYYSWMSDGAQATYTN 60
QY 61 LEGGTYSISWGDGNNLVGKGMNPGLNARAIHFEQVYQPNGNSTYLAAYGWTNPVVEYI 120
DB 61 LEGGTYSISWGDGNNLVGKGMNPGLNARAIHFEQVYQPNGNSTYLAAYGWTNPVVEYI 120
QY 121 VENFGTYDPSSGATDLGTVECDSIYRLGKTTRVNAPSIDGTQTFPDQYWSYRQDKRTSGT 180
DB 121 VENFGTYDPSSGATDLGTVECDSIYRLGKTTRVNAPSIDGTQTFPDQYWSYRQDKRTSGT 180
QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225
DB 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225

RESULT 4
AEB00305
ID AEB00305 standard; protein; 225 AA.
XX
AC AEB00305;
XX
DT 08-SEP-2005 (first entry)
XX
DE Xylanase SEQ ID NO:15.
XX
KM enzyme; xylanase; feedstuff; alcohol; fermentation; brewing; filtration.
XX
OS Thermomyces lanuginosus.
XX
PN WO2005059084-A1.
XX
PD 30-JUN-2005.
XX
PF 17-DEC-2004; 2004WO-DK000880.
XX
PR 19-DEC-2003; 2003DK-00001895.
XX
PA (NOVO) NOVOZYMS AS.
XX
PI Feesteren RM, Vikebo-Nielsen A, Joergensen CT, Christensen LM;
XX
DR WPI; 2005-458776/46.
XX
PT Preparation of a mash (having enhanced filterability and/or improved
XX
PT extract yield after filtration) comprises preparing a mash in the
XX
PT presence of enzyme activities comprising xylanase of GH family 10 and
XX
XX filtering to obtain wort.

PS Disclosure; SEQ ID NO 15; 68pp; English.
XX
XX The invention relates to a process for preparing a mash (A) (having
XX
XX enhanced filterability and/or improved extract yield after filtration)
XX
XX which comprises preparing a mash in the presence of enzyme activities
XX
XX (comprising a xylanase of GH family 10 at at least 1% w/w of the total
XX
XX xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a
XX
XX wort. Also described is a composition is useful for reducing the
XX
XX viscosity of an aqueous solution comprising a starch hydrolysate, which
XX
XX is a mash for beer making or a feed composition. The process is useful
XX
XX for the production of an alcoholic beverage, such as beer or whiskey and
XX
XX the composition is useful in the mashing and filtration step in brewing
XX
XX process. The present sequence represents a xylanase used in the mashing
XX
XX process of the invention.
SQ Sequence 225 AA;

Query Match 100.0%; Score 1238; DB 9; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3e-108;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFTPVALLAALAAATGALAPAGNATELEKQQTTPNSEGWHIDGYYSWMSDGAQATYTN 60
DB 1 MVGFTPVALLAALAAATGALAPAGNATELEKQQTTPNSEGWHIDGYYSWMSDGAQATYTN 60
QY 61 LEGGTYSISWGDGNNLVGKGMNPGLNARAIHFEQVYQPNGNSTYLAAYGWTNPVVEYI 120
DB 61 LEGGTYSISWGDGNNLVGKGMNPGLNARAIHFEQVYQPNGNSTYLAAYGWTNPVVEYI 120
QY 121 VENFGTYDPSSGATDLGTVECDSIYRLGKTTRVNAPSIDGTQTFPDQYWSYRQDKRTSGT 180
DB 121 VENFGTYDPSSGATDLGTVECDSIYRLGKTTRVNAPSIDGTQTFPDQYWSYRQDKRTSGT 180
QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225
DB 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225

RESULT 5
AAE18456
ID AAE18456 standard; protein; 194 AA.
XX
AC AAE18456;
XX
DT 16-MAY-2002 (first entry)
XX
DE Thermomyces lanuginosus xylanase, Xyn.
XX
KM Modified xylanase; thermostability; alkalophilicity; industrial process;
XX
KM pulp manufacture; poultry; swine feed; enzyme; Xyn.
XX
OS Thermomyces lanuginosus.
XX
PN WO200192487-A2.
XX
PD 06-DEC-2001.
XX
PF 31-MAY-2001; 2001WO-CA000769.
XX
PR 31-MAY-2000; 2000US-0213803P.
XX
PA (CANADA) NAT RES COUNCIL CANADA.
XX
PI Sung WL;
XX
DR WPI; 2002-171435/22.
XX
PT Modified xylanase exhibiting increased thermostability and
XX
PT alkalophilicity useful for industrial processing e.g. for pulp
XX
XX manufacturing.

PS Disclosure; Page 83-84; 109pp; English.
XX
XX The present invention relates to a modified xylanase exhibiting increased
XX
XX thermostability and alkalophilicity. Modified xylanase is useful in
XX
XX industrial process such as pulp manufacturing. Modified xylanase is also
XX
XX useful for bleaching of pulp, processing of precision devices and
XX
XX improving digestibility of poultry and swine feed. Modified xylanase has
XX
XX exhibits improved performance at conditions of high temperature and pH and
XX
XX corresponds improved thermostability and/or alkalophilicity in comparison to
XX
XX lanuginosus xylanase, Xyn
SQ Sequence 194 AA;
Query Match 87.9%; Score 1088; DB 5; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7e-94;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QTPNSEGWHIDGYYSWMSDGAQATYTNLEGGTYSISWGDGNNLVGKGMNPGLNARAI 91

Db 1 OTTNSGMDHGYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGNPGLNARAI 60
Qy 92 HFEVYQPNNGSYLAVYGMTNPLVEYYIVENFGYTPSSGATDLGTVECDGSIYRLGKT 151
Db 61 HFEVYQPNNGSYLAVYGMTNPLVEYYIVENFGYTPSSGATDLGTVECDGSIYRLGKT 120
Qy 152 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVDHYQIVATEGY 211
Db 121 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVDHYQIVATEGY 180
Qy 212 FSSGYARTTVADVG 225
Db 181 FSSGYARTTVADVG 194

RESULT 6
AAB48543
ID AAB48543 standard; protein; 194 AA.

XX AAB48543;
AC AAB48543;
XX 05-MAR-2001 (first entry)
XX Thermomyces lanuginosus xylanase.
DE Thermomyces lanuginosus xylanase.
XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
KM bleaching agent.
XX Thermomyces lanuginosus.
OS WO200068396-A2.
XX PN 16-NOV-2000.
XX PD 12-MAY-2000; 2000WO-US013172.
XX PF 12-MAY-1999; 99US-0133714P.
XX PR 12-MAY-1999; 99US-0133714P.
XX PA (XENC-) XENCOR INC.
XX P1 Bentzien JM;
XX P1 Bentzien JM;
XX DR WPI; 2000-679800/66.
XX

XX Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.

XX Disclosure; Fig 16L; 114pp; English.

XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative
CC to the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX

XX Sequence 194 AA;

Query Match 87.5%; Score 1083; DB 3; Length 194;
Best Local Similarity 100.0%; Pred. No. 5.1e-94;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 TTPNSEGMDHGYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGNPGLNARAIH 92
Db 2 TTPNSEGMDHGYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGNPGLNARAIH 61
Qy 93 FEGVYQPNNGSYLAVYGMTNPLVEYYIVENFGYTPSSGATDLGTVECDGSIYRLGKT 152
Db 62 FEGVYQPNNGSYLAVYGMTNPLVEYYIVENFGYTPSSGATDLGTVECDGSIYRLGKT 121

Qy 153 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVDHYQIVATEGY 212
Db 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVDHYQIVATEGY 181
Qy 213 SSGYARTTVADVG 225
Db 182 SSGYARTTVADVG 194

RESULT 7
AAO18649
ID AAO18649 standard; protein; 194 AA.

XX AAO18649;
AC AAO18649;
XX 24-OCT-2002 (first entry)
XX T lanuginosus xylanase.
XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KM liquid clarification; coffee extraction; plant oil extraction;
KM starch extraction; food thickener; animal food additive; mutant; mutein.
XX Thermomyces lanuginosus.
OS WO200238746-A2.
XX PN 16-MAY-2002.
XX PD 09-NOV-2001; 2001WO-US048018.
XX PF 10-NOV-2000; 2000US-00710050.
XX PR 10-NOV-2000; 2000US-00710050.
XX PA (XENC-) XENCOR INC.
XX P1 Bentzien J; Dahiyat B;
XX P1 Bentzien J; Dahiyat B;
XX DR WPI; 2002-608200/65.
XX

XX Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.

XX Disclosure; Fig 16L; 121pp; English.

XX The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductor. The present sequence is a xylanase protein
XX described in the exemplification of the invention
XX

XX Sequence 194 AA;

Query Match 87.5%; Score 1083; DB 5; Length 194;
Best Local Similarity 100.0%; Pred. No. 5.1e-94;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 TTPNSEGMDHGYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGNPGLNARAIH 92
Db 2 TTPNSEGMDHGYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGNPGLNARAIH 61
Qy 93 FEGVYQPNNGSYLAVYGMTNPLVEYYIVENFGYTPSSGATDLGTVECDGSIYRLGKT 152

Db 62 PEGVYQPNNGSYLAIVGWTNRNPLVEYYIVENFGTYDPSGATDLGTCDCGSIYRLGKTT 121
Qy 153 RVNAPSIDGTQTFQYQVSVNRDCKRTSGTVQTCGFDAARAGLVNNGDHYQIVATEGYF 212
Db 122 RVNAPSIDGTQTFQYQVSVNRDCKRTSGTVQTCGFDAARAGLVNNGDHYQIVATEGYF 181
Qy 213 SSGYARITVADVG 225
Db 182 SSGYARITVADVG 194

RESULT 8
ADI6751
ID ADI6751 standard; protein; 194 AA.
XX
AC ADI6751;
XX
DT 22-APR-2004 (first entry)
XX
DE T. lanuginosus xylanase.
XX
KM Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
KM paper industry; food; animal feed; thermostability; alkaliphilic;
KM hot alkali treatment.
XX
OS Thermomyces lanuginosus.
XX
PN US6682923-B1.
XX
PD 27-JAN-2004.
XX
PF 12-MAY-2000; 2000US-00570856.
XX
PR 12-MAY-1999; 99US-0133714P.
PR 07-JUN-1999; 99US-0138156P.
PA (XENC-) XENCOR.
XX
PI Bentzien J, Dahljat BJ;
XX
DR WPI; 2004-118575/12.
XX
PT New mutant xylanase (XA) protein comprising at least four amino acid
PT substitutions as compared to Bacillus circulans xylanase; useful for
PT bleaching (paper) pulp, and in the food and animal feed industries..
XX
PS Disclosure; SEQ ID NO 24; 84p; English.
XX
CC The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
CC xylanase from Bacillus circulans) protein appearing as ADI6730. Also
CC included is a bleaching agent comprising the XA protein. The non-
CC naturally occurring XA protein comprises at least four amino acid
CC substitutions as compared to Bacillus circulans xylanase ADI6728. The
CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
CC useful for bleaching pulp in the paper and related industries, but is
CC also useful in the food and animal feed industries. The new protein is
CC active at higher pH and temperature ranges than naturally occurring
CC xylanases, simplifying incorporation of the xylanase treatment step into
CC pulp processing, especially where the enzyme is added after hot alkali
CC treatment. The present sequence is a xylanase from another species
CC included for comparison.
XX
SQ Sequence 194 AA;

Query Match 87.5%; Score 1083; DB 8; Length 194;
Best Local Similarity 100.0%; Pred. No. 5,1e-94;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 TTPNSEGMHDGYYSWMSDGAQATYTNLBGGTYEISWGDGSLVGGKGNPGLNARAIH 92
Db 2 TTPNSEGMHDGYYSWMSDGAQATYTNLBGGTYEISWGDGSLVGGKGNPGLNARAIH 61

Qy 93 PEGVYQPNNGSYLAIVGWTNRNPLVEYYIVENFGTYDPSGATDLGTCDCGSIYRLGKTT 152
Db 62 PEGVYQPNNGSYLAIVGWTNRNPLVEYYIVENFGTYDPSGATDLGTCDCGSIYRLGKTT 121
Qy 153 RVNAPSIDGTQTFQYQVSVNRDCKRTSGTVQTCGFDAARAGLVNNGDHYQIVATEGYF 212
Db 122 RVNAPSIDGTQTFQYQVSVNRDCKRTSGTVQTCGFDAARAGLVNNGDHYQIVATEGYF 181
Qy 213 SSGYARITVADVG 225
Db 182 SSGYARITVADVG 194

RESULT 9
AAB48542
ID AAB48542 standard; protein; 194 AA.
XX
AC AAB48542;
XX
DT 05-MAR-2001 (first entry)
XX
DE Paecilomyces variotii xylanase.
XX
KM Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
KM bleaching agent.
XX
OS Paecilomyces variotii.
XX
PN WO20068396-A2.
XX
PD 16-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US013172.
XX
PR 12-MAY-1999; 99US-0133714P.
XX
PA (XENC-) XENCOR INC.
XX
PI Bentzien JM;
XX
DR WPI; 2000-679800/66.
XX
PT Non naturally occurring XA protein with enhanced thermostability,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
PS Disclosure; Fig 16K, 114p; English.
XX
CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermostability, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 194 AA;

Query Match 77.9%; Score 965; DB 3; Length 194;
Best Local Similarity 87.6%; Pred. No. 7,5e-83;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 33 TTPNSEGMHDGYYSWMSDGAQATYTNLBGGTYEISWGDGSLVGGKGNPGLNARAIH 92
Db 2 TTPNSEGMHDGYYSWMSDGDSTYTNNSGTYEITWNGNGLVGGKGNPGLNARAIH 61
Qy 93 PEGVYQPNNGSYLAIVGWTNRNPLVEYYIVENFGTYDPSGATDLGTCDCGSIYRLGKTT 152
Db 62 PEGVYQPNNGSYLAIVGWTNRNPLVEYYIVENFGTYDPSGATDLGTCDCGSIYRLGKTT 121
Qy 153 RVNAPSIDGTQTFQYQVSVNRDCKRTSGTVQTCGFDAARAGLVNNGDHYQIVATEGYF 212
Db 2 TTPNSEGMHDGYYSWMSDGAQATYTNLBGGTYEISWGDGSLVGGKGNPGLNARAIH 61

Db 122 RYNAPSIDGTQTQFNQYWSVRQDKSSGTVGTGCHFDAMASAGLNVTDHYYQIVATEGYF 181
 QY 213 SSGYARITVADVG 225
 |||||
 Db 182 SSGYARITVADVG 194

RESULT 10
 ID AAO18648 standard; protein; 194 AA.
 AC AAO18648;

XX 24-OCT-2002 (first entry)
 DT
 XX P variotcii xylanase.

XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
 KM liquid clarification; coffee extraction; plant oil extraction;
 KM starch extraction; food thickener; animal food additive; mutant; mutein.
 OS Paecilomyces variotcii.

XX WO200238746-A2.
 XX 16-MAY-2002.

XX 09-NOV-2001; 2001WO-US048018.
 XX 10-NOV-2000; 2000US-00710050.

XX (XENC-) XENCOR INC.

PI Bentzien J, Dahljat B;

XX WPI; 2002-608200/65.

PT Novel xylanase activity protein, useful in bleaching process of pulp and
 PT in food and animal feed industry, has enhanced thermostability and
 PT alkalophilicity.

PS Disclosure; Fig 16K; 121pp; English.

XX The present invention relates to a non-naturally occurring xylanase
 CC activity (XA) protein comprising an amino acid sequence less than 97%
 CC identical to a naturally occurring Bacillus circulans xylanase, where the
 CC protein has been modified to exhibit enhanced thermostability, or
 CC alkalophilicity, or thermostability relative to naturally occurring B.
 CC circulans xylanase, and has at least 5 amino acid substitutions. A
 CC bleaching agent comprising a modified xylanase is useful for bleaching
 CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
 CC clarifying juice and wine, extracting coffee, plant oils and starch,
 CC producing food thickeners, altering texture in bakery products, e.g.
 CC improving the quality of dough, helping bread to rise and processing of
 CC wheat and corn for starch production, use as animal food additives to aid
 CC in the digestibility of feedstuffs and in the washing of super precision
 CC devices and semiconductor. The present sequence is a xylanase protein
 CC described in the exemplification of the invention

XX Sequence 194 AA;

Query Match 77.9%; Score 965; DB 5; Length 194;
 Best Local Similarity 87.6%; Pred. No. 7.5e-83;
 Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 33 TTPNSEGHHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGMPGLNARAIH 92
 |||||
 Db 2 TTPNSEGHHDGYYYSWMSDGGDSTYTNNSGTYEITWNGNGNLVGGKMPGLNARAIH 61
 |||||
 QY 93 FEGVYQPNNGSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDVGTCDSGYIRLQKTT 152
 |||||
 Db 62 FTGVQPNGSTYLSIVGWTNPLVEYYIVENFGSSNPSSGSTDLDGTCDSGYIRLQOST 121

QY 153 RYNAPSIDGTQTQFDQYWSVRQDKRTSGTVGTGCHFDAMAAAGLNVNDHYYQIVATEGYF 212
 |||||
 Db 122 RYNAPSIDGTQFNQYWSVRQDKSSGTVGTGCHFDAMASAGLNVTDHYYQIVATEGYF 181
 QY 213 SSGYARITVADVG 225
 |||||
 Db 182 SSGYARITVADVG 194

RESULT 11
 ID ADI66750 standard; protein; 194 AA.
 AC ADI66750;

XX 22-APR-2004 (first entry)
 DT
 XX P. variotcii xylanase.

XX Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
 KM paper industry; food; animal feed; thermostability; alkalophilic;
 KM hot alkali treatment.

XX Paecilomyces variotcii.
 XX US6682923-B1.

XX 27-JAN-2004.

XX 12-MAY-2000; 2000US-00570856.

XX 12-MAY-1999; 99US-0133714P.

XX 07-JUN-1999; 99US-0138156P.

XX (XENC-) XENCOR.

PI Bentzien J, Dahljat B;

XX WPI; 2004-118575/12.

PT New mutant xylanase (XA) protein comprising at least four amino acid
 PT substitutions as compared to Bacillus circulans xylanase, useful for
 PT bleaching (paper) pulp, and in the food and animal feed industries.

PS Disclosure; SEQ ID NO 23; 84pp; English.

XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
 CC xylanase from Bacillus circulans) protein appearing as ADI66730. Also
 CC included is a bleaching agent comprising the XA protein. The non-
 CC naturally occurring XA protein comprises at least four amino acid
 CC substitutions as compared to Bacillus circulans xylanase ADI66728. The
 CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
 CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
 CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
 CC useful for bleaching pulp in the paper and related industries, but is
 CC also useful in the food and animal feed industries. The new protein is
 CC active at higher pH and temperature ranges than naturally occurring
 CC xylanases, simplifying incorporation of the xylanase treatment step into
 CC pulp processing, especially where the enzyme is added after hot alkali
 CC treatment. The present sequence is a xylanase from another species
 CC included for comparison.

XX Sequence 194 AA;

Query Match 77.9%; Score 965; DB 8; Length 194;
 Best Local Similarity 87.6%; Pred. No. 7.5e-83;
 Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 33 TTPNSEGHHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGMPGLNARAIH 92
 |||||
 Db 2 TTPNSEGHHDGYYYSWMSDGGDSTYTNNSGTYEITWNGNGNLVGGKMPGLNARAIH 61
 |||||
 QY 93 FEGVYQPNNGSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDVGTCDSGYIRLQKTT 152

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Db      62 FTGVQPNGTSTYLSYVGWTRNPLVEYYIVENFGSSNPSSGSTDLCTVSCDGSYTLAQST 121
Qy      153 RVNAPSIDGTQTFPDQYMSVRDOKRTSGTVQGCCHDAPARAGLNNGDHYQIVATEGYF 212
Db      122 RYNAPSIDGTQTFPDQYMSVRDOKRTSGTVQGCCHDAPARAGLNNGDHYQIVATEGYF 181
Qy      213 SSGYARITVADVG 225
Db      182 SSGYARITVADVG 194

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RESULT 12
AAB48548
ID AAB48548 standard; protein; 221 AA.
XX
AC AAB48548;
XX
DT 05-MAR-2001 (first entry)
XX
DE Cochliobolus carbonum xylanase.
XX
KW Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
KM bleaching agent.
XX
OS Cochliobolus carbonum.
XX
PN WO200068396-A2.
XX
PD 16-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US013172.
XX
PR 12-MAY-1999; 99US-0133714P.
XX
PA (XENC-) XENCOR INC.
XX
PI Bentzen JM;
XX
DR WPI; 2000-679800/66.
XX
PT Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
PS Disclosure; Fig 16Q; 114pp; English.
XX
CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 221 AA;

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```

Query Match      65.1%; Score 806.5; DB 3; Length 221;
Best Local Similarity 67.9%; Pred. No. 9e-68;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;
Qy      1 MVGFTPVALLAATGALAPAGNATELEKRTTPNSGMDGYYSWSDGGAQATYTN 60
Db      1 MVSFTSITTAATAAATGALAPATDVS-LVARQNTPNBGTNCGFMSWSDGARATYTN 59
Qy      61 LEGGTVEISMGDGNLVGKGMNPGLNARAIHFEQVYQPNGNSYLAAYGTRNPLVEYYI 120
Db      60 GAGGSYSVSWSGGNLVGKGMNPG-TARTITTSGETVYNGNSYLAAYGTRNPLVEYYI 118
Qy      121 VENFGTVPSSGATDLCTVECDGSYRLGKTTVNAPSIDGTQTFPDQYMSVRDOKRTSGT 180
Db      119 VENFGTVPSSGATDLCTVECDGSYRLGKTTVNAPSIDGTQTFPDQYMSVRDOKRTSGT 178

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Qy      181 VQGCCHDAPARAGLNNGDHYQIVATEGYFSSGYARITV 221
Db      179 VNMKTHFDAMASKGMNL-GQHYQIVATEGYFSGNAQITV 218

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RESULT 13
AAO18654
ID AAO18654 standard; protein; 221 AA.
XX
AC AAO18654;
XX
DT 24-OCT-2002 (first entry)
XX
DE C carbonum xylanase.
XX
KW Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KW liquid clarification; coffee extraction; plant oil extraction;
KW starch extraction; food thickener; animal food additive; mutant; mutein.
XX
OS Cochliobolus carbonum.
XX
PN WO200238746-A2.
XX
PD 16-MAY-2002.
XX
PF 09-NOV-2001; 2001WO-US048018.
XX
PR 10-NOV-2000; 2000US-00710050.
XX
PA (XENC-) XENCOR INC.
XX
PI Bentzen J, Dahljat B;
XX
DR WPI; 2002-608200/65.
XX
PT Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
PS Disclosure; Fig 16Q; 121pp; English.
XX
CC The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioreconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductor. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
SQ Sequence 221 AA;

```

```

Query Match      65.1%; Score 806.5; DB 5; Length 221;
Best Local Similarity 67.9%; Pred. No. 9e-68;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;
Qy      1 MVGFTPVALLAATGALAPAGNATELEKRTTPNSGMDGYYSWSDGGAQATYTN 60
Db      1 MVSFTSITTAATAAATGALAPATDVS-LVARQNTPNBGTNCGFMSWSDGARATYTN 59
Qy      61 LEGGTVEISMGDGNLVGKGMNPGLNARAIHFEQVYQPNGNSYLAAYGTRNPLVEYYI 120
Db      60 GAGGSYSVSWSGGNLVGKGMNPG-TARTITTSGETVYNGNSYLAAYGTRNPLVEYYI 118
Qy      121 VENFGTVPSSGATDLCTVECDGSYRLGKTTVNAPSIDGTQTFPDQYMSVRDOKRTSGT 180
Db      119 VENFGTVPSSGATDLCTVECDGSYRLGKTTVNAPSIDGTQTFPDQYMSVRDOKRTSGT 178

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Db 120 VEYVIESYGTYNPGSOAQYKGFYTDQDYDIFVSTRYNQPSIDGTRTFQYWSIRKNK 179
Qy 176 RTSGTYOTGCHFDAMAPAGLNVNGDHYVQIVATEGYFSSGYARITV 221
Db 180 RVGGSVMQNHFNAMQOHGMP-L-GOHYYQVATEGYOSSGESDITV 224

Search completed: February 10, 2006, 14:54:12
Job time : 153.432 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 14:54:33 ; Search time 27.9236 Seconds
(without alignments)
775.285 Million cell updates/sec

Title: US-09-467-368-2

Perfect score: 1238
Sequence: 1 MVGFTPVLAALAAATGALAF.....VATEGFSSGVARTTADVG 225

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------------|
| 1 | 691.5 | 55.9 | 219 | 2 | S71472 endo-1,4-beta-xylo- |
| 2 | 689.5 | 55.7 | 227 | 2 | S43919 endo-1,4-beta-xylo- |
| 3 | 689 | 55.7 | 241 | 2 | S71473 endo-1,4-beta-xylo- |
| 4 | 684.5 | 55.3 | 223 | 2 | S39883 endo-1,4-beta-xylo- |
| 5 | 680.5 | 55.0 | 225 | 1 | S57477 endo-1,4-beta-xylo- |
| 6 | 667 | 53.9 | 222 | 2 | S39154 xyloamase 1 - fungu |
| 7 | 663 | 53.6 | 197 | 1 | A44597 endo-1,4-beta-xylo- |
| 8 | 659 | 53.2 | 232 | 2 | UC7577 endo-1,4-beta-xylo- |
| 9 | 637.5 | 51.5 | 221 | 1 | S57469 endo-1,4-beta-xylo- |
| 10 | 636.5 | 51.4 | 190 | 1 | A44593 endo-1,4-beta-xylo- |
| 11 | 636.5 | 51.4 | 190 | 1 | A44595 endo-1,4-beta-xylo- |
| 12 | 634.5 | 51.3 | 190 | 1 | A44594 endo-1,4-beta-xylo- |
| 13 | 599.5 | 48.4 | 221 | 2 | UC7307 endo-1,4-beta-xylo- |
| 14 | 585.5 | 47.3 | 335 | 2 | T50601 endo-1,4-beta-xylo- |
| 15 | 573 | 46.3 | 333 | 1 | J50590 endo-1,4-beta-xylo- |
| 16 | 554.5 | 44.8 | 241 | 2 | T37005 endo-1,4-beta-xylo- |
| 17 | 553 | 44.7 | 240 | 1 | S47512 endo-1,4-beta-xylo- |
| 18 | 540 | 43.6 | 240 | 1 | J50591 endo-1,4-beta-xylo- |
| 19 | 529 | 42.7 | 644 | 1 | T40712 endo-1,4-beta-xylo- |
| 20 | 528 | 42.6 | 661 | 1 | S59633 endo-1,4-beta-xylo- |
| 21 | 505.5 | 40.8 | 210 | 2 | C83762 endo-1,4-beta-xylo- |
| 22 | 498 | 40.2 | 656 | 1 | S59631 endo-1,4-beta-xylo- |
| 23 | 470.5 | 38.0 | 213 | 1 | I40569 endo-1,4-beta-xylo- |
| 24 | 469.5 | 37.9 | 213 | 1 | S48126 endo-1,4-beta-xylo- |
| 25 | 468.5 | 37.8 | 213 | 1 | S01734 endo-1,4-beta-xylo- |
| 26 | 452 | 36.5 | 354 | 1 | S51779 endo-1,4-beta-xylo- |
| 27 | 427 | 34.5 | 511 | 1 | JQ1935 endo-1,4-beta-xylo- |
| 28 | 400 | 32.3 | 261 | 1 | S12745 endo-1,4-beta-xylo- |
| 29 | 397.5 | 32.1 | 228 | 1 | WMBSXP endo-1,4-beta-xylo- |

| | | | | | |
|----|-------|------|------|---|----------------------------|
| 30 | 390 | 31.5 | 211 | 2 | S49542 endo-1,4-beta-xylo- |
| 31 | 389.5 | 31.5 | 789 | 2 | SS8235 endo-1,4-beta-xylo- |
| 32 | 388 | 31.3 | 211 | 1 | JC1198 endo-1,4-beta-xylo- |
| 33 | 385 | 31.1 | 211 | 1 | S48229 endo-1,4-beta-xylo- |
| 34 | 372 | 30.0 | 229 | 2 | S39155 xyloamase 2 - fungu |
| 35 | 371 | 30.0 | 954 | 1 | S20907 endo-1,4-beta-xylo- |
| 36 | 365 | 29.5 | 781 | 2 | S51592 XynB precursor - R |
| 37 | 356 | 28.8 | 209 | 2 | JC4909 endo-1,4-beta-xylo- |
| 38 | 355.5 | 28.7 | 802 | 2 | A36910 xyloamase, beta(1,3 |
| 39 | 299.5 | 24.2 | 607 | 2 | S49528 endoxyloamase - rum |
| 40 | 296 | 23.9 | 607 | 2 | S24754 endo-1,4-beta-xylo- |
| 41 | 248 | 20.0 | 608 | 2 | B53295 xyloamase (EC 3.2.1 |
| 42 | 240.5 | 19.4 | 266 | 1 | S48865 endo-1,4-beta-xylo- |
| 43 | 145 | 11.7 | 50 | 2 | A61149 endo-1,4-beta-xylo- |
| 44 | 115 | 9.3 | 2817 | 2 | B97033 uncharacterized pr |
| 45 | 113 | 9.1 | 40 | 2 | PQ0202 endo-1,4-beta-xylo- |

ALIGNMENTS

RESULT 1

S71472
endo-1,4-beta-xyloamase (EC 3.2.1.8) A precursor - Chaetomium gracile
N:Alternate names: xyloamase A
C:Species: Chaetomium gracile
C:Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
C:Accession: S71472; S78206
R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
Curr. Genet. 29, 73-80, 1995
A:Title: Two family G xyloamase genes from Chaetomium gracile and their expression in Asp
A:Reference number: S71472; MUID:96118924; PMID:8595661
A:Accession: S71472
A:Molecule type: DNA
A:Residues: 1-219 <YOS>
A:Cross-references: UNIPROT:Q12579; UNIPARC:UP10000421A6; EMBL:D49850; NID:G1339857; PIR:
A:Cross-References: UNIPARC:UP10000175A79; UNIPARC:UP10000175A82; UNIPARC:UP10000175A83
A:Accession: S78206
A:Molecule type: Protein
A:Residues: 31-45782-94152-160 <YOH>
A:Cross-References: UNIPARC:UP10000175A79; UNIPARC:UP10000175A82; UNIPARC:UP10000175A83
C:Genetics:
A:Introns: 81/2
C:Function:
A:Pathway: xyloan degradation
C:Superfamily: endo-1,4-beta-xyloamase; endo-1,4-beta-xyloamase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-219/Product: endo-1,4-beta-xyloamase A #status experimental <MAT>
F:42-219/Domain: endo-1,4-beta-xyloamase homology <XYL>
F:115,206/Active site: Glu #status predicted

Query Match 55.9%; Score 691.5; DB 2; Length 219;

Best Local Similarity 59.1%; Pred. No. 5.3e-48;
Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;

| | | | |
|----|-----|---|-----|
| QY | 1 | MVGFTPVLAALAAATGALAPAGNAT---ELEKQQTTPNEBGMHGGYVMSGGGAQAT | 57 |
| DB | 1 | MVSEKAL--LLGAAGLAPFP-NVTQMNELVAPAGTPSGTGTNGYFYSFMWDGGSTVN | 56 |
| QY | 58 | YTNLEGGTVEISWDGNTLVGCKGMPGLNARAIHFEQVYQPNQNSYLAAYGWTNPLVE | 117 |
| DB | 57 | YONGAGGSYVQVQVQNCNPFVGGKQWNGA-AKRTNFGTSPQNGGLAIYGTQNLVE | 115 |
| DB | 116 | YVIVSEFGTVPSSQSKFGTIOODGSTYIAKTRRNQPSIGSTFTDFQFWSVQRHRS | 175 |
| QY | 118 | YVIVSEFGTVPSSGATDLATVECDGSIYFLGKTRRVNAPSIDGOTFEDQYMSVRQDKRT | 177 |
| QY | 178 | SGTQTGCHPDANARAGLANNNGHYVOIVATGEGFSSGVARTYA | 222 |
| DB | 176 | SGSVNVAHFNAQAQGLKL-GSHNTQIVATGEGSSSSSITVS | 219 |

RESULT 2

S43919
endo-1,4-beta-xylosidase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)
C|Species: Humicola insolens
C|Date: 19-Mar-1997 #sequence_rev19-Mar-1997 #text_change 09-Jul-2004
C|Accession: S43919
R|Dalboge, H.; Heidt-Hansen, H.P.
Mol. Gen. Genet. 243, 253-260, 1994
A|Title: A novel method for efficient expression cloning of fungal enzyme genes.
A|Reference number: S43919; MUID:94247364; PMID:8190078
A|Accession: S43919
A|Molecule type: mRNA
A|Residues: 1-227 <DNL>
A|Cross-references: UNIPROT:P55334; UNIPARC:UPI00000421A4; EMBL:X76047; NID:9505260; PIR
C|Genetics:
A|Gene: XYL1
C|Function:
A|Pathway: xylan degradation
C|Superfamily: endo-1,4-beta-xylosidase; endo-1,4-beta-xylosidase homology
C|Keywords: glycosidase; hydrolase; polysaccharide degradation
F|1-19/Domain: signal sequence #status predicted <SIG>
F|20-227/Product: endo-1,4-beta-xylosidase #status predicted <MAT>
F|48-228/Domain: endo-1,4-beta-xylosidase homology <XYL>
F|112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
F|121,212/Active site: Glu #status predicted

Query Match 55.7%; Score 689.5; DB 2; Length 227;
Best Local Similarity 55.8%; Pred. No. 8e-48;
Matches 126; Conservative 31; Mismatches 62; Indels 7; Gaps 3;

QY 1 MVGFTPALAALATGALAA-----PPAGNATELEKQRTTPNSEGMHGGYYSWSDGAQ 55
Db 1 MVSFSLAGVAAISGTLAARPAEVSVAVEKRTITPCTGYNNGYFYSYNDHGGYTY 60
QY 56 ATYNLEGGTYEISGDCGNLVGGKGNPGUNARAIHBEVYQPNNGSYLAIVGWTNPL 115
Db 61 VQTNLEBSRYQVRKRNKGNVGGKGNPG--TGRTINIGYTFNPGNGYLAIVGWTNPL 119
QY 116 VEYIVENFGTYDPSGATDLGTYECDSIYRLKRTTRVNAPSIDGTQTPDQYSVRODK 175
Db 120 VEYIVESYGTYNPSQAYQVGTFTDGDQDIFSTRYNGPSIDGTRTFQGYMSIRNKK 179
QY 176 RTSGVTGTCFDMARAGLVNNGDHYQIYATGTSYSSGARITV 221
Db 180 RVGGSVMQNHFNMAQHGMP--GQHYVVAATEGYSSGSIDIV 224

RESULT 3

S71473
endo-1,4-beta-xylosidase (EC 3.2.1.8) B precursor - Chaetomium gracile
C|Species: Chaetomium gracile
C|Date: 09-Dec-1997 #sequence_rev19-Dec-1997 #text_change 09-Jul-2004
C|Accession: S71473; S78207
R|Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
Curr. Genet. 29, 73-80, 1995
A|Title: Two family G xylosidase genes from Chaetomium gracile and their expression in Asf
A|Reference number: S71473; MUID:96118924; PMID:8595661
A|Accession: S71473
A|Molecule type: DNA
A|Residues: 1-241 <YOS>
A|Cross-references: UNIPROT:Q12580; UNIPARC:UPI00000421AB; EMBL:D49851; NID:g1339859; PIR
A|Accession: S78207
A|Molecule type: protein
A|Residues: 38-44; 89-91; 153-161 <YOH>
A|Cross-references: UNIPARC:UPI0000175A77; UNIPARC:UPI0000175A78; UNIPARC:UPI0000175A79
C|Genetics:
A|Introns: 88/2
C|Function:
A|Pathway: xylan degradation
C|Superfamily: endo-1,4-beta-xylosidase; endo-1,4-beta-xylosidase homology
C|Keywords: glycosidase; hydrolase; polysaccharide degradation
F|1-30/Domain: signal sequence #status predicted <SIG>
F|31-241/Product: endo-1,4-beta-xylosidase B #status predicted <MAT>
F|43-220/Domain: endo-1,4-beta-xylosidase homology <XYL>

F|116,207/Active site: Glu #status predicted
Query Match 55.7%; Score 689; DB 2; Length 241;
Best Local Similarity 59.5%; Pred. No. 9.4e-48;
Matches 132; Conservative 31; Mismatches 55; Indels 4; Gaps 4;

QY 1 MVGFTPALAALATGALAAFPAGNATELEKQRTTPNSEGMHGGYYSWSDGAQATYT 59
Db 1 MVSFSLAGVAAISGTLAARPAEVSVAVEKRTITPCTGYNNGYFYSYNDHGGYTY 59
QY 60 NLEGGTYEISGDCGNLVGGKGNPGUNARAIHBEVYQPNNGSYLAIVGWTNPLVEY 119
Db 60 NEAGGQYSVMSGKGNMVGKGNMPC--SARTINTANTNNGSYLAIVGWTNPLVEY 118
QY 120 IVENFGTYDPSGATDLGTYECDSIYRLKRTTRVNAPSIDGTQTPDQYSVRODKRTSG 179
Db 119 IVENFGTYNPGTATRLGSLYTDGSCVDYRTQVNGPSIEGTSFYQFMSVRNKRSGG 176
QY 180 TVOTGTCFDMARAGLVNNGDHYQIYATGTSYSSGARITV 221
Db 179 SVMMAAFHMAAAGIQL--GTHDYQIYATGTSYSSGSATVNV 219

RESULT 4

S39883
endo-1,4-beta-xylosidase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)
N|Alternate names: endoxylosidase II
C|Species: Trichoderma reesei
C|Date: 19-Mar-1997 #sequence_rev19-Mar-1997 #text_change 09-Jul-2004
C|Accession: S39883; S39884
R|Saarelainen, R.; Palonen, M.; Fagerstroem, R.; Suominen, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A|Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxylan
A|Reference number: S39883; MUID:94088442; PMID:8264524
A|Accession: S39883
A|Molecule type: DNA
A|Residues: 1-223 <SAA>
A|Cross-references: UNIPROT:Q02244; UNIPARC:UPI00000421AB; EMBL:S67387; NID:g455906; PIR
A|Experimental source: strain QM6a
A|Accession: S39884
A|Molecule type: protein
A|Residues: 34-43; 49-57; 121-151; 178-191 <SAP>
A|Cross-references: UNIPARC:UPI0000175A7C; UNIPARC:UPI0000175A7D; UNIPARC:UPI0000175A7E;
C|Genetics:
A|Gene: xln2
A|Introns: 91/2
C|Function:
A|Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A|Pathway: xylan degradation
C|Superfamily: endo-1,4-beta-xylosidase; endo-1,4-beta-xylosidase homology
C|Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F|1-19/Domain: signal sequence #status predicted <SIG>
F|20-33/Domain: propeptide #status predicted <PRO>
F|34-223/Product: endo-1,4-beta-xylosidase II #status experimental <MAT>
F|45-223/Domain: endo-1,4-beta-xylosidase homology <XYL>
F|71,94/Binding site: carbohydrate (Asn) (covalent) #status predicted
F|110,121/Binding site: substrate (Tyr) #status predicted
F|119,210/Active site: Glu #status predicted

Query Match 55.3%; Score 684.5; DB 2; Length 223;
Best Local Similarity 57.1%; Pred. No. 2e-47;
Matches 128; Conservative 32; Mismatches 61; Indels 3; Gaps 2;

QY 1 MVGFTPALAALATGALAAFPAG--NATELEKQRTTPNSEGMHGGYYSWSDGAQATY 58
Db 1 MVSFSLAGVAAISGTLAARPAEVSVAVEKRTITPCTGYNNGYFYSYNDHGGYTY 60
QY 59 TNLEGGTYEISGDCGNLVGGKGNPGUNARAIHBEVYQPNNGSYLAIVGWTNPLVEY 118
Db 61 TNNGGQFVSVMWSNGNFGVGGKGMQPGTKNVINFSGSYNNGNSYLSVYQMSRNPLEY 120
QY 119 YIVENFGTYDPSGATDLGTYECDSIYRLKRTTRVNAPSIDGTQTPDQYSVRODKRTS 178
Db 119 YIVENFGTYDPSGATDLGTYECDSIYRLKRTTRVNAPSIDGTQTPDQYSVRODKRTS 178

Db 121 YIVENFGTNPSTGATKLGESVSDSVYDIYRTQRVNQPSTIGTATFYQYWSVRNRHRS 180
 Qy 179 GTVQTGCHFDAMARAGLNVGDHYQIVATGEGYSSGARITVA 222
 Db 181 GSVNTANHFMAAQOGLTL-GTMDYQIVAVEGIFSSGSASITVS 223

RESULT 5

857477

endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - *Emeticella nidulans*
 N/Alternate names: xylanase 1
 C/Species: *Emeticella nidulans*, *Aperergillus nidulans*
 C/Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
 C/Accession: S57477
 R/Perez-Gonzalez, J.A.

submitted to the EMBL Data Library, June 1995

A/Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes frc
 A/Reference number: S57469

A/Accession: S57477

A/Molecule type: DNA

A/Residues: 1-225 <PER>

A/Cross-references: UNIPROT:P55332; UNIPARC:UPI0000139073; EMBL:Z49892; NID:9870832; PII
 C/Genetic:

A/Intons: 93/2

C/Function:

A/Description: catalyzes the hydrolysis of 1,4-beta-xyloisidic bonds in xylans

C/Superfamily: xylan degradation
 C/Keyword: glycosidase; hydrolase; polysaccharide degradation

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>

F/48-225/Domain: endo-1,4-beta-xylanase homology <XYL>

F/121,212/Active site: Glu #status predicted

Query Match 55.0%; Score 680.5; DB 1; Length 225;
 Best Local Similarity 56.6%; Pred. No. 4.1e-47;
 Matches 129; Conservative 31; Mismatches 57; Indels 11; Gaps 4;

Qy 1 MNGFTPALAALATGALAPAG-----ATLEKRTTPNSEGHNDGYSSWSDG 53
 Db 1 MVSFKSLVLCALGFAFPPVSGSEDLAREASLLER-STPSGTGNSNGYYSFWTDG 58

Qy 54 AQTATYTLLEGTYEISWGDGNTLVGKGMNPGMLNARAIHFGVYQPNQNSYLAAYGWTN 113
 Db 59 GADVTTNGAGSGSTVQSNVNGNPFVGGKGNPFG-STRTINVGSGNPNBGNGLAVYGMTQN 117

Qy 114 PLVEYYIVENFGTYDPSSGATDGLTVBCDSIYRLGKTRVNAPSIDGTQFPQYMSVRQ 173
 Db 118 PLLEYIVIVESYGTYNPSSGGHGTGVSDDGATVDIYATATYNAPSIEGTATPFGFMSVRQ 177

Qy 174 DKRTSGTVQGFHDAMARAGLNVGDHYQIVATGEGYSSGARITV 221
 Db 178 SKRTGTVTANHFMAAQOGLTL-GTMDYQIVAVEGIFSSGSASITV 224

RESULT 6
 839154
 xylanase 1 - fungus (*Trichoderma reesei*)
 C/Species: *Trichoderma reesei*
 C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
 C/Accession: S39154
 R/Toetooenen, A.; Mach, R.L.; Mesener, R.; Gonzalez, R.; Kalkkinen, N.; Härkki, A.; Kubi
 Biotechnology 10, 1461-1465, 1992
 A/Title: The two major xylanases from *trichoderma reesei*: characterization of both enzym
 A/Reference number: S39154
 A/Accession: S39154
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-222 <TOE>
 A/Cross-references: UNIPROT:P36217; UNIPARC:UPI00000421A9; EMBL:X69573; NID:9396563; PII
 C/Genetic:
 A/Gene: xyn1
 A/Intons: 90/2

C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 F/44-222/Domain: endo-1,4-beta-xylanase homology <XYL>

Query Match 53.9%; Score 667; DB 2; Length 222;
 Best Local Similarity 57.1%; Pred. No. 4.8e-46;
 Matches 128; Conservative 32; Mismatches 60; Indels 4; Gaps 3;

Qy 1 MNGFTPALAALATGALAPAG--NATELEKRTTPNSEGHNDGYSSWSDGAAQATY 58
 Db 1 MVSFTSL-LAASPPSPASCRPAEVESVAVERKQTIQPGYGNNGYFYSTYNDGHGCVTY 59

Qy 59 TNLGGTYEISWGDGNTLVGKGMNPGMLNARAIHFGVYQPNQNSYLAAYGWTNPLVEY 118
 Db 60 TNGPGGQFSVWNSNGNPFVGGKGMQPGTKKVINFGSYVNPNGNSYLSYVGMGRNPLIEY 119

Qy 119 YIVENFGTNPSTGATKLGESVSDSVYDIYRTQRVNQPSTIGTATFYQYWSVRNRHRS 179
 Db 120 YIVENFGTNPSTGATKLGESVSDSVYDIYRTQRVNQPSTIGTATFYQYWSVRNRHRS 179

Qy 179 GTVQTGCHFDAMARAGLNVGDHYQIVATGEGYSSGARITVA 222
 Db 180 GSVNTANHFMAAQOGLTL-GTMDYQIVAVEGIFSSGSASITVS 222

RESULT 7

A44597

endo-1,4-beta-xylanase (EC 3.2.1.8) A - bracket fungus (*Schizophyllum commune*)

N/Alternate names: xylanase A
 C/Species: *Schizophyllum commune*

C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
 C/Accession: A44597; S41411; A05147; S38973

R/Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A/Reference number: A44593
 A/Accession: A44597

A/Molecule type: protein

A/Residues: 1-197 <YAG>
 A/Cross-references: UNIPROT:P35809; UNIPARC:UPI0000034D33

A/Experimental source: strain Delmar ATCC 38548

R/Bray, W.R.; Clarke, A.J.
 Eur. J. Biochem. 219, 821-827, 1994

A/Title: Identification of a glutamate residue at the active site of xylanase A from *Sch*
 A/Reference number: S41411; PMID:9415888; PMID:7906649

A/Accession: S41411

A/Status: preliminary
 A/Molecule type: protein

A/Residues: 83-123 <BRA>
 A/Cross-references: UNIPARC:UPI0000172966

R/Palce, M.G.; Jurasek, L.; Carpenter, M.R.; Smillie, L.B.
 Appl. Environ. Microbiol. 36, 802-808, 1978

A/Reference number: A05147; PMID:79102289; PMID:32833

A/Accession: A05147

A/Molecule type: protein

A/Residues: 1-27 <PAL>
 A/Cross-references: UNIPARC:UPI0000172967

R/Oku, T.; Roy, C.; Watson, D.C.; Makarchuk, W.; Campbell, R.; Yaguchi, M.; Jurasek, L.;
 FBS Lett. 334, 296-300, 1993

A/Title: Amino acid sequence and thermostability of xylanase A from *Schizophyllum commune*
 A/Reference number: S38973; PMID:94063044; PMID:8243636

A/Accession: S38973

A/Molecule type: protein
 A/Residues: 1197 <OKU>

A/Cross-references: UNIPARC:UPI0000034D33
 A/Experimental source: ATCC 38548

C/Function:
 A/Description: catalyzes the hydrolysis of 1,4-beta-xyloisidic bonds in xylans

C/Superfamily: xylan degradation
 C/Keyword: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F/12-197/Domain: endo-1,4-beta-xylanase homology <XYL>

F/87,184/Active site: Glu #status predicted

F/111-160/Disulfide bonds: #status experimental

Query Match 53.6%; Score 663; DB 1; Length 197;
 Best Local Similarity 61.3%; Pred. No. 8.8e-46;
 Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 34 TPNSSEGHNDYYYSWSDGGAQATYTTLEGGTYISM-GDGGNLVGGKGNPGLNAAIH 92
 DB 3 TPSSGTGDDGGYYSWMTDGDADATYQNNGGSYTLTWSGNNGNLVGGKGNPGAAASHSIS 62

QY 93 PEGYOPNGNSYLAIVGCTRNPLVEYIVENFTGYDSSSGATDGTVECDGSIYRLGKTT 152
 DB 63 YSGTYQNGNSYLSVYGTNRSLSLEYIVESYGSYDSSSAASHGSGTTCATYDILSTW 122

QY 153 RVNAPSIDGTQTFDQYWSVRQDKRT-----SGTVQSGCHPDAMARAGLNVGDHYQIVA 207
 DB 123 RVNAPSIDGTQTFQFPMWSVRNPKKAPGSGISGTYDVQCHPDAMKGLGMLGSEHNYQIVA 182

QY 208 TEGYFSSGYARITV 221
 DB 183 TEGYQSSGTYRITV 196

RESULT 8

QY 577 JCT577
 endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
 N/Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
 C/Species: Aspergillus oryzae
 C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
 C/Accession: JCT577; PC7120
 R/Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka, B. *Biotechnol. Biochem.* 64, 2734-2738, 2000
 A/Title: Molecular cloning, overexpression, and purification of a major xylanase from *Aspergillus oryzae*
 A/Reference number: JCT577; MUID: 21077500; PMID: 11210150
 A/Molecule type: DNA
 A/Accession: JCT577
 A/Residues: 1-232 <KTM>
 A/Cross-references: UNIPROT:Q9HEP4; UNIPARC:UPI0000069976; DDBJ:AB044941
 A/Experimental source: strain KEN616
 A/Accession: PC7120
 A/Molecule type: protein
 A/Residues: 45-64 <KIT>
 A/Cross-references: UNIPARC:UPI0000175A84
 C/Comment: This enzyme has strong similarity to other fungal family 11 endoxylanases, de
 C/Genetics:
 A/Gene: xynG2
 A/Intons: 100/2
 C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C/Keywords: glycosidase; hydrolase

Query Match 53.2%; Score 659; DB 2; Length 232;
 Best Local Similarity 54.9%; Pred. No. 2.2e-45;
 Matches 128; Conservative 30; Mismatches 61; Indels 14; Gaps 4;

QY 1 MVGTPLVALAALATGALAP-----AGNATELEK--RQTTPSEGMHGGYYSW 48
 DB 1 MVSPSSILACSAIIGALATPIELADHPNPAFETAENDLVGSGTSTYNNGYYSF 60

QY 49 WSDGGAQATYTNLEGGTYEISWGDGNLVGGKGNPGLNAAIHPEGYOPNGNSYLAIV 108
 DB 61 WTDGGQVTTYTNNGSGSYVQMSNVGNVGGKGNP--SSRALITYSGSFNPSGNYLAVY 119

QY 109 GMTNPLVEYIVENFTGYDSSSGATDGTVECDGSIYRLGKTRVNAPSIDGTQTFDQY 168
 DB 120 GMTDPLEYIVESYGTNRSLSLEYIVESYGSYDSSSAASHGSGTTCATYDILSTW 179

QY 169 WSVRQDKRTSGTVQTFDQYWSVRQDKRT-----SGTVQSGCHPDAMARAGLNVGDHYQIVA 221
 DB 180 WSVRTSKRVGGTYVTGNHFNMAKYGTLT--GTHNYQIVATGEGYSSGSSAIVT 231

RESULT 9

QY 57469 S57469
 endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emeritella nidulans
 N/Alternate names: xylanase 2

C/Species: Emeritella nidulans, Aspergillus nidulans
 C/Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
 C/Accession: S57469
 R/Perez-Gonzalez, J.A.
 submitted to the EMBL Data Library, June 1995
 A/Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes from
 A/Reference number: S57469
 A/Accession: S57469
 A/Molecule type: DNA
 A/Residues: 1-221 <PER>
 A/Cross-references: UNIPROT:P55333; UNIPARC:UPI0000139075; EMBL:Z49893; NID:G870834; PID
 A/Intons: 89/3
 C/Function:
 A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 A/Pathway: xylan degradation
 C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/19-221/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
 F/44-221/Domain: endo-1,4-beta-xylanase homology <XYL>
 F/117,208/Active site: Glu #status predicted

Query Match 51.5%; Score 637.5; DB 1; Length 221;
 Best Local Similarity 54.0%; Pred. No. 1.1e-43;
 Matches 122; Conservative 36; Mismatches 59; Indels 9; Gaps 4;

QY 1 MVGTPLVALAALATGALAPAGNATELEK-----QTPNSEGMHGGYYSWSDGGAQA 56
 DB 1 MVSPSSILACSAVLT--ANAPSDDGSIARSLSEKSTPSTGSGYISFTDGGDV 57

QY 57 TYTNLEGGTYEISWGDGNLVGGKGNPGLNAAIHPEGYOPNGNSYLAIVGCTRNPLV 116
 DB 58 TYTNNGDGSYTVEMTKVGNVGGKGNP--SGQTSYSGSFIRSGNYLSVYGTQNPPLI 116

QY 117 EYIVENFTGYDSSSGATDGTVECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKR 176
 DB 117 EYIVESYGDYNPGRATGTHGTLSDSTDIYATTEANPSLEGATFTQFWSVRQSKR 176

QY 177 TSGTVQSGCHPDAMARAGLNVGDHYQIVATGEGYFSSGYARITVA 222
 DB 177 TSGSVTTQNHFDMSQLGMLT--GTHNYQIVAVEGYSSGSSASITVS 221

RESULT 10

QY 44593 A44593
 endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (*Trichoderma harzianum*) (strain
 N/Alternate names: Xylanase
 C/Species: *Trichoderma harzianum*
 C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
 C/Accession: A44593
 R/Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994
 A/Reference number: A44593
 A/Accession: A44593
 A/Molecule type: protein
 A/Residues: 1-190 <YAG>
 A/Cross-references: UNIPARC:UPI00000493CB
 A/Experimental source: strain E58
 R/Campbell, R.L.; Rose, D.R.
 submitted to the Brookhaven Protein Data Bank, June 1994
 A/Reference number: A52868; PDB:1XND
 A/Function: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, 'A' 48-190

A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 A/Pathway: xylan degradation
 C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation
 F/1-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F/186,177/Active site: Glu #status experimental

Query Match 51.4%; Score 636.5; DB 1; Length 190;
 Best Local Similarity 60.7%; Pred. No. 1.1e-43;

Matches 116; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

Qy 32 QTTNSGMDHGYYSWMDGGAQATYTNLEGGTYEISWMDGGLVGGKGNPGLNRAI 91
Db 1 QTIPTGCTISNGYIYSTYNDHAGVTTNNGGGSTVWMSNGFVGKQPGTKNVI 60

Qy 92 HFEGVQPNNGNSYLAIVYGMTNPLVEYIYVENFGTYDPSGATDLGTYECDGSIYRLGKT 151
Db 61 NFSGTYPNNGNSYLSIVYGMSRNPLEYIYVENFGTYNPSTGATLGEVTSIDGSIYDIYRT 120

Qy 152 TRVNAPEIDGTQTFDQVYSVRQDKRTSGTVQTCGFDPAMAPAGLVNNDHYQIVATEGY 211
Db 121 QRVNQPSTIGTATFTFYQVYSVRNRHSSGVSNTANHFMAHSHGLTL-GTMDYQIVAAVEGY 179

Qy 212 FSSGVARITVA 222
Db 180 FSSGSASITVS 190

RESULT 11
A44595
endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (protease-sensitive) - fungus (Trichoderma viride)
N/Alternate names: xylanase IIB
C/Species: Trichoderma viride
C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: A44595
R/Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A/Reference number: A44593
A/Accession: A44595
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-190 <YAG>
A/Cross-references: UNIPROT:Q7M520, UNIPARC:UPI0000172968
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylanidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/12-190/Domain: endo-1,4-beta-xylanase homology <XVL>
F/86,177/Active site: Glu #status predicted
F/126-127/cleavage site: Pro-Ser (unidentified proteinase) #status predicted
F/129-130/cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 51.4%; Score 636.5; DB 1; Length 190;
Best Local Similarity 60.2%; Pred. No. 1.1e-43;
Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;

Qy 32 QTTNSGMDHGYYSWMDGGAQATYTNLEGGTYEISWMDGGLVGGKGNPGLNRAI 91
Db 1 QTIPTGCTISNGYIYSTYNDHAGVTTNNGGGSTVWMSNGFVGKQPGTKNVI 60

Qy 92 HFEGVQPNNGNSYLAIVYGMTNPLVEYIYVENFGTYDPSGATDLGTYECDGSIYRLGKT 151
Db 61 NFSGTYPNNGNSYLSIVYGMSRNPLEYIYVENFGTYNPSTGATLGEVTSIDGSIYDIYRT 120

Qy 152 TRVNAPEIDGTQTFDQVYSVRQDKRTSGTVQTCGFDPAMAPAGLVNNDHYQIVATEGY 211
Db 121 QRVNQPSTIGTATFTFYQVYSVRNRHSSGVSNTANHFMAHSHGLTL-GTMDYQIVAAVEGY 179

Qy 212 FSSGVARITVA 222
Db 180 FSSGSASITVS 190

RESULT 12
A44594
endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
N/Alternate names: xylanase IIA
C/Species: Trichoderma viride
C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: A44594
R/Yaguchi, M.

submitted to the Protein Sequence Database, March 1994
A/Reference number: A44593
A/Accession: A44594
A/Molecule type: protein
A/Residues: 1-190 <YAG>
A/Cross-references: UNIPROT:Q7M519, UNIPARC:UPI0000034D34
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylanidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/12-190/Domain: endo-1,4-beta-xylanase homology <XVL>
F/77,88/Binding site: substrate (Tyr) #status predicted
F/86,177/Active site: Glu #status predicted

Query Match 51.3%; Score 634.5; DB 1; Length 190;
Best Local Similarity 60.2%; Pred. No. 1.6e-43;
Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;

Qy 32 QTTNSGMDHGYYSWMDGGAQATYTNLEGGTYEISWMDGGLVGGKGNPGLNRAI 91
Db 1 QTIPTGCTISNGYIYSTYNDHAGVTTNNGGGSTVWMSNGFVGKQPGTKNVI 60

Qy 92 HFEGVQPNNGNSYLAIVYGMTNPLVEYIYVENFGTYDPSGATDLGTYECDGSIYRLGKT 151
Db 61 NFSGTYPNNGNSYLSIVYGMSRNPLEYIYVENFGTYNPSTGATLGEVTSIDGSIYDIYRT 120

Qy 152 TRVNAPEIDGTQTFDQVYSVRQDKRTSGTVQTCGFDPAMAPAGLVNNDHYQIVATEGY 211
Db 121 QRVNQPSTIGTATFTFYQVYSVRNRHSSGVSNTANHFMAHSHGLTL-GTMDYQIVAAVEGY 179

Qy 212 FSSGVARITVA 222
Db 180 FSSGSASITVS 190

RESULT 13
JC7307
endo-1,4-beta-xylanase (EC 3.2.1.8) - Penicillium sp.
N/Alternate names: endo-1,3-beta-xylanase; xylanase
C/Species: Penicillium sp.
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
R/Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, K.; Ohmura, Biochem. Biotechnol. Biochem. 64, 1230-1237, 2000
A/Title: Purification, characterization, and molecular cloning of acidophilic xylanase f.
A/Reference number: JC7307
A/Accession: JC7307
A/Molecule type: DNA
A/Residues: 1-221 <KIM>
A/Cross-references: UNIPROT:Q9U0Q2, UNIPARC:UPI00000421AD, DDBJ:AB035540
A/Accession: PC7086
A/Molecule type: protein
A/Residues: 32-51 <K12>
A/Cross-references: UNIPARC:UPI0000175A85
C/Genetics:
A/Gene: xynA
A/Intons: 89/2
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycoprotein; glycosidase; hydrolase

Query Match 48.4%; Score 599.5; DB 2; Length 221;
Best Local Similarity 51.1%; Pred. No. 1.1e-40;
Matches 114; Conservative 41; Mismatches 65; Indels 3; Gaps 3;

Qy 1 MVEGTPVALAALATGALAPFAGNATELEKROTPNSE-GMHDGYYSWMDGGAQATYT 59
Db 1 MKSFIALTLASVAVTGMALPBGYHKKRQRTITTSQGTNNGYISFPTNGGATQYT 60

Qy 60 NLEGGTYEISWMDGGLVGGKGNPGLNRAI HFEGVQPNNGNSYLAIVYGMTNPLVEYI 119
Db 61 NGAAGEYSVTWENCDFPTSGKMGSTG-SARDITFEGFTFSGNAYLAIVYGMTISPLVEYI 119

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 14:49:37 ; Search time 227.148 Seconds

(without alignments)
698.857 Million cell updates/sec

Title: US-09-467-368-2
Perfect score: 1238
Sequence: 1 MVGFTVALALATGALAF.....VATEGVSSGVARITVADVG 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------|-----------------------|
| 1 | 1238 | 100.0 | 225 | 1 XYN2_THELA | Q43097 thermomyces |
| 2 | 965 | 77.9 | 194 | 1 XYN2_PABVA | P81536 paecilomyces |
| 3 | 821.5 | 66.4 | 227 | 2 Q9UVZ3_9PLEO | Q9UVZ3 setosphaeria |
| 4 | 806.5 | 65.1 | 221 | 1 XYN1_COCCA | Q06562 cochlidiobolus |
| 5 | 785 | 63.4 | 235 | 2 Q9CIR2_FUSOX | Q9CIR2 fusarium ox |
| 6 | 775.5 | 62.6 | 227 | 2 Q00263_9PEZI | Q00263 ascochyta p |
| 7 | 728 | 58.8 | 231 | 2 Q92245_MAGGR | Q92245 magnaporthe |
| 8 | 716.5 | 57.9 | 231 | 2 Q13447_COCSA | Q13447 cochlidiobolus |
| 9 | 711 | 57.4 | 204 | 2 Q518A1_MAGGR | Q518A1 magnaporthe |
| 10 | 710.5 | 56.7 | 231 | 2 Q70728_9PLEO | Q70728 setosphaeria |
| 11 | 701.5 | 55.9 | 227 | 2 Q00350_COCCA | Q00350 cochlidiobolus |
| 12 | 692.5 | 55.9 | 227 | 2 Q9HGB1_HUMGT | Q9HGB1 humicola gr |
| 13 | 691.5 | 55.9 | 219 | 2 Q12579_9PEZI | Q12579 chaetomium |
| 14 | 689.5 | 55.7 | 227 | 1 XYN1_HUMIN | P55334 humicola in |
| 15 | 689 | 55.7 | 241 | 2 Q12580_9PEZI | Q12580 chaetomium |
| 16 | 685.5 | 55.4 | 235 | 2 Q766V1_9ASCO | Q766V1 ascochyta |
| 17 | 685 | 55.3 | 220 | 2 Q7SDQ1_NEUCR | Q7SDQ1 neurospora |
| 18 | 684.5 | 55.3 | 223 | 2 Q02244_TIRRE | Q02244 trichoderma |
| 19 | 684 | 55.3 | 223 | 2 Q871E8_NEUCR | Q871E8 neurospora |
| 20 | 681.5 | 55.0 | 221 | 2 Q4WLV2_ASPTU | Q4WLV2 aspergillus |
| 21 | 681 | 55.0 | 228 | 2 Q4WGI1_ASPTU | Q4WGI1 aspergillus |
| 22 | 680.5 | 55.0 | 223 | 2 Q728Q3_TRIVI | Q728Q3 trichoderma |
| 23 | 680.5 | 55.0 | 225 | 1 XYN2_EMENT | P55332 emericella |
| 24 | 680.5 | 55.0 | 225 | 2 Q5B767_EMENT | Q5B767 aspergillus |
| 25 | 678.5 | 54.8 | 261 | 2 Q8J1V6_9PEZI | Q8J1V6 chaetomium |
| 26 | 676.5 | 54.6 | 231 | 2 Q9CIR1_FUSOX | Q9CIR1 fusarium ox |
| 27 | 672.5 | 54.3 | 231 | 2 Q4HYK9_GIBZE | Q4HYK9 gibberella |
| 28 | 672.5 | 54.3 | 231 | 2 Q7ZAS7_GIBZE | Q7ZAS7 gibberella |
| 29 | 672.5 | 54.3 | 267 | 2 Q6UN40_9PEZI | Q6UN40 chaetomium |
| 30 | 671.5 | 54.2 | 223 | 2 Q99015_TIRRE | Q99015 trichoderma |
| 31 | 670 | 54.1 | 220 | 2 Q8J0T4_9HYPO | Q8J0T4 trichoderma |

ALIGNMENTS

| RESULT 1 | ID | XYNA_THELA | STANDARD; | PRT; | 225 AA. |
|----------|--|------------|-----------|------|----------------------|
| AC | Q43097; | | | | |
| DT | 15-DEC-1998 (Rel. 37, Created) | | | | |
| DT | 15-DEC-1998 (Rel. 37, Last sequence update) | | | | |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | | | |
| DE | Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan xylanohydrolase). | | | | |
| GN | Name=XYNA; | | | | |
| OS | Thermomyces lanuginosus (Humicola lanuginosa). | | | | |
| OC | Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces. | | | | |
| OX | NCBI_TaxID=5541; | | | | |
| RN | [1] | | | | |
| RP | NOTBLOTED SEQUENCE. | | | | |
| RC | STRAIN=DSM 5826 / Tsiklinsky; | | | | |
| RA | MDLLINE=97033440; PubMed=8879171; DOI=10.1016/0168-1656(96)01516-7; | | | | |
| RT | Schlaecher A., Holzmann K., Hayn W., Steiner W., Schwab H.; | | | | |
| RT | "Cloning and characterization of the gene for the thermostable xylanase Xyna from Thermomyces lanuginosus."; | | | | |
| RL | J. Biotechnol. 49:211-218(1996). | | | | |
| RN | [2] | | | | |
| RP | X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS). | | | | |
| RC | STRAIN=DSM 5826 / Tsiklinsky; | | | | |
| RX | MDLLINE=98426042; PubMed=9753433; DOI=10.1021/bi19808641; | | | | |
| RA | Gruber K., Klintschar G., Hayn W., Schlaecher A., Steiner W.; | | | | |
| RA | Kratky C.; | | | | |
| RT | "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution X-ray structure and modeling studies."; | | | | |
| RL | Biochemistry 37:13475-13485(1998). | | | | |
| CC | -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans. | | | | |
| CC | -1- BIOPHYSICOCHEMICAL PROPERTIES: Thermolabile; | | | | |
| CC | Temperature dependence: | | | | |
| CC | -1- PATHWAY: Xylan degradation. | | | | |
| CC | -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G) family. | | | | |
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| DR | EMBL; U53436; AAB94633.1; -; Genomic DNA. | | | | P36217 trichoderma |
| DR | PDB; 1YNA; X-ray; @32-225. | | | | P35809 schizomyli |
| DR | InterPro; IPR001137; Glyco_hydro_11. | | | | 0811V5 chaetomium |
| DR | Pfam; PF00457; Glyco_hydro_11; 1. | | | | P87037 aspergillus |
| DR | PRINTS; PR00911; GHYDRASB11. | | | | P55335 magnaporthe |
| DR | PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1. | | | | Q419N4 aspergillus |
| DR | PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1. | | | | Q419N4 aspergillus |
| DR | 3D-structure; Glycosylase; Hydrolase; Pyridinolone carboxylic acid; | | | | Q5nd21 gibberella |
| KW | Signal; Xylan degradation. | | | | Q5q475 aspergillus |
| | | | | | Q9hey9 phanerochaete |
| | | | | | Q9hez0 phanerochaete |
| | | | | | P55333 emericella |
| | | | | | Q7m520 trichoderma |

FT SIGNAL 1 31
FT CHAIN 32 225
FT ACT_SITE 117 117
FT ACT_SITE 209 209
FT MOD_RES 32 185
FT DISULFID 141 185
FT STRAND 33 33
FT STRAND 37 41
FT TURN 42 43
FT STRAND 44 50
FT STRAND 56 60
FT TURN 63 64
FT STRAND 65 70
FT STRAND 82 82
FT STRAND 90 100
FT STRAND 103 112
FT TURN 113 115
FT TURN 116 124
FT TURN 129 132
FT STRAND 134 141
FT TURN 142 143
FT STRAND 144 158
FT TURN 159 160
FT STRAND 161 172
FT STRAND 179 182
FT HELIX 183 192
FT TURN 193 194
FT STRAND 200 211
FT STRAND 214 223
SQ SEQUENCE 225 AA; 24356 MW; FAA79A914C5C676C CRC64;

Query Match 100.0%; Score 1238; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-96;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGFTPALAALAAATGALAPAGNATELEKROTPNSBGMDGYYSWMSDGAQATYTN 60
DB 1 MCGFTPALAALAAATGALAPAGNATELEKROTPNSBGMDGYYSWMSDGAQATYTN 60
QY 61 LEGGTYSISWGDGNLVGKGMNPGINARATHEGTYVOPNNSYLAVYGMTRNPLVEYI 120
DB 61 LEGGTYSISWGDGNLVGKGMNPGINARATHEGTYVOPNNSYLAVYGMTRNPLVEYI 120
QY 121 VENEGTIDPSSGATDLGTVECDGSIYRLGKTRVNAPSIDGTQTFDQYWSYRQDKTSGT 180
DB 121 VENEGTIDPSSGATDLGTVECDGSIYRLGKTRVNAPSIDGTQTFDQYWSYRQDKTSGT 180
QY 181 VOTGCHFDAMARAGINVGHDHYQIVATGTFSSGYARITVADV 225
DB 181 VOTGCHFDAMARAGINVGHDHYQIVATGTFSSGYARITVADV 225

RESULT 2
XVNA_PAEVA STANDARD; PRT; 194 AA.
ID XVNA_PAEVA
AC PA1536;
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
DE xylanohydrolase) (PYX).
OS Paecilomyces variotii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.
CN NCBI_TaxID=45996;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (1.59 ANGSTROMS), AND PROTEIN SEQUENCE OF 50-58
RP AND 123-128.
RC STRAIN=Bainier;
RX MEDLINE=2009955; PubMed=10623548; DOI=10.1006/jmbi.1999.3348;
RA Kumar P.R., Bswaramoorthy S., Vilhavyachai P.J., Vismawitra M.A.;
RT "The tertiary structure at 1.59 A resolution and the proposed amino
RT acid sequence of a family-11 xylanase from the thermophilic fungus

RT Paecilomyces variotii bainier.";
RL J. Mol. Biol. 295:581-593 (2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
CC Temperature dependence:
CC Thermostable;
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PDB; 1PVX; X-ray; A=1.194.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR 3D-structure; Acetylation; Direct protein sequencing; Glycosidase;
KW Hydrolyase; Xylan degradation.
FT ACT_SITE 86 86 Nucleophile (By similarity).
FT ACT_SITE 178 178 Proton donor (By similarity).
FT MOD_RES 1 1 N-acetylglutamine.
FT DISULFID 110 154
SQ SEQUENCE 194 AA; 20947 MW; 1D5C50AA4F6EDB90 CRC64;

Query Match 77.9%; Score 965; DB 1; Length 194;
Best Local Similarity 87.6%; Pred. No. 3.8e-73;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 33 TTNSSEGMHGGTYYSWMSDGAQATYTNLEGTYEISWEGCNLVGKGMNPGINARAIIH 92
DB 2 TTNSSEGMHGGTYYSWMSDGAQATYTNNSGGTYEISWEGCNLVGKGMNPGINARAIIH 61
QY 93 FEGYVOPNNSYLAVYGMTRNPLVEYIYVENFGTYDPPSSGATDLGTVECDGSIYRLGKT 152
DB 62 FTYGTYQNGNSYLSVYGMTRNPLVEYIYVENFGSSNPSSTDLGTYSCGISTYTLQOST 121
QY 153 RVNAPSIDGTQTFDQYWSYRQDKTSGTQVGTGCHFDAMARAGINVGHDHYQIVATGTF 212
DB 122 RVNAPSIDGTQTFDQYWSYRQDKTSGTQVGTGCHFDAMARAGINVGHDHYQIVATGTF 181
QY 213 SSGYARITVADV 225
DB 182 SSGYARITVADV 194

RESULT 3
Q9UVZ3_9PLEO PRELIMINARY; PRT; 227 AA.
ID Q9UVZ3_9PLEO
AC Q9UVZ3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Xylanase precursor.
GN Name=Xyl1;
OS Setosphaeria turcica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Setosphaeria.
CN NCBI_TaxID=93612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=H2;
RA Degefu Y., Paulin L., Lubbeck P.S.;
RT "Cloning, sequencing and expression of a xylanase gene from the maize
RT pathogen Helminthosporium turcicum Pass.";
RL Eur. J. Plant Pathol. 107:457-465 (2001).
DR EMBL; AJ238895; CAB52417.1; -; Genomic_DNA.

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DR HSBP; O43097; 1YNA.
DR SMR; O9UV23; 37-224.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0005493; P:Xylan catabolism; IEA.
DR InterPro; IPR01137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Signal; xylan degradation.
DR Signal; xylan degradation.
DR SIGNAL 19 Potential.
FT CHAIN 20 xylanase.
SQ SEQUENCE 227 AA; 24123 MW; BA86FC075EE5306E CRC64;

Query Match 66.4%; Score 821.5; DB 2; Length 227;
Best Local Similarity 67.7%; Pred. No. 5.3e-61;
Matches 153; Conservative 25; Mismatches 41; Indels 7; Gaps 3;

QY 1 MVGFTPALAALATGALAPAGN-----ATELEKROTPNSEGMHGDGYYYSWMSDGAQ 55
DB 1 MVSFTSIITAAVAATGALAPATDAAAPSDLVAKOSTPNEGTHNGCFYSWMSDGAAR 60
QY 56 ATYNLEGGTYEISMGDGNLVGKGMPGLNAPAIHEGVYQPNGNSYLAAYGWTNRNPL 115
DB 61 ATYNGAGGSYSVSGTGNLVGKGMPG-TARTITVSGQYNPNNSYLAAYGWTNRNPL 119
QY 116 VEYIVVERFCTYDSSGATDGTVECDGSIYRLGKTRIVNAPSIDGTOTFQOYVSVRQDK 175
DB 120 VEYIVVERFCTYDSSGATDGTVECDGSIYRLGKTRIVNAPSIDGTOTFQOYVSVRQDK 179
QY 176 RTSGTVOTGCHFDAMARAGLVNVDGPHYQIVATGEGYFSSGYARITV 221
DB 180 RSSGSVMKTHFDAMASKGMNL-GSHYQIVATGEGYFSSGSASITV 224

RESULT 4
XYN1 COCCA STANDARD; PRT; 221 AA.
ID XYN1 COCCA STANDARD; PRT; 221 AA.
AC Q06562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I) (1,4-
DE beta-D-xylan xylohydrolase 1).
GN Name=XYL1;
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Race 1 / Isolate SB111;
RX MEDLINE=94003417; PubMed=8400376;
RA Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT "Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase
RT gene from the maize pathogen Cochliobolus carbonum.";
RL Mol. Plant Microbe Interact. 6:467-473(1993).
RN [2]
RP PARTIAL PROTEIN SEQUENCE.
RA Holden F.R., Walton J.D.;
RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum.";
RL Physiol. Mol. Plant Pathol. 40:39-47(1992).
CC -1- FUNCTION: Major xylan-degrading enzyme. Contributes to the
CC hydrolysis of arabinoxylan, the major component of maize cell-
CC wall.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.

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CC -----
DR EMBL; L13596; AAA33024.1; -; Genomic_DNA.
DR HSBP; O43097; 1YNA.
DR SMR; O06562; 31-218.
DR InterPro; IPR01137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Direct protein sequencing; Glycosidase; Hydrolyase; Signal;
KM Xylan degradation.
KM SIGNAL 30 Potential.
FT CHAIN 31 221 Endo-1,4-beta-xylanase I.
FT ACT_SITE 115 115 Nucleophile (By similarity).
FT ACT_SITE 206 206 Proton donor (By similarity).
FT CONFLICT 81 81 W -> I (in Ref. 2).
FT CONFLICT 107 107 G -> A (in Ref. 2).
FT CONFLICT 131 131 S -> W (in Ref. 2).
SQ SEQUENCE 221 AA; 23728 MW; 59DBD983FC5B08C CRC64;

Query Match 65.1%; Score 806.5; DB 1; Length 221;
Best Local Similarity 67.9%; Pred. No. 9.3e-60;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY 1 MVGFTPALAALATGALAPAGNATELEKROTPNSEGMHGDGYYYSWMSDGAQATYTN 60
DB 1 MVSFTSIITAAVAATGALAPATDVS-LVARQNTPNBEGTHNGCFYSWMSDGAARITYN 59
QY 61 LGGTYEISMGDGNLVGKGMPGLNAPAIHEGVYQPNGNSYLAAYGWTNRNPLVEYYI 120
DB 60 GAGGSYSVSGTGNLVGKGMPG-TARTITVSGYTNPNNSYLAAYGWTNRNPLVEYYV 118
QY 121 VENFGTYDPSGAGDGTVECDGSIYRLGKTRIVNAPSIDGTOTFQOYVSVRQDKRISGT 180
DB 119 VENFGTYDPSGAGDGTVECDGSIYRLGKTRIVNAPSIDGTOTFQOYVSVRQDKRISGS 178
QY 181 VOTGCHFDAMARAGLVNVDGPHYQIVATGEGYFSSGYARITV 221
DB 179 VMKTHFDAMASKGMNL-GSHYQIVATGEGYFSGNNAQITV 218

RESULT 5
O9CIR2 FUSOX PRELIMINARY; PRT; 295 AA.
ID O9CIR2 FUSOX PRELIMINARY; PRT; 295 AA.
AC O9CIR2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase 5 protein.
GN Name=XYL5;
OS Fusarium oxysporum f. sp. lycopersici.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
OC Fusarium oxysporum complex.
OX NCBI_TaxID=59765;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21654148; PubMed=11795847; DOI=10.1007/s00294-001-0260-0;
RA Gomez-Gomez E., Roncero M.I.G., Di Pietro A., Hera C.;
RT "Molecular characterization of a novel endo-beta-1,4-xylanase gene
RT from the vascular wilt fungus Fusarium oxysporum.";
RL Curr. Genet. 40:268-275 (2001).
DR EMBL; AF246830; AKK27974.1; -; Genomic_DNA.
DR HSBP; O43097; 1YNA.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0005493; P:Xylan catabolism; IEA.

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DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation.
KW SEQUENCE 295 AA; 30858 MW; CA441056DCD3C104 CRC64;

Query Match
Best Local Similarity 63.4%; Score 785; DB 2; Length 295;
Matches 146; Conservative 30; Mismatches 45; Indels 4; Gaps 3;

QY 1 MGVETPVALLAALATGALAPPA--GNATELEKQRTTNSGMDHGYYSWMSDGAQATY 58
DB 1 MVEFTSVFAGLSVAGSLAAPSKEGLPSKITKRAQTNSGTTNNGFYYSWMSDGAQATY 60
QY 59 TNLBGGTIEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNQNSYLAIVGTRNPLVEY 118
DB 61 TNGEGGYSWEMKXGNNVGGKGPS-KARTISYESEYKPNQNSYLSYVGWTRNPLVEY 119
QY 119 YIVENFGTYPSSGATDLGTVCECDGSYRLGKTRVNAPSIDGTQTFDQYWSVRQDRTS 178
DB 120 YIVESFTYPPSSGATKKGIVTADGSTYDIFETTRTAPSIDGTQTFDQYWSVRQDRTS 179
QY 179 GTVQTGCHPDAMARAGLVNGDHYQIVATEGYFSSGVARITVAD 223
DB 180 GSVDTGLHFDAMWAKGMKL-GTHDYQIVATEGYFSSGSHMTVSE 223

RESULT 6
Q00263_9PEZ1 PRELIMINARY; PRT; 227 AA.
ID Q00263_9PEZ1 PRELIMINARY; PRT; 227 AA.

AC Q00263;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1,4-beta-xylanase precursor.
OS Ascochyta pisi.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC mitosporic Pezizomycotina; Ascochyta.
OX NCBI_TaxID=47971;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lubbeck P.S., Paulin L., Degefu Y., Lubbeck M., Collinge D.;
RT "Molecular cloning and DNA sequencing of a xylanase gene from the
RT phytopathogenic fungus Ascochyta pisi lib. ";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z68891; CA93120.1; -; Genomic_DNA.
DR HSSP; O43097; 1YNA.

DR SMR; Q00263; 39-224.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro: IPR01137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal; xylan degradation.
FT SIGNAL 1 19 Potential.
FT CHAIN 1 227 Potential.
SQ SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0F CRC64;

Query Match
Best Local Similarity 62.6%; Score 775.5; DB 2; Length 227;
Matches 148; Conservative 25; Mismatches 46; Indels 7; Gaps 4;

QY 1 MGVETPVALLAALATGALAPPA--GNATELEKQRTTNSGMDHGYYSWMSDGAQ 55
DB 1 MVEFTSVFAGLSVAGSLAAPSKEGLPSKITKRAQTNSGTTNNGFYYSWMSDGAQ 60
QY 56 ATYTNBGGTIEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNQNSYLAIVGTRNPL 115

DB 61 ATYTNBGGTIEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNQNSYLAIVGTRNPL 119
QY 116 VEXYIVENFGTYPSSGATDLGTVCECDGSYRLGKTRVNAPSIDGTQTFDQYWSVRQD 175
DB 120 IEXYIVENFGTYPSSGATKKGIVTADGSTYDIFETTRTAPSIDGTQTFDQYWSVRQD 179
QY 176 RTSGTVQTGCHPDAMARAGLVNGDHYQIVATEGYFSSGVARITV 221
DB 180 RSSGSYVMKTHFDAMWAKGMKL-GTHDYQIVATEGYFSSGSAQITV 224

RESULT 7
Q92245_MAGGR PRELIMINARY; PRT; 231 AA.
ID Q92245_MAGGR PRELIMINARY; PRT; 231 AA.

AC Q92245;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-beta-1,4-D-xylanase.
GN Name=Xyl4;
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=148305;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mycelium;
RA Wu S.-C., Darvill A.G., Albersheim P.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY144349; AB06573.2; -; Genomic_DNA.
DR HSSP; O43097; 1YNA.

DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro: IPR01137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation.
SQ SEQUENCE 231 AA; 25305 MW; CECF0249D5A795B CRC64;

Query Match
Best Local Similarity 58.8%; Score 728; DB 2; Length 231;
Matches 137; Conservative 29; Mismatches 53; Indels 12; Gaps 4;

QY 1 MGVETPVALLAALATGALAPPA-----NATELEKQRTTNSGMDHGYYSWMS 50
DB 1 MVEFTTVLVAATLAAVNAFVPSIDEMREIYKSRDLHARGGTSSGTGHDGFYSMT 60
QY 51 DGAQATYTNLEGGTIEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNQNSYLAIVGW 110
DB 61 DNGAQATYTNNAGGSYISITSGNGLVGGKGNP-G-SARVITYSANRPNQNSYLSYGW 119
QY 111 TRNPLVEYIVENFGTYPSSGATDLGTVCECDGSYRLGKTRVNAPSIDGTQTFDQYWS 170
DB 120 TRNPLVEYIVENFGTYPSSGASRKGTINVDGATVVAOSTRTNCPISDGTRTFOQYWS 179

QY 171 VRQDKRTSGTVQCHPDAMARAGLVNGDHYQIVATEGYFSSGVARITV 221
DB 180 VRQDKRTSGTVQCHPDAMARAGLVNGDHYQIVATEGYFSSGSAQITV 229

RESULT 8
O13447_COCOA PRELIMINARY; PRT; 231 AA.
ID O13447_COCOA PRELIMINARY; PRT; 231 AA.

AC O13447;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-1,4-xylanase.
GN Name=Xyl2;
OS Cochliobolus sativus (Bipolaris sorokiniana).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; Cochliobolus.
 OC NCBI_TaxID=45130;
 RN [1]
 RA Nucleotide sequence.
 RA Emsm1 K., Hack E.;
 RT "Characterization of a xylanase gene from Cochliobolus sativus and its
 expression";
 RL Mycol. Res. 105:352-359(2001).
 DR EMBL, AJ004802; CA06151.1; -; Genomic_DNA.
 DR HSBP, Q8U1V6; 1H1A.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0045493; P:xylan catabolism; IEA.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Xylan degradation.
 SQ SEQUENCE 231 AA; 25577 MW; 33366DD1F065A6B CRC64;

Query Match 57.9%; Score 716.5; DB 2; Length 231;
 Best Local Similarity 58.7%; Pred. No. 3.6e-52;
 Matches 135; Conservative 29; Mismatches 55; Indels 11; Gaps 4;

QY 1 MVGTPVALALATGALAP-----AGNATE-LEKRTTNSGMDHYGYWMSD 51
 DB 1 MVSFSLTLAAVATSVLAAPDPPLRERDDNATLLEKRTSSSEYHNGFYSWWTD 60
 QY 52 GGAQATYTNLEGTYEISWGDGNI.VGSGKGNPGI.NARAIHFEVYOPNGSYLAAYGWT 111
 DB 61 GGSQAQYTMGSGSYVYWRMTGNFVGSKGNPG--TGKIVYGGAFNPGNGIYLAAYGWT 119
 QY 112 RNPLVEYIVENFGTYDPSGATDLGVECDGSIYRLKTRVNAVPSIDGTQFDQYWSV 171
 DB 120 RNPLVEYIVESYGTVPSSGAQYKVSFQTDGTYVNAVSTRYNQPSIDGTRTFQYWSV 179
 QY 172 RQDKRTGTGTGCHFDMAAGANVNDHYGVVATREGYSSGYARITV 221
 DB 180 RQDKRGVGSVMQNFHMSRYGLNL-QGHYVQIVATEGYSSGSDIYV 228

RESULT 9
 OS18A1_MAGGR PRELIMINARY; PRT; 204 AA.
 AC OS18A1;
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=M080424.4;
 OS Magnaporthe oryzae 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; Sordariaceae; Magnaportheaceae; Magnaporthe.
 OC NCBI_TaxID=242507;
 RN [1]
 RA Nucleotide sequence.
 RC STRAIN=70-15;
 RA Biren B., Nisbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Archolli H., Ambuster J., Bachantang P., Baldwin J., Barry A.,
 RA Bayul T., Bilschstein B., Bloom T., Blye J., Bogunlavsky L.,
 RA Botovsky K., Bouhgalier B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarota J., Campo K., Chang J., Cheshtang Y., Citroen M.,
 RA Collins A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Fatina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gierke S.,
 RA Guitke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Homan T., Horn A., Houde N., Hughes L., Hulme W., Hubdy E., Iliev I.,

RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyssele M., Karlsson E.,
 RA Kells C., Kieu A., Klinger P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marbella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., McShane T., Meldrum J., Menue L.,
 RA Meierov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Moses J., Mulrain L., Munson G., Naylor J., Nemes C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Notbu C.,
 RA Notbu N., O'donnell P., Oloawo O., O'leary S., Omotsho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunhang P., Pignat B.,
 RA Purcell S., Rachupka T., Ramasamy U., Ramau R., Ray V., Raymond C.,
 RA Ratta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smitov S., Smith C., Souguez C.,
 RA Spencer B., Stalker J., Stange-Chomun N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Testaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vasilev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wymann D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe oryzae";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RA Nucleotide sequence.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RA Nucleotide sequence.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; ALCU01001255; EAA49509.1; -; Genomic_DNA.
 DR InterPro; IPR002453; Beta_tubulin.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
 KM Hypothetical protein.
 SQ SEQUENCE 204 AA; 22624 MW; 2396D83ED2B92260 CRC64;

Query Match 57.4%; Score 711; DB 2; Length 204;
 Best Local Similarity 65.1%; Pred. No. 9.2e-52;
 Matches 127; Conservative 26; Mismatches 40; Indels 2; Gaps 2;

QY 27 ELEKRTTPNSBGMHDGYYSWMSDGAQATYTNLEGTYEISWGDGNI.VGSGKGNPGI 86
 DB 10 DLNARGSTPSTGTHBFTISWMTDNGAQATYTNNAAGSISTISWSGKGNLVGSGKGNPG- 68
 QY 87 NABAIHBEVYOPNGNSYLAAYGATNPLVEYIVENFGTYDPSGATDLGVECDGSIY 146
 DB 69 SANRVYVSANRYRNGNSYLSVYGMTNPLVEYIVENFGTYDPSGASRGTINVDGATY 128
 QY 147 RLGKTRVNAVPSIDGTQFDQYWSVRODKRTSGTGTGCHFDMAAGANVNDHYGYV 206
 DB 129 QVASTRTNQPSTIDGTRTFQYWSVRODKRTSGTGTGCHFDMAAGANVNDHYGYV 187
 QY 207 ATGEYFSSGYARITV 221
 DB 188 ATGEYFSSGSSTYIT 202

RESULT 10
 Q70728_gPLEO

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ID 070728_9PLEO PRELIMINARY; PRT; 231 AA.
AC 070728;
RT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Xylanase precursor.
GN Name=xyl12;
OS Setosphaeria turcica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Setosphaeria.
OX NCBI_TaxId=93612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15016446; DOI=10.1016/j.biochi.2004.01.001;
RA Degeln Y., Lohender K., Paulin L.G.;
RT "Expression patterns and phylogenetic analysis of two xylanase genes
RT (hxy1.1 and hxy1.2) from Helminthosporium turcicum, the cause of
RT leaf blight of maize."
RL Biochimie 86:83-90(2004).
DR EMBL; AJ548879; CAD70174.1; -; Genomic_DNA.
DR HSP; P09850; 1BCX.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Signal; xylan degradation.
FT SIGNAL 19 Potential.
FT CHAIN 1 20 231 xyl12.
SQ SEQUENCE 231 AA; 25611 MW; 440785B52BAF15 CRC64;

Query Match 57.4%; Score 710.5; DB 2; Length 231;
Best Local Similarity 57.4%; Pred. No. 1.2e-51;
Matches 133; Conservative 30; Mismatches 56; Indels 11; Gaps 4;

QY 1 MGFTPVALLAALATGALAPP-----AGNATE-LEKRTTPNSGMDGYYSWMSD 51
ID 09HGE1 HUMGT PRELIMINARY; PRT; 227 AA.
AC 09HGE1;
RT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Beta-1,4-xylanase.
GN Name=xyl2;
OS Humicola grisea var. thermoides.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxId=5528;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF155594; AAG16891.1; -; Genomic_DNA.
DR HSP; O43097; 1YNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation.
FT SIGNAL 227 AA; 25615 MW; 991815AD84EB2939 CRC64;

SQ SEQUENCE 227 AA; 25615 MW; 991815AD84EB2939 CRC64;

Query Match 55.9%; Score 692.5; DB 2; Length 227;
Best Local Similarity 56.6%; Pred. No. 3.7e-50;
Matches 128; Conservative 29; Mismatches 62; Indels 7; Gaps 3;

QY 1 MGFTPVALLAALATGALA-----FPAGNATELEKRTTPNSGMDGYYSWMSD 55

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RT "Cloning, disruption, and expression of two endo-beta 1, 4-xylanase
RT genes, xyl2 and xyl3, from Cochliobolus carbonum.";
RL Appl. Environ. Microbiol. 62:4129-4135(1996).
DR EMBL; U58915; AAC62815.1; -; Genomic_DNA.
DR HSP; O43106; 1H1A.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Signal.
FT SIGNAL 1 41 Potential.
FT CHAIN 1 231 xyl12.
SQ SEQUENCE 231 AA; 25576 MW; 237C3D49C4D0B871 CRC64;

Query Match 56.7%; Score 701.5; DB 2; Length 231;
Best Local Similarity 57.4%; Pred. No. 6.7e-51;
Matches 132; Conservative 31; Mismatches 56; Indels 11; Gaps 4;

QY 1 MGFTPVALLAALATGALAPPAG-----NATE-LEKRTTPNSGMDGYYSWMSD 51
ID 09HGE1 HUMGT PRELIMINARY; PRT; 227 AA.
AC 09HGE1;
RT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Beta-1,4-xylanase.
GN Name=xyl2;
OS Humicola grisea var. thermoides.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxId=5528;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF155594; AAG16891.1; -; Genomic_DNA.
DR HSP; O43097; 1YNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation.
FT SIGNAL 227 AA; 25615 MW; 991815AD84EB2939 CRC64;

SQ SEQUENCE 227 AA; 25615 MW; 991815AD84EB2939 CRC64;

Query Match 55.9%; Score 692.5; DB 2; Length 227;
Best Local Similarity 56.6%; Pred. No. 3.7e-50;
Matches 128; Conservative 29; Mismatches 62; Indels 7; Gaps 3;

QY 1 MGFTPVALLAALATGALA-----FPAGNATELEKRTTPNSGMDGYYSWMSD 55

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Db 1 MWSIKSVLAATAVSSALAAFPDFVRPNRSTALQARQVTPABEGMNGYFSWMSDGGCQ 60
Qy 56 ATYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQYOPNGNSYLAIVGWTNPL 115
Db 61 VQYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQYOPNGNSYLAIVGWTNPL 119
Qy 116 VEYIVENFGTYDPSGATDLGTVBCDGSYRLGKTRTVNAPSIDGTQTFDQYWSVRQDK 175
Db 120 VEYIVESYGTYPNGSOAQYKGTFTYDDQYDIFVSTRYNQPSIDGRTFOQYWSIRKNK 179
Qy 176 RTSGTVQTCGHPDAMARAGLNVNGDHYOIVATEGYFSSGYARITV 221
Db 180 RVGGSVMQNHFNAMQOHGML-GQHYOIVATEGYFSSGSDITV 224

RESULT 13
Q12579_9PEZI PRELIMINARY; PRT; 219 AA.
ID Q12579_9PEZI
AC Q12579_9PEZI
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Endo-beta1,4-xylosidase A (EC 3.2.1.8).
GN Name=CGXA;
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.
OX NCBI_TaxID=47794;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118924; PubMed=8595661; DOI=10.1007/BF00311196;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
RT "Two family G xylosidase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans."
RL Curr. Genet. 29:73-80(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tsukagoshi N.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D49850; BAA08649.1; -; Genomic_DNA.
DR PIR; S71472; S71472.
DR HSP; P36217; IXYO.
DR GO; GO:0031176; F:endo-1,4-beta-xylosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylian catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 219 AA; 23325 MW; 4729299E08FD9FBA CRC64;

Query Match 55.9%; Score 691.5; DB 2; Length 219;
Best Local Similarity 59.1%; Pred. No. 4.3e-50;
Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;
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RESULT 14
XNNI_HUMIN STANDARD; PRT; 227 AA.
ID XNNI_HUMIN
AC P55334; Q12625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylosidase 1 precursor (EC 3.2.1.8) (Xylanase 1) (1,4-
DE beta-D-xylan xylosidase 1).
GN Name=XYL1;
OS Humicola insolens.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxID=34413;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94247364; PubMed=8190078; DOI=10.1007/BF00301060;
RA Dalboege H., Hansen H.P.H.;
RT "A novel method for efficient expression cloning of fungal enzyme
RT genes."
RL Mol. Genet. 243:253-260(1994).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X76047; CA53632.1; -; mRNA.
DR PIR; S43919; S43919.
DR HSP; O43097; IYNA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 227 Endo-1,4-beta-xylosidase 1.
FT ACT_SITE 121 121 Nucleophile (By similarity).
FT ACT_SITE 212 212 Proton donor (By similarity).
SQ SEQUENCE 227 AA; 25601 MW; 5C2FF6ADCFFADAF CRC64;

Query Match 55.7%; Score 689.5; DB 1; Length 227;
Best Local Similarity 55.8%; Pred. No. 6.7e-50;
Matches 126; Conservative 31; Mismatches 62; Indels 7; Gaps 3;
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Qy 1 MWSIKSVLAATAVSSALAAFPDFVRPNRSTALQARQVTPABEGMNGYFSWMSDGGCQ 60
Db 1 MWSIKSVLAATAVSSALAAFPDFVRPNRSTALQARQVTPABEGMNGYFSWMSDGGCQ 60
Qy 56 ATYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQYOPNGNSYLAIVGWTNPL 115
Db 61 VQYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQYOPNGNSYLAIVGWTNPL 119
Qy 116 VEYIVENFGTYDPSGATDLGTVBCDGSYRLGKTRTVNAPSIDGTQTFDQYWSVRQDK 175
Db 120 VEYIVESYGTYPNGSOAQYKGTFTYDDQYDIFVSTRYNQPSIDGRTFOQYWSIRKNK 179
Qy 176 RTSGTVQTCGHPDAMARAGLNVNGDHYOIVATEGYFSSGYARITV 221
Db 180 RVGGSVMQNHFNAMQOHGML-GQHYOIVATEGYFSSGSDITV 224

RESULT 15
Q12580_9PEZI PRELIMINARY; PRT; 241 AA.
ID Q12580_9PEZI
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AC Q12580;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Endo-beta1,4-xylosylase (EC 3.2.1.8).
 GN Name=cgx8;
 OS Chaetomium gracile.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Chaetomaceae; Chaetomium.
 OX NCBI_TaxID=47794;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96118924; PubMed=8595661; DOI=10.1007/BF00313196;
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
 RT "Two family G xylanase genes from Chaetomium gracile and their
 RT expression in Aspergillus nidulans.";
 RL Curr. Genet. 29:73-80(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Tsukagoshi N.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D49851; BA00650.1; -, Genomic_DNA.
 DR PIR; S71473; S71473.
 DR HSSP; Q8J1V6; 1H1A.
 DR SMR; Q12580; 31-220.
 DR GO; GO:0031176; F:endo-1,4-beta-xylosylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 KM Glycosidase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 241 AA; 25564 MW; DCD4B012272F77F CRC64;

Query Match 55.7%; Score 689; DB 2; Length 241;
 Best Local Similarity 59.5%; Pred. No. 7.9e-50;
 Matches 132; Conservative 31; Mismatches 55; Indels 4; Gaps 4;

QY 1 MVGFTPALALATATGALAFAGNATELEKRTTPNSE-GWHDGYYYSWSDGGAQATYT 59
 DB 1 MNFSSIFLAAALAVAVAAAB-GEIPGMHKQTLTSOTGTNNNGYYSFTWDGQNVQYT 59

QY 60 NLEGGTYEISWGDGNI.VGKGWNPGLNARAIHFEGVYQPNGNSYLAIVGWTNPLVEYY 119
 DB 60 NEAGGQYSVTWSGNGWVGKGMNPG-SARTINYTANNPNNGNSYLAIVGWTNPLIEYY 118

QY 120 IVENFGTYDPSSGATDGTVCDCGSYRLGKTRVNAPSIDGTQTPDOYWSVRODKRTSG 179
 DB 119 VVENFGTYNPSYATRLGSLVTTDSCYDIYRTORVNOPISIGTSTFYQFWSVRONKRSYG 178

QY 180 TVOTGCHPDAMARAGLNVNGDHYVQIVATEGYFSSGVARTV 221
 DB 179 SVMMAAHFNMAAAGLQL-GTHDYQIVATEGYSSGSATVNV 219

Search completed: February 10, 2006, 15:01:22
 Job time : 230.148 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using BW model

Run on: February 10, 2006, 15:01:51 ; Search time 38.1265 Seconds
(without alignments)
487.903 Million cell updates/sec

Title: US-09-467-368-2
Perfect score: 1238
Sequence: 1 MVGFTPVALLAALATGALAF.....VATEGYFSSGYARITVADVG 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodaca/1/1aa/6.COMB.pep:*
3: /cgn2_6/ptodaca/1/1aa/H.COMB.pep:*
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5: /cgn2_6/ptodaca/1/1aa/RE.COMB.pep:*
6: /cgn2_6/ptodaca/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1 | 1238 | 100.0 | 225 | 1 US-08-886-765-2 | Sequence 2, Appl1 |
| 2 | 1238 | 100.0 | 225 | 2 US-09-115-660-2 | Sequence 2, Appl1 |
| 3 | 1083 | 87.5 | 194 | 2 US-09-570-8568-24 | Sequence 24, Appl1 |
| 4 | 965 | 77.9 | 194 | 2 US-09-570-8568-23 | Sequence 23, Appl1 |
| 5 | 806.5 | 65.1 | 221 | 2 US-09-570-8568-29 | Sequence 29, Appl1 |
| 6 | 688.5 | 55.6 | 227 | 1 US-08-458-0238-4 | Sequence 4, Appl1 |
| 7 | 684.5 | 55.3 | 223 | 1 US-09-254-733-7 | Sequence 7, Appl1 |
| 8 | 684.5 | 55.3 | 223 | 1 US-08-121-436A-2 | Sequence 2, Appl1 |
| 9 | 678.5 | 54.8 | 261 | 2 US-08-768-373-2 | Sequence 2, Appl1 |
| 10 | 678.5 | 54.8 | 261 | 2 US-09-849-242A-2 | Sequence 2, Appl1 |
| 11 | 663 | 53.6 | 197 | 1 US-08-044-621D-29 | Sequence 29, Appl1 |
| 12 | 663 | 53.6 | 197 | 1 US-08-709-912-9 | Sequence 9, Appl1 |
| 13 | 663 | 53.6 | 197 | 1 US-09-047-370-9 | Sequence 9, Appl1 |
| 14 | 663 | 53.6 | 197 | 1 US-09-570-8568-18 | Sequence 18, Appl1 |
| 15 | 662.5 | 53.5 | 230 | 2 US-08-768-373-4 | Sequence 4, Appl1 |
| 16 | 662.5 | 53.5 | 230 | 2 US-09-849-242A-4 | Sequence 4, Appl1 |
| 17 | 636.5 | 51.4 | 190 | 1 US-08-044-621D-28 | Sequence 28, Appl1 |
| 18 | 636.5 | 51.4 | 190 | 1 US-08-709-912-14 | Sequence 14, Appl1 |
| 19 | 636.5 | 51.4 | 190 | 1 US-09-047-370-14 | Sequence 14, Appl1 |
| 20 | 635.5 | 51.3 | 190 | 1 US-08-044-621D-26 | Sequence 26, Appl1 |
| 21 | 635.5 | 51.3 | 190 | 1 US-08-709-912-16 | Sequence 16, Appl1 |
| 22 | 635.5 | 51.3 | 190 | 1 US-09-047-370-16 | Sequence 16, Appl1 |
| 23 | 634.5 | 51.3 | 190 | 1 US-08-044-621D-27 | Sequence 27, Appl1 |
| 24 | 634.5 | 51.3 | 190 | 2 US-09-570-8568-19 | Sequence 19, Appl1 |
| 25 | 632.5 | 51.1 | 190 | 1 US-08-709-912-17 | Sequence 17, Appl1 |
| 26 | 632.5 | 51.1 | 190 | 1 US-09-047-370-17 | Sequence 17, Appl1 |
| 27 | 632 | 51.1 | 225 | 2 US-09-570-8568-26 | Sequence 26, Appl1 |

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| 28 | 630.5 | 50.9 | 190 | 2 US-09-570-8568-20 | Sequence 20, Appl1 |
| 29 | 630.5 | 50.9 | 190 | 2 US-09-570-8568-22 | Sequence 22, Appl1 |
| 30 | 628 | 50.7 | 225 | 1 US-08-290-979A-8 | Sequence 8, Appl1 |
| 31 | 610.5 | 49.3 | 223 | 2 US-09-462-246-2 | Sequence 2, Appl1 |
| 32 | 577.5 | 48.3 | 226 | 2 US-09-367-891A-2 | Sequence 2, Appl1 |
| 33 | 588.5 | 47.5 | 296 | 1 US-08-507-431-6 | Sequence 6, Appl1 |
| 34 | 588.5 | 47.5 | 296 | 2 US-09-116-622-6 | Sequence 6, Appl1 |
| 35 | 588.5 | 47.5 | 296 | 2 US-09-219-277-6 | Sequence 6, Appl1 |
| 36 | 588.5 | 47.5 | 296 | 2 US-09-599-661-6 | Sequence 6, Appl1 |
| 37 | 587.5 | 47.5 | 335 | 2 US-09-570-8568-15 | Sequence 15, Appl1 |
| 38 | 586.5 | 47.4 | 231 | 1 US-08-902-655A-6 | Sequence 6, Appl1 |
| 39 | 571.5 | 46.2 | 215 | 1 US-08-044-621D-34 | Sequence 34, Appl1 |
| 40 | 568 | 45.9 | 189 | 1 US-08-709-912-13 | Sequence 13, Appl1 |
| 41 | 568 | 45.9 | 189 | 1 US-09-047-370-13 | Sequence 13, Appl1 |
| 42 | 566.5 | 45.8 | 206 | 1 US-08-315-695-19 | Sequence 19, Appl1 |
| 43 | 566 | 45.7 | 344 | 1 US-08-468-812-2 | Sequence 2, Appl1 |
| 44 | 566 | 45.7 | 344 | 2 US-08-590-563-2 | Sequence 2, Appl1 |
| 45 | 566 | 45.7 | 344 | 2 US-09-770-621-2 | Sequence 2, Appl1 |

ALIGNMENTS

```
RESULT 1
US-08-886-765-2
: Sequence 2, Application US/0886765
: Patent No. 5817500
:
: GENERAL INFORMATION:
: APPLICANT: Hansen, Peter Kamp
: APPLICANT: Wagner, Peter
: APPLICANT: Mullertz, Anette
: APPLICANT: Knap, Inge Helmer
: TITLE OF INVENTION: Animal Feed Additives
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESSES:
: ADDRESSER: No. 5817500 No. 5817500disk of No. 5817500th America, Inc.
: STREET: 405 Lexington Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10174
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/886,765
: FILING DATE: 1-JUL-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambitis, Elias J
: REFERENCE/DOCKET NUMBER: 33,728
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 225 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-886-765-2
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Query Match 100.0%; Score 1238; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 7.9e-110;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVGFTPVALLAALATGALAFPAAGNATELEKRTTPNSGCHDGYYSWSDGGAQATYTN 60
DB 1 MVGFTPVALLAALATGALAFPAAGNATELEKRTTPNSGCHDGYYSWSDGGAQATYTN 60
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| | | | |
|----|-----|---|-----|
| QY | 61 | LEBGTAEISMGDSGNLVGKGNPPGIMNAAHFEESVQPNQNSYLAAYGWRNDLVYYI | 120 |
| Db | 61 | LEBGTAEISMGDSGNLVGKGNPPGIMNAAHFEESVQPNQNSYLAAYGWRNDLVYYI | 120 |
| QY | 121 | VENRGTYDPSSGATDGLTVECDOSYIRLGLKTRVNAPSIDGTQFPDQWSVRQDKRTSGT | 180 |
| Db | 121 | VENRGTYDPSSGATDGLTVECDOSYIRLGLKTRVNAPSIDGTQFPDQWSVRQDKRTSGT | 180 |
| QY | 181 | VQTCHEFDAMARAGLVNNGDHYQYLVALEGVSSGABRTVAADVG | 225 |
| Db | 181 | VQTCHEFDAMARAGLVNNGDHYQYLVALEGVSSGABRTVAADVG | 225 |

RESULT 2

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US-09-115-660-2
Sequence 2, Application US/09115660
Patent No. 6245546
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mulietz, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No. 62455460 No. 6245546dlak of No. 6245546th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,660
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-115-660-2

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| Query Match | 100.0% | Score 1238; | DB 2; | Length 225; |
|-----------------------|--------|--|---------------|------------------|
| Beet Local Similarity | 100.0% | Pred. No. 7.9e-110; | | |
| Matches | 225; | Conservative 0; | Mismatches 0; | Indels 0; Gaps 0 |
| Qy | 1 | MVGFPPVLAALATGALAFPAAGNATELEKQRTTPNSEGMHDGYYYSWNSDGAQATYTN | 60 | |
| Db | 1 | MVGFPVLAALATGALAFPAAGNATELEKQRTTPNSEGMHDGYYYSWNSDGAQATYTN | 60 | |
| Qy | 61 | LEGGTYEISWDGCGNIVGSGKNNPGINAPAIHPEGYQPNGNSYLAVGMTNPLVEYTI | 120 | |
| Db | 61 | LEGGTYEISWDGCGNIVGSGKNNPGINAPAIHPEGYQPNGNSYLAVGMTNPLVEYTI | 120 | |
| Qy | 121 | VENPGYDSSGATDGTVECDGSIYRLGKTRRVNAPSIDGQTPDQVSWVDKRTSGT | 180 | |
| Db | 121 | VENPGYDSSGATDGTVECDGSIYRLGKTRRVNAPSIDGQTPDQVSWVDKRTSGT | 180 | |

[illegible]

RESULT 3
US-09-570-856B-24

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Sequence 24, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RP/BRM/RMK
CURRENT APPLICATION NUMBER: US/09/570, 856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133, 714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 194
TYPE: PRT
ORGANISM: Thermomyces lanuginosus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1) - (1)
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3+ "-"
US-09-570-856B-24

```

| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 87.5%; | Score 1083; | DB 2; | Length 194; |
| Best Local Similarity | 100.0%; | Pred. No. 3.6e-95; | | |
| Matches 193; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | | | | |
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| Qy | 93 | FEGVYQPNQNSYLA | VYGVWTRNPLVEYYIVENFGTYDPS | SGATDLGTV | CECDGSIYRLGKTT | 152 |
| Db | 62 | FEGVYQPNQNSYLA | VYGVWTRNPLVEYYIVENFGTYDPS | SGATDLGTV | CECDGSIYRLGKTT | 121 |
| Qy | 153 | RVNAPSIDGTQTF | DDYMSYRQDKRPSGTYQTG | CHDPAMRAGL | INNVGDHYIQVVAIEGYF | 212 |
| Db | 122 | RVNAPSIDGTQTF | DDYMSYRQDKRPSGTYQTG | CHDPAMRAGL | INNVGDHYIQVVAIEGYF | 181 |
| Qy | 213 | SSGYARITVADYG | 225 | | | |
| Db | 182 | SSGYARITVADYG | 194 | | | |

RESULT 4

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US-09-570-856B-23
;; Sequence 23, Application US/09570856B
;; Patent No. 6682923
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;; GENERAL INFORMATION:
;; APPLICANT: Bentzen, Joerg M
;; APPLICANT: Dahiyat, Bassil I
;; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
;; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
;; CURRENT APPLICATION NUMBER: US/09/570,856B
;; CURRENT FILING DATE: 2002-04-15
;; PRIOR APPLICATION NUMBER: US 60/133,714
;; PRIOR FILING DATE: 1999-05-12
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 23
;;
;; LENGTH: 194
;; TYPE: prt
;; ORGANISM: Paecilomyces varioti
US-09-570-856B-23

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Query Match      77.9%; Score 965; DB 2; Length 194;
Best Local Similarity 87.6%; Pred. No. 66-84;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY      33 TTPNSEGMDGYYISWMSDGAQATYTNLEGGTYEISWGDGNIYVGGKGNPGLNARAIH 92
DB      2 TTPNSEGMDGYYISWMSDGGDSSTYTNNSGGTYEITWNGGNIYVGGKGNPGLNARAIH 61

QY      93 PEGYOPNGNSYLVVGGTRNPLVEYYIVENFGTYDPSSGATDLGTVBCDGSIRLGTT 152
DB      62 PTGYOPNGNSYLVVGGTRNPLVEYYIVENFGSSNPSSGTDLGTVSCDGSITTLGQST 121

QY      153 RVNAPSIDGTQTPQYMSVRQDKRTSGTVQTCGCHFDAMARAGLNVNGDHYQIVATEGYF 212
DB      122 RVNAPSIDGTQTPQYMSVRQDKSSGTVQTCGCHFDAMASGLNVNGDHYQIVATEGYF 181

QY      213 SSGYARITVADVG 225
DB      182 SSGYARITVADVG 194

RESULT 5
US-09-570-856B-29
Sequence 29, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzen, Joerg M
APPLICANT: Dahiyat, Basbil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RPT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 607133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 221
TYPE: PRT
ORGANISM: Cochliobolus carbonum
US-09-570-856B-29

Query Match      65.1%; Score 806.5; DB 2; Length 221;
Best Local Similarity 67.9%; Pred. No. 84e-69;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY      1 MVGFTPVALLAALATGALAPPAGNATBLEKQTPNSEGMHDGYYISWMSDGAQATYTN 60
DB      1 MVSFTSIITAAVAATGALAAPATDVS-LVAQNTPNNGSTNGCFWMSDGAQATYTN 59

QY      61 LEGGTYEISWGDGNIYVGGKGNPGLNARAIHFBGCVIQPNQNSYLAAYGWTNPLVEYYI 120
DB      60 GAGGSYSYWSGSGNLVGGKGNPGLNARAIHFBGCVIQPNQNSYLAAYGWTNPLVEYYI 118

QY      121 VENFGTYDPSSGATDLGTVBCDGSIRLGTVTRNAPSIDGTQTPQYMSVRQDKRTSGT 180
DB      119 VENFGTYDPSSGATDLGTVBCDGSIRLGTVTRNAPSIDGTQTPQYMSVRQDKRTSGT 178

QY      181 VOTGCHFDAMARAGLNVNGDHYQIVATEGYSSGYARITV 221
DB      179 VNMKTHFDAMASKGMNL-GQHYIYQIVATEGYFSTGMNQITV 218

RESULT 6
US-08-458-023B-4
Sequence 4, Application US/08458023B
Patent No. 5667990
GENERAL INFORMATION:
APPLICANT: Beika, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boomnathan, Karuppan C.
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM

```

```

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 56679900 No. 56679900disk of No. 56679900th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086,010-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-023B-4

```

```

Query Match      55.6%; Score 688.5; DB 1; Length 227;
Best Local Similarity 55.8%; Pred. No. 1.5e-57;
Matches 126; Conservative 30; Mismatches 63; Indels 7; Gaps 3;

QY      1 MVGFTPVALLAALATGALAPPAGNATBLEKQTPNSEGMHDGYYISWMSDGAQ 55
DB      1 MVSLSYLAALATVASSIAAPFDPVFPDNTALQARQVTRNGEHNHGYFISWMSDGGQ 60

QY      56 ATYTNLEGGTYEISWGDGNIYVGGKGNPGLNARAIHFBGCVIQPNQNSYLAAYGWTNPL 115
DB      61 VQYTNLEGSRQYVWRMTGPFVGGKGNPGLNARAIHFBGCVIQPNQNSYLAAYGWTNPL 119

QY      116 VEVYIVNFGTYDPSSGATDLGTVBCDGSIRLGTVTRNAPSIDGTQTPQYMSVRQDK 175
DB      120 VEVYIVNFGTYDPSSGATDLGTVBCDGSIRLGTVTRNAPSIDGTQTPQYMSVRQDK 179

QY      176 RTSQVOTGCHFDAMARAGLNVNGDHYQIVATEGYSSGYARITV 221
DB      180 RVGGSVNMGNHFNAMQOHMPL-GQHYIYQIVATEGYSSGGSIDITV 224

RESULT 7
US-09-254-733-7
Sequence 7, Application US/09254733
Patent No. 6277596
GENERAL INFORMATION:
APPLICANT: WATANABE, MANABU
APPLICANT: MORIYA, TATSUKI
APPLICANT: AOYAGI, KAORU
APPLICANT: SUMIDA, NAOMI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE Gb1 GENES ORIGINATING
FROM TRICHOCHLORUS VIRIDE AND SYSTEM FOR MASS-PRODUCING
TITLE OF INVENTION: IN TRICHOCHLORUS VIRIDE AND SYSTEM FOR MASS-PRODUCING
OPERATING SYSTEM: PC-DOS/MS-DOS
FILE REFERENCE: 99-0266*/LIC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 223

```

TYPE: PRT
ORGANISM: TRICHODERMA VIRIDE MC300-1
US-09-254-733-7

Query Match 55.4%; Score 685.5; DB 2; Length 223;
Best Local Similarity 56.7%; Pred. No. 2,7e-57;
Matches 127; Conservative 32; Mismatches 62; Indels 3; Gaps 2;

QY 1 MVGFTPALAALATGALAPAG--NATELEKROTTNSEGMDGYYXSWMSDGAQATY 58
DB 1 MVSFTSLAGVAPISGLAPAAEVESVDEKQTIOPGTGYNNGYTSYWNDSHGAVTY 60
QY 59 TNLGGTYEISWDDGNLVGGKGNPGLNARAIHFEVYOPNGNSYLAAYGWTENPLVEY 118
DB 61 TNGPGGQPSVWMSNSGNFVGKGMQPGTKNKVINFSGTYNPNNGNSYLSYVGMSRNPLEY 120
QY 119 YIVENFGTYDPSGATDLGTVECDGSIYRLGKTRTVNAPSIDGTQTDQYWSVRQDKRTS 178
DB 121 YIVENFGTYDPSGATDLGTVECDGSIYRLGKTRTVNAPSIDGTQTDQYWSVRQDKRTS 180
QY 179 GTVQTGCHPDAMAPAGLVNNGDHYQIVATEGYFSSGSARITVA 222
DB 181 GSVTANHFNAASHGLTL-CTMDYQIVAVEGYFSSGSASITVS 223

RESULT 8

US-08-121-436A-2
Sequence 2, Application US/08121436A

GENERAL INFORMATION:
APPLICANT: Suominen, Pirkko
APPLICANT: Nevalainen, Helena
APPLICANT: Saarelainen, Riitta
APPLICANT: Palohelmo, Marja
APPLICANT: Lahtinen, Tarja
APPLICANT: Fagerstr m, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,436A
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI93/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-436A-2

Query Match 55.3%; Score 684.5; DB 1; Length 223;
Best Local Similarity 57.1%; Pred. No. 3,4e-57;
Matches 128; Conservative 32; Mismatches 61; Indels 3; Gaps 2;

QY 1 MGVFTPALAALATGALAPAG--NATELEKROTTNSEGMDGYYXSWMSDGAQATY 58
DB 1 MVSFTSLAGVAPISGLAPAAEVESVAVEKQTIOPGTGYNNGYTSYWNDSHGAVTY 60
QY 59 TNLGGTYEISWDDGNLVGGKGNPGLNARAIHFEVYOPNGNSYLAAYGWTENPLVEY 118
DB 61 TNGPGGQPSVWMSNSGNFVGKGMQPGTKNKVINFSGTYNPNNGNSYLSYVGMSRNPLEY 120
QY 119 YIVENFGTYDPSGATDLGTVECDGSIYRLGKTRTVNAPSIDGTQTDQYWSVRQDKRTS 178
DB 121 YIVENFGTYDPSGATDLGTVECDGSIYRLGKTRTVNAPSIDGTQTDQYWSVRQDKRTS 180
QY 179 GTVQTGCHPDAMAPAGLVNNGDHYQIVATEGYFSSGSARITVA 222
DB 181 GSVTANHFNAQAQGLTL-CTMDYQIVAVEGYFSSGSASITVS 223

RESULT 9

US-08-768-373-2
Sequence 2, Application US/08768373
Patent No. 6228629

GENERAL INFORMATION:

APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: M NYL, ARJA
APPLICANT: VEHMANPER, JARI
APPLICANT: LANTTO, RAIIJA
APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: Protein
LOCATION: 1..261
OTHER INFORMATION: /label= XLNA
US-08-768-373-2

Query Match 54.8%; Score 678.5; DB 2; Length 261;
Best Local Similarity 57.7%; Pred. No. 1.6e-56;
Matches 128; Conservative 31; Mismatches 56; Indels 7; Gaps 3;

QY 1 MVGFTVALAALATGALAPAGNATELEKQQT-TPNSEGMHGGYYSWMSDGAQATYT 59
DB 1 MWNSTFLAATAAAPS-----IEKQTLTSSATGTHNGYYSFMTDGGNIREN 55
QY 60 NLEGGTIEISMGDGNLVGKGNPGLNARAIHPEGYQPNNGNSYLAAYGTRPLVEYY 119
DB 56 LESGGQYSVTWSGNGWVGKGNPGLNARAIHPEGYQPNNGNSYLAAYGTRPLVEYY 115
QY 120 IVENFTYDPSGATDGTVECDGSIYRLGKTRRVNAPSIDGTQTFDQYMSVRODKRTSG 179
DB 116 VVESFGTYDPSGTATRGMSVTTDGTGTYNIYRTQRVNAPSISGRTFTFYQMSVRSKRTGG 175
QY 180 TVQTCGHPDAMARAGLVNNDHYQIVATGEGYSSGATVTV 221
DB 176 TVTMANHFNAWRQAGQL-GSHDYQIVATGEGYSSGATVTV 216

RESULT 10
US-09-849-242A-2
Sequence 2, Application US/09849242A
Patent No. 6635464
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
HAKOLA, SATU
MONTILO, ARJA
VERMANPERO, JARI
LAHTI, RAIIJA
LAHTINEN, TARJA
PAGERSTROM, RICHARD
SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,242A
FILING DATE: 07-May-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/768,373
FILING DATE: 17-DEC-1996

APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: Protein
LOCATION: 1..261
OTHER INFORMATION: /label= XLNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-849-242A-2

Query Match 54.8%; Score 678.5; DB 2; Length 261;
Best Local Similarity 57.7%; Pred. No. 1.6e-56;
Matches 128; Conservative 31; Mismatches 56; Indels 7; Gaps 3;

QY 1 MVGFTVALAALATGALAPAGNATELEKQQT-TPNSEGMHGGYYSWMSDGAQATYT 59
DB 1 MWNSTFLAATAAAPS-----IEKQTLTSSATGTHNGYYSFMTDGGNIREN 55
QY 60 NLEGGTIEISMGDGNLVGKGNPGLNARAIHPEGYQPNNGNSYLAAYGTRPLVEYY 119
DB 56 LESGGQYSVTWSGNGWVGKGNPGLNARAIHPEGYQPNNGNSYLAAYGTRPLVEYY 115
QY 120 IVENFTYDPSGATDGTVECDGSIYRLGKTRRVNAPSIDGTQTFDQYMSVRODKRTSG 179
DB 116 VVESFGTYDPSGTATRGMSVTTDGTGTYNIYRTQRVNAPSISGRTFTFYQMSVRSKRTGG 175
QY 180 TVQTCGHPDAMARAGLVNNDHYQIVATGEGYSSGATVTV 221
DB 176 TVTMANHFNAWRQAGQL-GSHDYQIVATGEGYSSGATVTV 216

RESULT 11
US-08-044-621D-29
Sequence 29, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Ming L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS

RESULT 13

US-09-047-370-9

Sequence 9, Application US/09047370
Patent No. 5866408

GENERAL INFORMATION:

APPLICANT: Sung Dr., Wang L

APPLICANT: Yaguchi Dr., Makoto

APPLICANT: Iehikawa Dr., Kazuhiko

TITLE OF INVENTION: Modification of Xylanase to Improve

TITLE OF INVENTION: Thermophilicity, Alkalophilicity and

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSER: Fitzpatrick, Cella, Harper, and Scinto

STREET: 277 Park Ave.

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10172-0194

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/047,370

FILING DATE:

CLASSIFICATION: 9

PRIOR APPLICATION NUMBER: US 08/709,912

FILING DATE: 09-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr., Warren E

REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039,2000

TELEPHONE: (212) 758-2400

TELEFAX: (212) 758-2982

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 197 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE: Schizophyllum commune

ORGANISM: Schizophyllum commune

STRAIN: Xylanase A

PUBLICATION INFORMATION:

AUTHORS: Oku, T

AUTHORS: Yaguchi, M

AUTHORS: Parise, M

AUTHORS: Juraeek, L

JOURNAL: Canadian Fed. Biol. Soc. annual meeting

PAGES: Abstract #676

DATE: 1988

US-09-047-370-9

Query Match

Best Local Similarity 53.6%; Score 663; DB 1; Length 197;

Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

34 TPNSGMDGYYSWMSDGAQATYTNLEGGTYEISW-GDGGNIVGGKGNPGIAPAIIH 92

3 TPSSGTGIDGGYYSWMTDGAQDATYNNGGSYTLTWSGNNGNLVGGKGNPGIAPASIS 62

93 FEGYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDGTGVCDSIYRLGKTT 152

Db 63 YSGTYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDGTGVCDSIYRLGKTT 122

Qy 153 RVNAPSIDGTQTFPOQVSVYRDKRT-----SGTYQTCGHPDAMARAGIANNVGHYYQIVA 207

Db 123 RYNAPSIDGTQTFPOQVSVRPNKAPGSGISGTVVQCHFDAMKGLGNLGSSEHYQIVA 182

Qy 208 TEGYSSGVARITV 221

Db 183 TEGYSSGVARITV 196

RESULT 14

US-09-570-856B-18

Sequence 18, Application US/09570856B

Patent No. 6682823

GENERAL INFORMATION:

APPLICANT: Bentzlen, Joerg M

APPLICANT: Dahljat, Basel I

TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE

FILE REFERENCE: A-67478-1/RPT/RMS/RMK

CURRENT APPLICATION NUMBER: US/09/570,856B

PRIOR FILING DATE: 2002-04-15

PRIOR APPLICATION NUMBER: US 60/133,714

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.1

SEQ ID NO 18

LENGTH: 197

TYPE: PRT

ORGANISM: Schizophyllum commune

US-09-570-856B-18

Query Match 53.6%; Score 663; DB 2; Length 197;
Best Local Similarity 61.3%; Pred. No. 3.2e-55;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

34 TPNSGMDGYYSWMSDGAQATYTNLEGGTYEISW-GDGGNIVGGKGNPGIAPAIIH 92

3 TPSSGTGIDGGYYSWMTDGAQDATYNNGGSYTLTWSGNNGNLVGGKGNPGIAPASIS 62

93 FEGYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDGTGVCDSIYRLGKTT 152

63 YSGTYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDGTGVCDSIYRLGKTT 122

153 RVNAPSIDGTQTFPOQVSVYRDKRT-----SGTYQTCGHPDAMARAGIANNVGHYYQIVA 207

123 RYNAPSIDGTQTFPOQVSVRPNKAPGSGISGTVVQCHFDAMKGLGNLGSSEHYQIVA 182

Qy 208 TEGYSSGVARITV 221

Db 183 TEGYSSGVARITV 196

RESULT 15

US-08-768-373-4

Sequence 4, Application US/08768373

Patent No. 6228629

GENERAL INFORMATION:

APPLICANT: PALOHEIMO, MARJA

APPLICANT: HAKOLA, SATU

APPLICANT: M NTYL, ARJA

APPLICANT: VERMAANPER, JARI

APPLICANT: LANTTO, RAUJA

APPLICANT: LAHTINEN, TARJA

APPLICANT: PAGERSTR, M, RICHARD

APPLICANT: SUOMINEN, PIIRKO

TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.054003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: Protein
LOCATION: 1..230
OTHER INFORMATION: /label= XLNB
US-08-768-373-4

Query Match 53.5%; Score 662.5; DB 2; Length 230;
Best Local Similarity 58.8%; Pred. No. 4.4e-55;
Matches 130; Conservative 23; Mismatches 55; Indels 13; Gaps 4;
QY 12 LAATGALAF--AGNAT-----ELEKQTTPNSEGMHGGYYSWMSDGAQATYTN 60
DB 9 LTAATALAFPLEAFATGEGNATSLHETLVRACTSGTTHNGWYTSFWDGGGTWYTN 68
QY 61 LEGGYEISMGDGNLVGKGMNPGINARAIFEGVYQPNGNSYLAIVYGTNRNPLVEYYI 120
DB 69 GNGGSYSVNMQNGCFVGGKGRIGA-AATIKYSGNVNPSGNSYLAIVGTNRNPLVEYYI 127
QY 121 VENFGTYDPSGANDLGTVECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
DB 128 VESYGTYPSSGAQNLGTFOSDGTYKIAKSTRYNAPSEIGTKTFQYWSVRTSKRVGT 187
QY 181 VOTGCHPDAAWABAGLVNVDHYOIVATEGYFSSGARITV 221
DB 188 VTVANHFNAKSKGLNL-GSHDYQIVATEGYKSSGASITV 227

Search completed: February 10, 2006, 15:03:36
Job time : 39.1265 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 15:17:55 ; Search time 131.563 Seconds

(without alignments)
714.573 Million cell updates/sec

Title: US-09-467-368-2

Perfect score: 1338

Sequence: 1 MVEGTPVALMALAATGALAF.....VATEGYFSGYARITVADVG 225

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|--------------------|
| 1 | 1238 | 100.0 | 225 | US-09-467-368-2 | Sequence 2, Appl1 |
| 2 | 1238 | 100.0 | 225 | US-10-237-386-24 | Sequence 24, Appl1 |
| 3 | 1088 | 87.9 | 194 | US-10-307-441-20 | Sequence 20, Appl1 |
| 4 | 1088 | 87.9 | 194 | US-11-088-725A-46 | Sequence 46, Appl1 |
| 5 | 821.5 | 66.4 | 227 | US-10-237-386-21 | Sequence 21, Appl1 |
| 6 | 806.5 | 65.1 | 221 | US-10-237-386-20 | Sequence 20, Appl1 |
| 7 | 794.5 | 64.2 | 227 | US-10-425-115-221836 | Sequence 221836, |
| 8 | 789.5 | 63.8 | 221 | US-10-425-115-267585 | Sequence 267585, |
| 9 | 775.5 | 62.6 | 227 | US-10-237-386-22 | Sequence 22, Appl1 |
| 10 | 772.5 | 62.4 | 234 | US-10-425-115-361946 | Sequence 361946, |
| 11 | 716.5 | 57.9 | 231 | US-10-237-386-26 | Sequence 26, Appl1 |
| 12 | 701.5 | 56.7 | 231 | US-10-237-386-25 | Sequence 25, Appl1 |
| 13 | 691.5 | 55.9 | 219 | US-10-237-386-29 | Sequence 29, Appl1 |
| 14 | 689.5 | 55.7 | 227 | US-10-237-386-27 | Sequence 27, Appl1 |
| 15 | 689 | 55.7 | 241 | US-10-237-386-35 | Sequence 35, Appl1 |
| 16 | 684.5 | 55.3 | 223 | US-10-237-386-31 | Sequence 31, Appl1 |
| 17 | 681.5 | 55.0 | 221 | US-10-213-990-66 | Sequence 66, Appl1 |
| 18 | 671.5 | 54.2 | 223 | US-10-237-386-30 | Sequence 30, Appl1 |
| 19 | 671 | 54.2 | 234 | US-10-213-990-69 | Sequence 69, Appl1 |
| 20 | 667 | 53.9 | 222 | US-10-237-386-32 | Sequence 32, Appl1 |
| 21 | 663 | 53.6 | 197 | US-10-307-441-9 | Sequence 9, Appl1 |
| 22 | 663 | 53.6 | 197 | US-11-088-725A-36 | Sequence 36, Appl1 |
| 23 | 663 | 53.6 | 201 | US-10-237-386-23 | Sequence 23, Appl1 |
| 24 | 660.5 | 53.4 | 221 | US-10-237-386-44 | Sequence 44, Appl1 |
| 25 | 660 | 53.3 | 223 | US-10-237-386-28 | Sequence 28, Appl1 |
| 26 | 636.5 | 51.4 | 190 | US-10-307-441-14 | Sequence 14, Appl1 |
| 27 | 636.5 | 51.4 | 190 | US-11-088-725A-41 | Sequence 41, Appl1 |

| | | | | | |
|----|-------|------|-----|-------------------|--------------------|
| 28 | 635.5 | 51.3 | 190 | US-10-307-441-16 | Sequence 16, Appl1 |
| 29 | 633 | 51.1 | 189 | US-10-307-441-19 | Sequence 19, Appl1 |
| 30 | 633 | 51.1 | 189 | US-11-088-725A-28 | Sequence 28, Appl1 |
| 31 | 632.5 | 51.1 | 190 | US-10-307-441-17 | Sequence 17, Appl1 |
| 32 | 632.5 | 51.1 | 190 | US-11-088-725A-42 | Sequence 42, Appl1 |
| 33 | 632.5 | 51.1 | 223 | US-10-237-386-34 | Sequence 34, Appl1 |
| 34 | 631 | 51.0 | 225 | US-10-237-386-36 | Sequence 36, Appl1 |
| 35 | 630.5 | 50.9 | 190 | US-10-237-386-33 | Sequence 33, Appl1 |
| 36 | 624.5 | 50.4 | 190 | US-11-088-725A-1 | Sequence 1, Appl1 |
| 37 | 613.5 | 49.6 | 313 | US-10-213-990-72 | Sequence 72, Appl1 |
| 38 | 611.5 | 49.4 | 217 | US-09-790-070A-11 | Sequence 11, Appl1 |
| 39 | 610.5 | 49.3 | 223 | US-10-299-393-2 | Sequence 2, Appl1 |
| 40 | 610.5 | 49.3 | 223 | US-11-154-793-2 | Sequence 2, Appl1 |
| 41 | 599.5 | 48.4 | 221 | US-10-237-386-37 | Sequence 37, Appl1 |
| 42 | 573 | 46.3 | 228 | US-10-237-386-39 | Sequence 39, Appl1 |
| 43 | 573 | 46.3 | 240 | US-10-237-386-42 | Sequence 42, Appl1 |
| 44 | 568 | 45.9 | 189 | US-10-307-441-13 | Sequence 13, Appl1 |
| 45 | 568 | 45.9 | 189 | US-11-088-725A-40 | Sequence 40, Appl1 |

ALIGNMENTS

RESULT 1
US-09-467-368-2

Sequence 2, Application US/09467368

Patent No. US20020160080A1

GENERAL INFORMATION:

APPLICANT: Hansen, Peter Kamp

Mullertz, Anette

Knap, Inge Helmer

TITLE OF INVENTION: Animal Feed Additives

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSER: No. US20020160080A1o No. US20020160080A1disk of No. US200201600

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10174

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/467,368

FILING DATE: 21-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/866,765

FILING DATE: 1-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4324,204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 225 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-467-368-2

Query Match 100.0%; Score 1238; DB 3; Length 225;

Best Local Similarity 100.0%; Pred. No. 1.6e-109;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVEGTPVALAALATGALAPAGNATELEKQTPNSBGMHDGYYYSWMSDGAQATYTN 60
Db 1 MVEGTPVALAALATGALAPAGNATELEKQTPNSBGMHDGYYYSWMSDGAQATYTN 60
QY 61 LEGGTYSISWGDGNNLVGKGMNPGLNARAIHFEQVYQPNNSYLAAYGWTNPLVEYYI 120
Db 61 LEGGTYSISWGDGNNLVGKGMNPGLNARAIHFEQVYQPNNSYLAAYGWTNPLVEYYI 120
QY 121 VENFGTYDPSSGATDLGTVCECDGSYIRLGKTTTVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
Db 121 VENFGTYDPSSGATDLGTVCECDGSYIRLGKTTTVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225
Db 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225

RESULT 2

US-10-237-386-24
Sequence 24, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:

APPLICANT: Danisco A/S
APPLICANT: Sidsen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 225
TYPE: PRT
ORGANISM: T. lanuginosus
US-10-237-386-24

Query Match 100.0%; Score 1238; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-109;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVEGTPVALAALATGALAPAGNATELEKQTPNSBGMHDGYYYSWMSDGAQATYTN 60
Db 1 MVEGTPVALAALATGALAPAGNATELEKQTPNSBGMHDGYYYSWMSDGAQATYTN 60
QY 61 LEGGTYSISWGDGNNLVGKGMNPGLNARAIHFEQVYQPNNSYLAAYGWTNPLVEYYI 120
Db 61 LEGGTYSISWGDGNNLVGKGMNPGLNARAIHFEQVYQPNNSYLAAYGWTNPLVEYYI 120
QY 121 VENFGTYDPSSGATDLGTVCECDGSYIRLGKTTTVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
Db 121 VENFGTYDPSSGATDLGTVCECDGSYIRLGKTTTVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225
Db 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225

RESULT 3

US-10-307-441-20
Sequence 20, Application US/10307441
Publication No. US20030166236A1
GENERAL INFORMATION:

APPLICANT: SUNG, Wing L.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
TITLE OF INVENTION: and Alkalophilicity

FILE REFERENCE: 027367-5006US
CURRENT APPLICATION NUMBER: US/10/307,441
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: PCT/CA01/00769
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/213,803
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 194
TYPE: PRT
ORGANISM: Thermomyces lanuginosus
US-10-307-441-20

Query Match 87.9%; Score 1088; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 2.5e-95;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QTPNSBGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGMNPGLNARAI 91
Db 1 QTPNSBGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGMNPGLNARAI 60
QY 92 HFEQVYQPNNSYLAAYGWTNPLVEYYIENFGTYDPSSGATDLGTVCECDGSYIRLGKT 151
Db 61 HFEQVYQPNNSYLAAYGWTNPLVEYYIENFGTYDPSSGATDLGTVCECDGSYIRLGKT 120
QY 152 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGY 211
Db 121 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGY 180
QY 212 FSSGYARITVADV 225
Db 181 FSSGYARITVADV 194

RESULT 4

US-11-088-725A-46
Sequence 46, Application US/11088725A
Publication No. US20050214410A1
GENERAL INFORMATION:

APPLICANT: Iogen Bio-Products Corporation
APPLICANT: White, Theresa C
APPLICANT: Giroux, Genevieve R
APPLICANT: Wallace, Katie B.A.
TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
FILE REFERENCE: 080712
CURRENT APPLICATION NUMBER: US/11/088,725A
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/556,061
PRIOR FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.2
SEQ ID NO 46
LENGTH: 194
TYPE: PRT
ORGANISM: Thermomyces lanuginosus
US-11-088-725A-46

Query Match 87.9%; Score 1088; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 2.5e-95;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QTPNSBGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGMNPGLNARAI 91
Db 1 QTPNSBGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGMNPGLNARAI 60
QY 92 HFEQVYQPNNSYLAAYGWTNPLVEYYIENFGTYDPSSGATDLGTVCECDGSYIRLGKT 151
Db 61 HFEQVYQPNNSYLAAYGWTNPLVEYYIENFGTYDPSSGATDLGTVCECDGSYIRLGKT 120
QY 152 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGY 211
Db 121 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGY 180

Db 121 TRVNAPIIDGTQFDQYWSVRQDKRTSGTVQTGCHFDAMARAAGLVNNGDHYQIVATEGY 180
Qy 212 FSSGATITVADVG 225
Db 181 FSSGATITVADVG 194

RESULT 5

US-10-237-386-21

Sequence 21, Application US/10237386
Publication No. US20030180895A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sorensen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanase Variance Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/10/237,386

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 21

LENGTH: 227

TYPE: PRT

ORGANISM: H. turcicum

US-10-237-386-21

Query Match 66.4%; Score 821.5; DB 4; Length 227;
Best Local Similarity 67.7%; Pred. No. 7.3e-70;
Matches 153; Conservative 25; Mismatches 41; Indels 7; Gaps 3;

Qy 1 MGVFTPALAALATGALAPAGN-----ATELKRQTTPNSEGMHGGYYSWMSDGAQ 55
Db 1 MVSFTSLITAAVAATGALAPATDIAARAPSDLVARQSTPBGSTHNGCFYSWMSDGAQ 60
Qy 56 ATYNLEGGTYEISWGDGNIYVGKGNPGLNARAIHFEQYQPNNGSYLAVYGMTNPL 115
Db 61 ATYNNGAGSYSVSWGTGNLVGKGNPG-TARTITYSGYNNNGSYLAIVGMTNPL 119
Qy 116 VEYIVNFGTYDPSSGATDLGTYECDSIYRLGKTRVNAAPSIDGTQFDQYWSVRQDK 175
Db 120 VEYIVNFGTYDPSSQAKNGKTVTSIDSSYKIAOSTRTNQPSIDGTRTFQYWSVRQNK 179
Qy 176 RTSGTVGTGCHFDAMARAAGLVNNGDHYQIVATEGYSFGSARITV 221
Db 180 RSSGSVNMKTHFDAMASKGNL-GSHYYQIVATEGYSFGSASITV 224

RESULT 6

US-10-237-386-20

Sequence 20, Application US/10237386
Publication No. US20030180895A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sorensen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanase Variance Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/10/237,386

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 221
TYPE: PRT
ORGANISM: C. carbonum
US-10-237-386-20

Query Match 65.1%; Score 806.5; DB 4; Length 221;
Best Local Similarity 67.9%; Pred. No. 1.9e-68;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

Qy 1 MGVFTPALAALATGALAPAGNATELEKRQTTPNSEGMHGGYYSWMSDGAQATYTN 60
Db 1 MVSFTSLITAAVAATGALAPATDVS-LVARQNTPNBEGTHNGCFYSWMSDGAARATYTN 59
Qy 61 LEGTYEISWGDGNIYVGKGNPGLNARAIHFEQYQPNNGSYLAVYGMTNPLVEYI 120
Db 60 GAGGSYSVSWSGGNIYVGKGNPG-TARTITYSGYNNNGSYLAVYGMTNPLVEYI 118
Qy 121 VENFGTYDPSSGATDLGTYECDSIYRLGKTRVNAAPSIDGTQFDQYWSVRQDKRTSGT 180
Db 119 VENFGTYDPSSQAKNGKTVTSIDSSYKIAOSTRTNQPSIDGTRTFQYWSVRQNKSSGS 178
Qy 181 VGTGCHFDAMARAAGLVNNGDHYQIVATEGYSFGSARITV 221
Db 179 VNMKTHFDAMASKGNL-GSHYYQIVATEGYSFGSNQITV 218

RESULT 7

US-10-425-115-221836

Sequence 221836, Application US/10425115
Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 221836

LENGTH: 227

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_133906C.1.pep

US-10-425-115-221836

Query Match 64.2%; Score 794.5; DB 4; Length 227;
Best Local Similarity 63.7%; Pred. No. 2.7e-67;
Matches 144; Conservative 32; Mismatches 43; Indels 7; Gaps 3;

Qy 1 MGVFTPALAALATGALAPAGNAT-----ELEKRTTPNSGMDHGGYYSWMSDGAQ 55
Db 1 MVSFTSLITAAVAATGAFAPATDVARRSGDLVARQSTPNARCTHNGCFYSWMTDGSK 60
Qy 56 ATYNLEGGTYEISWGDGNIYVGKGNPGLNARAIHFEQYQPNNGSYLAVYGMTNPL 115
Db 61 VTTNNGAGSYSVNMWGSNGNPFVGGKGNPG-SARTIVYSSGNPNNGSYLAIVGMTNPL 119
Qy 116 VEYIVNFGTYDPSSGATDLGTYECDSIYRLGKTRVNAAPSIDGTQFDQYWSVRQDK 175
Db 120 VEYIVNFGTYDPSSQAKNGKTVTSIDSSYKIAOSTRTNQPSIDGTRTFQYWSVRQNK 179
Qy 176 RTSGTVGTGCHFDAMARAAGLVNNGDHYQIVATEGYSFGSARITV 221
Db 180 RSSGSVNMKTHFDAMASKGNL-GSHYYQIVATEGYSFGSASITV 224

RESULT 8

US-10-425-115-267585
 ; Sequence 267585, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 267585
 ; LENGTH: 221
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)-(221)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: clone ID: MFT4577_175642C.1.pep
 ; US-10-425-115-267585

Query Match 63.8%; Score 789.5; DB 4; Length 221;
 Best Local Similarity 66.5%; Pred. No. 7.9e-67;
 Matches 147; Conservative 26; Mismatches 45; Indels 3; Gaps 3;
 QY 1 MVEGTPVALAALAAATGALAPAGNATELEKQTPNSGMDGYYSWSDGGAQATYTN 60
 Db 1 MVSFTTITAAVAATGALAAATATVS-LVAAQNPNGSGTHNGCFWSWSDGGAATYTN 59
 QY 61 LEGGTYSWSDGGLVGGKGNPGLNARAIHFEBSYQPNNGSYLAAYGWTNPPL 120
 Db 60 GAGGSYSWSDGGLVGGKGNPGLNARAIHFEBSYQPNNGSYLAAYGWTNPPLVEYYV 118
 QY 121 VENFGTVPSSGATDGLTVECDGSYRLGKTTNVAPSIDGTQTFPDQYWSVRQDK 180
 Db 119 VENFGTVPSSGATDGLTVECDGSYRLGKTTNVAPSIDGTQTFPDQYWSVRQDK 178
 QY 181 VGTGCHPDAMARAGLNVNGDHYQIVATEGYSSSGYARITV 221
 Db 179 VNMKTHPDAMASKGMNL-GQHHYQIVATEGYSSSGYARITV 218

RESULT 9
 US-10-237-386-22
 ; Sequence 22, Application US/10237386
 ; Publication No. US20030180895A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Danisco A/S
 ; APPLICANT: Sidsen, Ole
 ; APPLICANT: Sorensen, Jens
 ; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
 ; FILE REFERENCE: 674509-2046
 ; CURRENT APPLICATION NUMBER: US/10/237,386
 ; CURRENT FILING DATE: 2002-12-06
 ; PRIOR APPLICATION NUMBER: PCT/IB01/00426
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: GB 0005585.5
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: GB 0015751.1
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: Patent version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: A. plst
 ; US-10-237-386-22

Query Match 62.6%; Score 775.5; DB 4; Length 227;
 Best Local Similarity 65.5%; Pred. No. 1.7e-65;
 Matches 148; Conservative 25; Mismatches 46; Indels 7; Gaps 4;
 QY 1 MVEGTPVALAALAAATGALAPAGNATELEKQTPNSGMDGYYSWSDGGAQ 55
 Db 1 MVSFTTITAAVAATGALAAATATVS-LVAAQNPNGSGTHNGCFWSWSDGGAQ 60
 QY 56 ATTNLEGGTYSWSDGGLVGGKGNPGLNARAIHFEBSYQPNNGSYLAAYGWTNPPL 115
 Db 61 ATTNAGGSYSVNMKTHPDAMASKGMNL-ARTTYSCTYSPSGNSYLAAYGWTNPPL 119
 QY 116 VEYIYVENFGTVPSSGATDGLTVECDGSYRLGKTTNVAPSIDGTQTFPDQYWSVRQDK 175
 Db 120 IXYIYVENFGTVPSSGATDGLTVECDGSYRLGKTTNVAPSIDGTQTFPDQYWSVRQDK 179
 QY 176 RTSGTQYTGCHPDAMARAGLNVNGDHYQIVATEGYSSSGYARITV 221
 Db 180 RSSGSVNMKTHPDAMASKGMNL-GTHNYQIVATEGYSSSGYARITV 224

RESULT 10
 US-10-425-115-361946
 ; Sequence 361946, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 361946
 ; SEQ ID NO 361946
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: clone ID: MFT4577_93271C.1.pep
 ; US-10-425-115-361946

Query Match 62.4%; Score 772.5; DB 4; Length 234;
 Best Local Similarity 63.0%; Pred. No. 3.5e-65;
 Matches 145; Conservative 27; Mismatches 47; Indels 11; Gaps 3;
 QY 1 MVEGTPVALAALAAATGALAPAGNATELEKQTPNSGMDGYYSWSD 51
 Db 1 MVSFTTITAAVAATGALAAATATVS-LVAAQNPNGSGTHNGCFWSWSD 60
 QY 52 GGAQATTTNLEGGTYSWSDGGLVGGKGNPGLNARAIHFEBSYQPNNGSYLAAYGWT 111
 Db 61 GGAQATTTNLEGGTYSWSDGGLVGGKGNPGLNARAIHFEBSYQPNNGSYLAAYGWT 119
 QY 112 RNPLVEYIYVENFGTVPSSGATDGLTVECDGSYRLGKTTNVAPSIDGTQTFPDQYWSV 171
 Db 120 RNPLVEYIYVENFGTVPSSGATDGLTVECDGSYRLGKTTNVAPSIDGTQTFPDQYWSV 179
 QY 172 RODKRTSGTQYTGCHPDAMARAGLNVNGDHYQIVATEGYSSSGYARITV 221
 Db 180 RQNRSSSGVNMKTHPDAMASKGMNL-GQHHYQIVATEGYSSSGYARITV 228

RESULT 11
 US-10-237-386-26
 ; Sequence 26, Application US/10237386
 ; Publication No. US20030180895A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Danisco A/S
 ; APPLICANT: Sidsen, Ole
 ; APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 231
TYPE: PRT
ORGANISM: C. sativus
US-10-237-386-26

Query Match 57.9%; Score 716.5; DB 4; Length 231;
Best Local Similarity 58.7%; Pred. No. 7,4e-60;
Matches 135; Conservative 29; Mismatches 55; Indels 11; Gaps 4;

QY 1 MVGTPVALAALATGALAPP-----AGNATE-LEKQTPNSEGMHDGYYSWMSD 51
DB 1 MVSFKSLILAATVATTSVLAAPDFLBERDDGNATALLERKQSTPSSEGYHNGYFSWMTD 60
QY 52 GGAATYTNLEGGTYEISWGDGNNLVGKGNPGLNARAIHPEGVYQPNNGSYLAIVGWT 111
DB 61 GGGAQTYMGSGRSYVMTWRTGNFVGKGNPFC-TGVIVYGAFFNQGNGYLAIVGWT 119
QY 112 RNPLVEYIVENFGTYDPSSGATDLGTVBCDSIYRLKTRVNAPSIDGTQTFDQYWSV 171
DB 120 RNPLVEYIVESYGTYNPSSGAQYKSGFTDGTGTYNNAVSTRNQPSIDGTRTQQTWSV 179
QY 172 RQDKRTSGTYGTGCHFDAMARAGLVNNGDHYQIVATEGYSSGYARITV 221
DB 180 RQDKRVGGSVMQNHFNAMSRYGLNL-GQHYQIVATEGYSSGSSSDIYV 228

RESULT 12
US-10-237-386-25
Sequence 25, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 231
TYPE: PRT
ORGANISM: C. carbonum
US-10-237-386-25

Query Match 56.7%; Score 701.5; DB 4; Length 231;
Best Local Similarity 57.4%; Pred. No. 2e-58;
Matches 132; Conservative 31; Mismatches 56; Indels 11; Gaps 4;
QY 1 MVGTPVALAALATGALAPP-----NATE-LEKQTPNSEGMHDGYYSWMSD 51
DB 1 MVSFKSLILAATVATTSVLAAPDFLBERDDGNATALLERKQSTPSSEGYHNGYFSWMTD 60

QY 52 GGAATYTNLEGGTYEISWGDGNNLVGKGNPGLNARAIHPEGVYQPNNGSYLAIVGWT 111
DB 61 GGGAQTYMGSGRSYVMTWRTGNFVGKGNPFC-SGVIVYGAFFNQGNGYLAIVGWT 119
QY 112 RNPLVEYIVENFGTYDPSSGATDLGTVBCDSIYRLKTRVNAPSIDGTQTFDQYWSV 171
DB 120 RNPLVEYIVESYGTYNPSSGAQYKSGFTDGTGTYNNAVSTRNQPSIDGTRTQQTWSV 179
QY 172 RQDKRTSGTYGTGCHFDAMARAGLVNNGDHYQIVATEGYSSGYARITV 221
DB 180 RQDKRVGGSVMQNHFNAMSRYGLNL-GQHYQIVATEGYSSGSSSDIYV 228

RESULT 13
US-10-237-386-29
Sequence 29, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 29
LENGTH: 219
TYPE: PRT
ORGANISM: C. gracile
US-10-237-386-29

Query Match 55.9%; Score 691.5; DB 4; Length 219;
Best Local Similarity 59.1%; Pred. No. 1,7e-57;
Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;

QY 1 MVGTPVALAALATGALAPPAGNAT---ELEKQTPNSEGMHDGYYSWMSGGAQAT 57
DB 1 MVSFKAL---LLGAAGLAPPF-NVTQMBELVAAAGTSPSGTNGYFYSFWTGGGTVN 56
QY 58 YTNLEGGTYEISWGDGNNLVGKGNPGLNARAIHPEGVYQPNNGSYLAIVGTRNPLVE 117
DB 57 YONGAGGSYVQWQNCNPFVGKGNPFGA-AKTINFGTSPQONGYLAIVGTRNPLVE 115
QY 118 YVIVENFGTYDPSSGATDLGTVBCDSIYRLKTRVNAPSIDGTQTFDQYWSVRQDKRT 177
DB 116 YVIVESFGTYDPSSGAQKFGTIQDGSYTIATKTRVNQSIESTSFDFQWMSVRQDKRT 175
QY 178 SGTYGTGCHFDAMARAGLVNNGDHYQIVATEGYSSGYARITV 222
DB 176 SGSVNVAHFNAQAQGLKL-GSHNYQIVATEGYSSGSSSDIYV 219

RESULT 14
US-10-237-386-27
Sequence 27, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426

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1 PRIOR FILING DATE: 2001-03-08
2 PRIOR APPLICATION NUMBER: GB 0005585.5
3 PRIOR FILING DATE: 2000-03-08
4 PRIOR APPLICATION NUMBER: GB 0015751.1
5 PRIOR FILING DATE: 2000-06-27
6 NUMBER OF SEQ ID NOS: 66
7 SOFTWARE: PatentIn version 3.0
8 SEQ ID NO: 27
9 LENGTH: 227
10 TYPE: PRN
11 ORGANISM: H. insulens
12 US-10-237-386-27

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|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 55.7% | Score 689.5; | DB 4; | Length 227; |
| Best Local Similarity | 55.8% | Pred. No. 2.7e-57; | | |
| Matches 126; | Conservative 31; | Mismatches 62; | Indels 7; | Gaps 3; |

| | | | |
|----|-----|---|-----|
| Qy | 1 | YVGFPPVLAALAAAGALA-----PAGNATELEKQQTTPNSGMDGYYSWSGGQA | 55 |
| Db | 1 | MVSLKSVLAAATAYVSAIAPDFPVPDRNSTALQAQVTPNMGWNGHGFYSWMSDGGQ | 60 |
| Qy | 56 | ATYTNLEGGTYEISWGDGGLVGKMGKPNGLNARAIHFEQGYVQPNGNSYLAVYGWRNPL | 115 |
| Db | 61 | VQYTNLESGRYVQRRNRNGNPFVGKMGKMG-NICRTINYGGFYFNPQNGYLAIVYGWRNPL | 119 |
| Qy | 116 | VEYYIVENFGTYDPSSGATDLGTCDSIYRLGKTRTVNAPSIDGTQTFPDQYWSYRQDK | 175 |
| Db | 120 | VEYYIVESGYTNPGSQAQYKGTPLYTDGQOYDIFVSTRVNPQSIDGTRTFQOYWSIRKNK | 179 |
| Qy | 176 | RTSGVQVQCHEDAMARAGLNNAGDHYQIIVATEGFSSGYAITY | 221 |
| Db | 180 | RVGSSVNNQNHFNAMQOHGMP-LGQHYVQVVAIEGYSQSSGESITIV | 224 |

RESULT 15
US-10-237-386-35

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; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsbeeen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 241
; TYPE: PRT
; ORGANISM: C. gracile
; US-10-237-386-35

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| | | | | |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match | 55.7%; | Score 689; | DB 4; | Length 241; |
| Best Local Similarity | 59.5%; | Pred. No. 3.3e-57; | | |
| Matches 132; Conservative | 31; | Mismatches 55; | Indels 4; | Gaps 4; |

QY 1 MNGFPTVALAALAAATGALPAPGNAVTELEGRQTPPNE-GMHGYYYSMMSDGGAQATYT 59
 Db 1 MNTFSLFLAASAAVAVANAP-GELEPMHGRQITLTSQTGTNNQYYYSFPTDGGANQYT 59
 QY 60 NLEGGTYEISMGEDGSLVGSGKMNPGILNAPLHEGYYQPNQNSYLAIVGTNRNPLVEYY 119
 Db 60 NKAQGGYSYTWISGNGMNVGGKGNPFC-SARTINTAYNNPNSGNSYLAIVGTNRNPLVEYY 119
 QY 120 IVENFGTYPSSGATLGTVECDGSIYRLKKTTRVANPSIDGTQTFDQYASVSRQDKRTSG 179

| | | | |
|----|-----|---|-----|
| Db | 119 | VVENFGITNPEITGATRLGSAVTITDSCYDIIYRQRNPISIEGTSIFEQFWSVRQNRKSSG | 178 |
| Qy | 180 | TVQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGARITV | 221 |
| Dd | 179 | SVNMAAHFNMAAAAGQL-GTHDHYIVATEGYSSSGARIVN | 219 |

Search completed: February 10, 2006, 15:22:35
Job time : 132.563 secs

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OM protein - protein search, using sw model

Run on: February 10, 2006, 15:18:39 / Search time 11.2768 Seconds
(without alignments)
261.826 Million cell updates/sec

Title: US-09-467-368-2

Perfect score: 1238
Sequence: 1 MVGFTPVLAALATGALAF.....VATGTFSSGVARITVADVG 225

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*
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2: /cgn2_6/ptcdatc/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptcdatc/1/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------------------------|
| 1 | 1238 | 100.0 | 225 | 7 | US-11-170-653-24 Sequence 24, App1 |
| 2 | 821.5 | 66.4 | 227 | 7 | US-11-170-653-21 Sequence 21, App1 |
| 3 | 806.5 | 65.1 | 221 | 7 | US-11-170-653-20 Sequence 20, App1 |
| 4 | 775.5 | 62.6 | 227 | 7 | US-11-170-653-22 Sequence 22, App1 |
| 5 | 716.5 | 57.9 | 231 | 7 | US-11-170-653-26 Sequence 26, App1 |
| 6 | 701.5 | 56.7 | 231 | 7 | US-11-170-653-25 Sequence 25, App1 |
| 7 | 691.5 | 55.9 | 219 | 7 | US-11-170-653-29 Sequence 29, App1 |
| 8 | 689.5 | 55.7 | 227 | 7 | US-11-170-653-27 Sequence 27, App1 |
| 9 | 689 | 55.7 | 241 | 7 | US-11-170-653-35 Sequence 35, App1 |
| 10 | 684.5 | 55.3 | 223 | 7 | US-11-170-653-31 Sequence 31, App1 |
| 11 | 671.5 | 54.2 | 223 | 7 | US-11-170-653-30 Sequence 30, App1 |
| 12 | 667 | 53.9 | 222 | 7 | US-11-170-653-32 Sequence 32, App1 |
| 13 | 663 | 53.6 | 201 | 7 | US-11-170-653-23 Sequence 23, App1 |
| 14 | 660.5 | 53.4 | 221 | 7 | US-11-170-653-44 Sequence 44, App1 |
| 15 | 660 | 53.3 | 223 | 7 | US-11-170-653-28 Sequence 28, App1 |
| 16 | 632.5 | 51.1 | 223 | 7 | US-11-170-653-34 Sequence 34, App1 |
| 17 | 631 | 51.0 | 225 | 7 | US-11-170-653-36 Sequence 36, App1 |
| 18 | 630.5 | 50.9 | 190 | 7 | US-11-170-653-33 Sequence 33, App1 |
| 19 | 608 | 49.1 | 432 | 6 | US-10-517-939-178 Sequence 178, App |
| 20 | 599.5 | 48.4 | 221 | 7 | US-11-170-653-37 Sequence 37, App1 |
| 21 | 585.5 | 47.3 | 335 | 6 | US-10-517-939-232 Sequence 232, App |
| 22 | 581 | 46.9 | 348 | 6 | US-10-517-939-166 Sequence 166, App |
| 23 | 573 | 46.3 | 228 | 7 | US-11-170-653-39 Sequence 39, App1 |
| 24 | 573 | 46.3 | 240 | 7 | US-11-170-653-42 Sequence 42, App1 |
| 25 | 567 | 45.8 | 344 | 7 | US-11-108-163B-10 Sequence 10, App1 |

| | | | | | |
|----|-------|------|-----|---|-------------------------------------|
| 26 | 563 | 45.5 | 239 | 7 | US-11-170-653-40 Sequence 40, App1 |
| 27 | 562.5 | 45.4 | 241 | 7 | US-11-170-653-43 Sequence 43, App1 |
| 28 | 561 | 45.3 | 242 | 7 | US-11-170-653-41 Sequence 41, App1 |
| 29 | 560 | 45.2 | 193 | 7 | US-11-108-163B-14 Sequence 14, App1 |
| 30 | 560 | 45.2 | 217 | 7 | US-11-108-163B-13 Sequence 13, App1 |
| 31 | 560 | 45.2 | 220 | 7 | US-11-108-163B-12 Sequence 12, App1 |
| 32 | 560 | 45.2 | 301 | 7 | US-11-108-163B-11 Sequence 11, App1 |
| 33 | 558.5 | 45.1 | 354 | 6 | US-10-517-939-216 Sequence 216, App |
| 34 | 553 | 44.7 | 240 | 7 | US-11-170-653-38 Sequence 38, App1 |
| 35 | 551 | 44.5 | 358 | 6 | US-10-517-939-182 Sequence 182, App |
| 36 | 541.5 | 43.7 | 347 | 6 | US-10-517-939-196 Sequence 196, App |
| 37 | 541 | 43.7 | 216 | 7 | US-11-170-653-45 Sequence 45, App1 |
| 38 | 540.5 | 43.7 | 542 | 6 | US-10-517-939-262 Sequence 262, App |
| 39 | 539.5 | 43.6 | 352 | 6 | US-10-517-939-226 Sequence 226, App |
| 40 | 532 | 43.0 | 445 | 6 | US-10-517-939-368 Sequence 368, App |
| 41 | 531.5 | 42.9 | 303 | 6 | US-10-517-939-214 Sequence 214, App |
| 42 | 531.5 | 42.9 | 358 | 6 | US-10-517-939-370 Sequence 370, App |
| 43 | 528 | 42.6 | 237 | 7 | US-11-170-653-47 Sequence 47, App1 |
| 44 | 527.5 | 42.6 | 346 | 6 | US-10-517-939-160 Sequence 160, App |
| 45 | 524 | 42.3 | 356 | 6 | US-10-517-939-234 Sequence 234, App |

ALIGNMENTS

RESULT 1

US-11-170-653-24
Sequence 24, Application US/11170653
Publication No. US20050271769A1

GENERAL INFORMATION:
APPLICANT: Danisco A/S

APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0
SEQ ID NO 24

LENGTH: 225
TYPE: PRT
ORGANISM: T. lanuginosus

US-11-170-653-24

Query Match 100.0%; Score 1238; DB 7; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.7e-106;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|----|-----|------|----------------|------------------|---------------------------|-----|
| QY | 1 | MVGF | TPVLAALATGALAF | PAGNATELEKRQTPNS | EGMHDGYYSWSDGAQATYTN | 60 |
| DB | 1 | MVGF | TPVLAALATGALAF | PAGNATELEKRQTPNS | EGMHDGYYSWSDGAQATYTN | 60 |
| QY | 61 | LEGG | TVYISWGDCGNLVG | GKGNPGLNARAIH | REGVYQPNGNSTLAYGTRNPLVYYI | 120 |
| DB | 61 | LEGG | TVYISWGDCGNLVG | GKGNPGLNARAIH | REGVYQPNGNSTLAYGTRNPLVYYI | 120 |
| QY | 121 | VENF | GTDPSSGATDCTG | VCDSIYRLGKTRVNA | PSIGTQTFDQYMSVRQDKRTSGT | 180 |
| DB | 121 | VENF | GTDPSSGATDCTG | VCDSIYRLGKTRVNA | PSIGTQTFDQYMSVRQDKRTSGT | 180 |
| QY | 181 | VQGC | HPDAMARAGLNV | NGDHYIQVAT | EGYFSSGVARITVADVG | 225 |
| DB | 181 | VQGC | HPDAMARAGLNV | NGDHYIQVAT | EGYFSSGVARITVADVG | 225 |


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RESULT 5
US-11-170-653-26
; Sequence 26, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 231
; TYPE: PRT
; ORGANISM: C. sativus
US-11-170-653-26

Query Match          57.9%; Score 716.5; DB 7; Length 231;
Best Local Similarity 58.7%; Pred. No. 1.8e-58;
Matches 135; Conservative 29; Mismatches 55; Indels 11; Gaps 4;

Qy      1  MWGTPVALAALAAATGALAFP-----AGNATE-LEKROTPNSGMDGYYSWMSD  51
Db      1  MWSEKSLILAAVATTSVLAAPFDLRERDDNATALLERKOSTPSSEGHNGYFYSWMTD  60
Qy      52  GGAATYTNLEGGTYEISWDGGLVGGKGNPGLNARAIHFEQVYQPNNGSYLAAYGWT  111
Db      61  GGSAQYTMGEGSRYSYWRNTGNFVGKGNPQ-TGIVINYGAFNPGNGYLAAYGWT  119
Qy      112  RNPLVEYYIVENFGTYDPSGATDLGTVBCDSIYRLGKTRVNAASIDGTQTFDQYWSV  171
Db      120  RNPLVEYYIVESYTYNPFSSGAQYKGSFQTDGCTYNNAVSTRYNQPSIDGTRTQQTWSV  179
Qy      172  RODRRTSGTYQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITV  221
Db      180  RQGRVGVGSVMQNHFNAMSRYGTLN-LGQHYQIVATEGYQSSGSSDIYV  228

RESULT 6
US-11-170-653-25
; Sequence 25, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 25
; LENGTH: 231
; TYPE: PRT
; ORGANISM: C. carbonum
US-11-170-653-25

Query Match          56.7%; Score 701.5; DB 7; Length 231;
Best Local Similarity 57.4%; Pred. No. 4.2e-57;
Matches 132; Conservative 31; Mismatches 56; Indels 11; Gaps 4;

Qy      1  MWGTPVALAALAAATGALAPAG-----NATE-LEKROTPNSGMDGYYSWMSD  51
Db      1  MWSEKSLILAAVATTSVLAAPFDLRERDDNATALLERKOSTPSAEGYHNGYFYSWMTD  60
Qy      52  GGAATYTNLEGGTYEISWDGGLVGGKGNPGLNARAIHFEQVYQPNNGSYLAAYGWT  111
Db      61  GGSAQYTMGEGSRYSYWRNTGNFVGKGNPQ-SGIVINYGAFNPGNGYLAAYGWT  119
Qy      112  RNPLVEYYIVENFGTYDPSGATDLGTVBCDSIYRLGKTRVNAASIDGTQTFDQYWSV  171
Db      120  RNPLVEYYIVESYTYNPFSSGAQYKGSFQTDGCTYNNAVSTRYNQPSIDGTRTQQTWSV  179
Qy      172  RODRRTSGTYQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITV  221
Db      180  RQGRVGVGSVMQNHFNAMSRYGTLN-LGQHYQIVATEGYQSSGSSDIYV  228

RESULT 7
US-11-170-653-29
; Sequence 29, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23; 386
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
US-11-170-653-29

Query Match          55.9%; Score 691.5; DB 7; Length 219;
Best Local Similarity 59.1%; Pred. No. 3.2e-56;
Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;

Qy      1  MWGTPVALAALAAATGALAPAGNAT---ELEKROTPNSGMDGYYSWMSDGAQAT  57
Db      1  MWSEKSLILAAVATTSVLAAPFDLRERDDNATALLERKOSTPSAEGYHNGYFYSWMTD  56
Qy      58  YTNLEGGTYEISWDGGLVGGKGNPGLNARAIHFEQVYQPNNGSYLAAYGWTNPLVE  117
Db      57  YONGAGSYSGYOWONCNFVGKGNPQA-ARTINFGTSPQONGYLAAYGWTQNLVE  115
Qy      118  YYIVENFGTYDPSGATDLGTVBCDSIYRLGKTRVNAASIDGTQTFDQYWSVRODKRT  177
Db      116  YYIVESFGTYDPSQAKFGTIOODGSTYITAKTRVNAQPSIDGTRTQQTWSVRODKRT  175
Qy      178  SGTVQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVA  222
Db      178  SGTVQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVA  222
```

Db 176 SGSVNVAHFNAQAQGLKL-GSHNYQIVATEGYQSSSSSITVS 219

RESULT 8

US-11-170-653-27
; Sequence 27, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:

APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

PRIOR FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 27

LENGTH: 227

TYPE: PRT

ORGANISM: H. insolens

US-11-170-653-27

Query Match 55.7%; Score 689.5; DB 7; Length 227;
Best Local Similarity 55.8%; Pred. No. 5.2e-56;
Matches 126; Conservative 31; Mismatches 62; Indels 7; Gaps 3;

QY 1 MVGFTPVALLAALATGALA-----FPAGNATELEKQRTTPNSEGMHDGYYSWMSDGAQ 55
Db 1 MVSLSKSVLAATAVASSALAPDFPFRDNRSTALQARQVTPNAEGWHNGYFYSWMSDGGQ 60
QY 56 ATYTNLEGTEIISMGDCGNLVGGKGNPGLNAPAIHBEGYQOPNGSYLAVGWTNPL 115
Db 61 VQYNLEBSRQVRNRNNGNFPVGGKGNPG-TGRITNGYGFNPGNGYLAIVGWTNPL 119
QY 116 VEYIVENFGTYDPSGATDGTVECDGSIYRLGKTRVNAPSIDGTQTFDQYMSVRQDK 175
Db 120 VEYIVIEBGTYNPSQAQYKGTFTYDGDQDIFPSTYNGPSIDGRTTFQYMSIRK 179
QY 176 RTSGTGTGCHFDAMARAAGLVNNGDHYQIVATEGYFSSGYARITV 221
Db 180 RVGGSVNNQNHFNAMQCHGMPL-GQHYVQVATBEGYQSSGESDIYV 224

RESULT 9

US-11-170-653-35

; Sequence 35, Application US/11170653
; Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

PRIOR FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 35

LENGTH: 241

TYPE: PRT

ORGANISM: C. gracile

US-11-170-653-35

Query Match 55.7%; Score 689; DB 7; Length 241;
Best Local Similarity 59.5%; Pred. No. 6.1e-56;
Matches 133; Conservative 31; Mismatches 55; Indels 4; Gaps 4;

QY 1 MVGFTPVALLAALATGALAAPPAGNATELEKQRTTPNSE-GMHQGYYSWMSDGAQATYT 59
Db 1 MVSFSLAALAAVAVAAAP-GEIPMHQRQTLTSQGTNNGYYSFWTDGQNVQYT 59
QY 60 NLEGTEIISMGDCGNLVGGKGNPGLNAPAIHBEGYQOPNGSYLAVGWTNPLVEY 119
Db 60 NEAGGQYSVTSGNGWVGKGNPG-SANTINTANYNNGSYLAVGWTNPLVEY 118
QY 120 IVENFGTYDPSGATDGTVECDGSIYRLGKTRVNAPSIDGTQTFDQYMSVRQDKRTSG 179
Db 119 VVENFGTYNPGTATRLGSLVTTDGSQYDIYRTQVNGPSIEGSTFYQFMSVRQDKRTSG 178
QY 180 TVOTGCHFDAMARAAGLVNNGDHYQIVATEGYFSSGYARITV 221
Db 179 SVNMAAHFNAMAAAQGLQ-LGTHDYQIVATEGYSSGSATYV 219

RESULT 10

US-11-170-653-31

; Sequence 31, Application US/11170653
; Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

PRIOR FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 31

LENGTH: 223

TYPE: PRT

ORGANISM: T. reesei

US-11-170-653-31

Query Match 55.3%; Score 684.5; DB 7; Length 223;
Best Local Similarity 57.1%; Pred. No. 1.4e-55;
Matches 128; Conservative 32; Mismatches 61; Indels 3; Gaps 2;

QY 1 MVGFTPVALLAALATGALAAPPAG--NATELEKQRTTPNSEGMHDGYYSWMSDGAQATY 58
Db 1 MVSFTSLAALAAISGVLAAPAAEVESVAVEKQRTIQGTGYNNNGYFYSWYNDGSGYTV 60
QY 59 TNLGTEIISMGDCGNLVGGKGNPGLNAPAIHBEGYQOPNGSYLAVGWTNPLVEY 118
Db 61 TNGGCGFVSVMNSNGNFGVGKGNQPGTKXNVINPFGSYNNGSYLSVGMSSRPILIEY 120
QY 119 YVENFGTYDPSGATDGTVECDGSIYRLGKTRVNAPSIDGTQTFDQYMSVRQDKRTS 178
Db 121 YVENFGTYNPGTATRLGSLVTTDGSQYDIYRTQVNGPSIEGRTFYQFMSVRQDKRTS 180
QY 179 GTVOTGCHFDAMARAAGLVNNGDHYQIVATEGYFSSGYARITVA 222

Db 181 GSVNTANHFNAQAQGLTL-CTMDYQIVAVEGYFSSGASITVS 223

RESULT 11

US-11-170-653-30

Sequence 30, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Sorensen, Ole

APPLICANT: Sorensen, Ole

TITLE OF INVENTION: Xylanase Variance Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

PRIOR FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 30

LENGTH: 223

TYPE: PRT

ORGANISM: T. reesei

US-11-170-653-30

Query Match

Best Local Similarity 54.2%; Score 671.5; DB 7; Length 223;

Matches 126; Conservative 32; Mismatches 63; Indels 3; Gaps 2;

Db 1 MVSFTSLAAGVLAISGVLAAPAEVPAVEKRTIQCTGCTGNNGYSTWNDHGGVTY 60

1 MVSFTSLAAGVLAISGVLAAPAEVPAVEKRTIQCTGCTGNNGYSTWNDHGGVTY 60

59 TNLGGTYEISWGDGNGLVGKGNPNGLNARAIHEGVYOPNGNSYLAIVGWTNPLVEY 118

61 TNGPGQGFVSWNSGNFVGKGNQPGTKNKVINFSGSYNPNNGSYLSVYGMSPNPLEY 120

119 YIYENFCTYPPSSGATDLGTYECDSYIRLCKTRRVNAPSIDGTQTPQYVSRQDKRTS 178

121 YIYENFCTYPPSSGATDLGTYECDSYIRLCKTRRVNAPSIDGTQTPQYVSRQDKRTS 180

179 GTVGTGCHPDAMARAGLANVGDHYQIVATEGYFSSGARITVA 222

181 GSVNTANHFNAQAQGLTL-CTMDYQIVAVEGYFSSGASITVS 223

RESULT 12

US-11-170-653-32

Sequence 32, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Sorensen, Ole

APPLICANT: Sorensen, Ole

TITLE OF INVENTION: Xylanase Variance Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

PRIOR FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

RESULT 13

US-11-170-653-23

Sequence 23, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Sorensen, Ole

APPLICANT: Sorensen, Ole

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

PRIOR FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 32

LENGTH: 222

TYPE: PRT

ORGANISM: T. reesei

US-11-170-653-32

Query Match

Best Local Similarity 53.9%; Score 667; DB 7; Length 222;

Matches 128; Conservative 32; Mismatches 60; Indels 4; Gaps 3;

Db 1 MVSFTSLAAGVLAISGVLAAPAEVPAVEKRTIQCTGCTGNNGYSTWNDHGGVTY 59

1 MVSFTSLAAGVLAISGVLAAPAEVPAVEKRTIQCTGCTGNNGYSTWNDHGGVTY 59

59 TNLGGTYEISWGDGNGLVGKGNPNGLNARAIHEGVYOPNGNSYLAIVGWTNPLVEY 118

60 TNGPGQGFVSWNSGNFVGKGNQPGTKNKVINFSGSYNPNNGSYLSVYGMSPNPLEY 119

119 YIYENFCTYPPSSGATDLGTYECDSYIRLCKTRRVNAPSIDGTQTPQYVSRQDKRTS 178

120 YIYENFCTYPPSSGATDLGTYECDSYIRLCKTRRVNAPSIDGTQTPQYVSRQDKRTS 179

179 GTVGTGCHPDAMARAGLANVGDHYQIVATEGYFSSGARITVA 222

180 GSVNTANHFNAQAQGLTL-CTMDYQIVAVEGYFSSGASITVS 222

RESULT 14

US-11-170-653-23

Sequence 23, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Sorensen, Ole

APPLICANT: Sorensen, Ole

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

PRIOR FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 23

LENGTH: 201

TYPE: PRT

ORGANISM: S. commune

US-11-170-653-23

Query Match

Best Local Similarity 53.6%; Score 663; DB 7; Length 201;

Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

Db 34 TPNSSEGHDDIYYSWMSDGAQATYTNLBEQTYEIS-GLGNGLVGKGNPNGLNARAIH 92

5 TPNSSTGDDGYYSWMTDGDAGATYQNNGGSYTLTWSGNGNLVGGKGNPAGASISIS 64

93 FEGYOPNGNSYLAIVGWTNPLVEYIYENFCTYPPSSGATDLGTYECDSYIRLCKTRT 152

65 YSGTYDNGNSYLAIVGWTNPLVEYIYENFCTYPPSSGATDLGTYECDSYIRLCKTRT 124

153 RVNAPSIDGTQTPQYVSRQDKRT-----SGTVGTGCHPDAMARAGLANVGDHYQIVA 207

125 RVNAPSIDGTQTPQYVSRQDKRT-----SGTVGTGCHPDAMARAGLANVGDHYQIVA 184

Qy 208 TEGYSSSGYARITV 221
Db 185 TEGYSSSGTATITV 198

RESULT 14

US-11-170-653-44
; Sequence 44, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 221
; TYPE: PRT
; ORGANISM: A. oryzae
US-11-170-653-44

Query Match 53.4%; Score 660.5; DB 7; Length 221;
Best Local Similarity 56.1%; Pred. No. 2.2e-53;
Matches 125; Conservative 34; Mismatches 59; Indels 5; Gaps 4;

Qy 1 MGFPTVALAALATG-ALAPPA--GNAT-----ELEKROTPNSEGMHGDGYYSWMSDGAQATY 58
1 MVSFSTIVTAVVVALAGSALAIAPADGNTGTGFPFQRLWRQSTPSTGRHNGYYSWMTDG 60
Db 59 TNLBEGTYEISWGDGSLVGGKGNPGLNAPAIHPEGYQYQVATGEGYSSGYARITV 118
60 TNGNGGQYSVKWTNCDNFVAGKGNMPG-SAKTVYSGEMESNSNSVSLYGTQNPVLEY 118
Qy 119 YIVNFGTYDPSSGATDLGTVBCDGSIVRLGKTRRVNAPSIDGTOTPDQYWSVRQDKRTS 178
119 YIVDKYGYDPSGTATGELGTVESDGGTYKTYITRENAPSLEGISTFNOYMSVRQSGRVG 178
Db 179 GTVQTCGHPDAMARAGLNVNGDHYQYQIVATEGYSSGYARITV 221
179 GTTANHFDMANVGLQI-GTHNMTILATEGYKSSGSATITV 220

RESULT 15

US-11-170-653-28
; Sequence 28, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 233
; TYPE: PRT
; ORGANISM: M. grisea
US-11-170-653-28

Query Match 53.3%; Score 660; DB 7; Length 233;
Best Local Similarity 53.7%; Pred. No. 2.6e-53;
Matches 124; Conservative 36; Mismatches 59; Indels 12; Gaps 6;

Qy 1 MGFPTVALAALATG-ALAPPA--GNAT-----ELEKROTPNSEGMHGDGYYSWMSDGAQATY 52
1 MVSFSTIVTAVVVALAGSALAIAPADGNTGTGFPFQRLWRQSTPSTGRHNGYYSWMTDG 60
Db 53 GAQATTYNLBEGTYEISWGDGSLVGGKGNPGLNAPAIHPEGYQYQVATGEGYSSGYARITV 110
61 ASPVQYQNGNGSGYSVQMGSGNPFVGGKGNMPG-GSKSITYSGTFNPNNGNAVLCITIGW 119
Qy 111 TRNPLVEYIIVENFGTYDPSSGATDLGTVBCDGSIVRLGKTRRVNAPSIDGTOTPDQYWS 170
120 TQNPVLEYIILENGETNPGNSAOSRGTLDAGSTYTLHSESTRVNPISIEGTRTFQYMA 179
Db 171 VRQDKRTSGTYQTCGHPDAMARAGLNVNGDHYQYQIVATEGYSSGYARITV 221
180 IROCKRNSGTIVNTGEPFQAWERAGMRM-GNHNMTIVATEGYRSAGNSNINV 229

Search completed: February 10, 2006, 15:23:01
Job time : 12.2768 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 14:49:18 / Search time 130.568 Seconds
(without alignments)
652.836 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225
Perfect score: 1088
Sequence: 1 QTTPNSEGMHDDGYYSWMSD.....VATGEYSSGYARITVADVG 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 1088 | 100.0 | 194 | 5 | AAE18456 Thermomyc |
| 2 | 1088 | 100.0 | 225 | 2 | AAW01112 Xylanase. |
| 3 | 1088 | 100.0 | 225 | 2 | AAW05187 Endo-1,4- |
| 4 | 1088 | 100.0 | 225 | 7 | ABR63119 Thermomyc |
| 5 | 1088 | 100.0 | 225 | 9 | AEB00305 Xylanase |
| 6 | 1083 | 99.5 | 194 | 3 | AAAB48543 Thermomyc |
| 7 | 1083 | 99.5 | 194 | 5 | AAO186449 T lanugin |
| 8 | 1083 | 99.5 | 194 | 8 | AD166751 T. lanugi |
| 9 | 965 | 88.7 | 194 | 3 | AAAB48542 Paecilomy |
| 10 | 965 | 88.7 | 194 | 5 | AAO186448 P. varioti |
| 11 | 965 | 88.7 | 194 | 8 | AD166750 P. varioti |
| 12 | 742 | 68.2 | 221 | 3 | AAAB48548 Cochlioba |
| 13 | 742 | 68.2 | 221 | 5 | AAO18654 C carbonu |
| 14 | 742 | 68.2 | 221 | 8 | AD166756 C. carbon |
| 15 | 663 | 60.9 | 197 | 2 | AAW60736 Xylanase |
| 16 | 663 | 60.9 | 197 | 3 | AAV98068 S. commun |
| 17 | 663 | 60.9 | 197 | 3 | AAAB48537 Schizophy |
| 18 | 663 | 60.9 | 197 | 5 | AAO186443 S. commun |
| 19 | 663 | 60.9 | 197 | 5 | AAE184445 Schizophy |
| 20 | 663 | 60.9 | 197 | 8 | AD166745 S. commun |
| 21 | 647.5 | 59.5 | 190 | 7 | AAO30298 Trichoder |
| 22 | 647.5 | 59.5 | 190 | 7 | AAO30297 Trichoder |
| 23 | 646.5 | 59.4 | 190 | 5 | AAE18492 Trichoder |
| 24 | 646.5 | 59.4 | 190 | 5 | AEBA7005 Thermophi |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 25 | 646 | 59.4 | 227 | 9 | AEB00301 Xylanase |
| 26 | 645 | 59.3 | 227 | 2 | AAE75421 Humicola |
| 27 | 645 | 59.3 | 227 | 2 | AAE78231 Humicola |
| 28 | 644.5 | 59.2 | 190 | 5 | AAE18496 Trichoder |
| 29 | 644.5 | 59.2 | 190 | 5 | AAE18494 Trichoder |
| 30 | 644.5 | 59.2 | 190 | 5 | AEBA7006 Thermophi |
| 31 | 643.5 | 59.1 | 190 | 7 | AAO30284 Trichoder |
| 32 | 643.5 | 59.1 | 190 | 7 | AAO30285 Trichoder |
| 33 | 643.5 | 59.1 | 190 | 7 | AAO30286 Trichoder |
| 34 | 643.5 | 59.1 | 190 | 7 | AAO30283 Trichoder |
| 35 | 643.5 | 59.1 | 190 | 7 | AAO30293 Trichoder |
| 36 | 643.5 | 59.1 | 190 | 7 | AAO30294 Trichoder |
| 37 | 641 | 58.9 | 234 | 6 | ABE80186 A. fumiga |
| 38 | 640.5 | 58.9 | 190 | 5 | AEBA7004 Thermophi |
| 39 | 640.5 | 58.9 | 190 | 5 | AEBA7001 Thermophi |
| 40 | 640.5 | 58.9 | 190 | 7 | AAO30304 Trichoder |
| 41 | 639.5 | 58.8 | 190 | 5 | AAE18493 Trichoder |
| 42 | 639.5 | 58.8 | 190 | 5 | AAE18495 Trichoder |
| 43 | 639.5 | 58.8 | 190 | 5 | AEBA7002 Thermophi |
| 44 | 639.5 | 58.8 | 190 | 7 | AAO30307 Trichoder |
| 45 | 639.5 | 58.8 | 190 | 7 | AAO30306 Trichoder |

ALIGNMENTS

| | | |
|----------|---|-------------------------------------|
| RESULT 1 | AAE18456 | AAE18456 standard; protein; 194 AA. |
| XX | XX | XX |
| AC | AAE18456; | |
| XX | XX | XX |
| DT | 16-MAY-2002 (first entry) | |
| XX | XX | XX |
| DE | Thermomyces lanuginosus xylanase, Xyn. | |
| XX | XX | XX |
| KM | Modified xylanase; thermostability; alkalophilicity; industrial process; | |
| KW | pulp manufacture; poultry; swine feed; enzyme; Xyn. | |
| OS | Thermomyces lanuginosus. | |
| XX | XX | XX |
| PN | W0200192487-A2. | |
| XX | XX | XX |
| PD | 06-DEC-2001. | |
| XX | XX | XX |
| PF | 31-MAY-2001; 2001MO-CA000769. | |
| XX | XX | XX |
| PR | 31-MAY-2000; 2000US-0213803P. | |
| XX | XX | XX |
| PA | (CANADA) NAT RES COUNCIL CANADA. | |
| XX | XX | XX |
| PI | Sung WL; | |
| XX | XX | XX |
| DR | WPI; 2002-171435/22. | |
| XX | XX | XX |
| PT | Modified xylanase exhibiting increased thermostability and | |
| PT | alkalophilicity useful for industrial processing e.g. for pulp | |
| XX | XX | XX |
| PS | Disclosure; Page 83-84; 109pp; English. | |
| XX | XX | XX |
| CC | The present invention relates to a modified xylanase exhibiting increased | |
| CC | thermostability and alkalophilicity. Modified xylanase is useful in | |
| CC | industrial process such as pulp manufacturing. Modified xylanase is also | |
| CC | useful for bleaching of pulp, processing of precision devices and | |
| CC | improving digestibility of poultry and swine feed. Modified xylanase has | |
| CC | improved performance at conditions of high temperature and pH and | |
| CC | exhibits improved thermostability and/or alkalophilicity in comparison to | |
| CC | corresponding native xylanase. The present sequence is Thermomyces | |
| XX | lanuginosus xylanase, Xyn | |
| XX | XX | XX |
| SQ | Sequence 194 AA; | |

Query Match 100.0%; Score 1088; DB 5; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTTPNSGMDGYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGMNPLNARAI 60
DB 1 OTTPNSGMDGYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGMNPLNARAI 60
QY HFEGVYQPNKNSLYAVGWTRNPLVEYIYVENFGTYPPSSGATDLGVECDGSIYRLGKT 120
DB HFEGVYQPNKNSLYAVGWTRNPLVEYIYVENFGTYPPSSGATDLGVECDGSIYRLGKT 120
QY 121 TRVAPSIDGTQTFDDQYMSVRQDKRTSGTYQTGCHFDAMARAGLNVNGDHYQIVATEGY 180
DB 121 TRVAPSIDGTQTFDDQYMSVRQDKRTSGTYQTGCHFDAMARAGLNVNGDHYQIVATEGY 180
QY 181 FSSGYARITVADVG 194
DB 181 FSSGYARITVADVG 194

RESULT 2
ID AAM01112 standard; protein; 225 AA.
AC AAM01112;
XX
DT 21-MAY-1997 (first entry)
DE xylanase.
KM xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermosaccus;
KM Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia;
KM Byssoschlamus; Pectilomyces; animal feed additive; in-vivo breakdown;
KM plant cell wall; growth rate; feed conversion.
XX
XX Thermomyces lanuginosus.
OS
PN W09623062-A1.
XX
PD 01-AUG-1996.
XX
PF 26-JAN-1996; 96WO-DK000046.
XX
PR 26-JAN-1995; 95DK-00000094.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Hansen PK; Wagner P; Muelleretz A; Knap IH;
XX
DR WPI; 1996-454790/45.
DR N-PSDB; AAT40742.
XX
PT Fungal xylanase preps. for use as animal feed additives - and DNA
PT construct for producing recombinant Thermomyces xylanase.
XX
PS Claim 5; Page 45-46; 69pp; English.
XX
CC This sequence represents the xylanase from Thermomyces lanuginosus strain
CC DSM 4109. This xylanase, and xylanases derived from Humicola,
CC Thermosaccus, Chaetomium, Mucor, Talaromyces, Malbranchea, Myceliophthora,
CC Thielavia, Byssoschlamus or Pectilomyces strains can be used in the
CC monocomponent xylanase preparations of the invention. The xylanase
CC preparations and the recombinant Thermomyces xylanase are useful as
CC animal feed additives, which promote in-vivo breakdown of plant cell wall
CC material and thus improve digestibility, growth rate and/or feed
CC conversion
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1088; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-98;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTTPNSGMDGYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGMNPLNARAI 60
DB 32 OTTPNSGMDGYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGMNPLNARAI 91
QY HFEGVYQPNKNSLYAVGWTRNPLVEYIYVENFGTYPPSSGATDLGVECDGSIYRLGKT 120
DB HFEGVYQPNKNSLYAVGWTRNPLVEYIYVENFGTYPPSSGATDLGVECDGSIYRLGKT 151
QY 121 TRVAPSIDGTQTFDDQYMSVRQDKRTSGTYQTGCHFDAMARAGLNVNGDHYQIVATEGY 180
DB 152 TRVAPSIDGTQTFDDQYMSVRQDKRTSGTYQTGCHFDAMARAGLNVNGDHYQIVATEGY 211
QY 181 FSSGYARITVADVG 194
DB 212 FSSGYARITVADVG 225

RESULT 3
ID AAM05187 standard; protein; 225 AA.
AC AAM05187;
XX
DT 16-OCT-2003 (revised)
DT 22-FEB-1997 (first entry)
XX
DE Endo-1,4-beta-D-xylanase.
XX
KM Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;
KM Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;
KM flour; baking; dough.
XX
OS Thermomyces lanuginosus; (strain DSM 4109) .
XX
PN W09632472-A1.
XX
PD 17-OCT-1996.
XX
PF 11-APR-1996; 96WO-DK000171.
XX
PR 11-APR-1995; 95DK-000000435.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Jorgensen OB; Si JQ; Jakobsen TS;
XX
DR WPI; 1996-477123/47.
DR N-PSDB; AAT43010.
XX
PT Bread improving additive contg. xylanase from Thermomyces - and opt.
PT alpha-amylase, increases volume, improves anti-staling properties etc.
XX
PS Claim 4; Page 31-32; 41pp; English.
XX
CC The sequence represents an endo-1,4-beta-D-xylanase from Thermomyces
CC lanuginosus (Humicola lanuginosa), which may be used as a bread-
CC improving additive. The enzyme may be expressed recombinantly from a
CC plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (clained),
CC and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour,
CC optionally along with other enzymes (amylase, maltogenase, lipase,
CC cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase,
CC protease and/or peroxidase). The enzyme combines particularly well with
CC amylolytic enzymes, and may be used to improve baking properties of flour
CC and/or dough, by increasing volume and improving texture, flavour, crumb
CC softness, freshness and anti-staling properties, while improving dough
CC machinability and stability. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1088; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-98;

Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 OTTPNSGMDGYYSWSDGGAQATYTNLEGGTYEISWGDGGLVGKGMNPELNARAI 60
Db 32 OTTPNSGMDGYYSWSDGGAQATYTNLEGGTYEISWGDGGLVGKGMNPELNARAI 91
Oy 61 HFEGVYQPNGNSYLA VYGMWRNPLVEYYIENFGTYDPSSGATDLGTVCDGSYIRLGKT 120
Db 92 HFEGVYQPNGNSYLA VYGMWRNPLVEYYIENFGTYDPSSGATDLGTVCDGSYIRLGKT 151
Oy 121 TRVVAPEIDGTQTFDQYWSVRQDKRTSGTYQTGCHFPAMARAAGLVNVDHYQIVATEGY 180
Db 152 TRVVAPEIDGTQTFDQYWSVRQDKRTSGTYQTGCHFPAMARAAGLVNVDHYQIVATEGY 211
Oy 181 FSSGYARITVADVG 194
Db 212 FSSGYARITVADVG 225
```

RESULT 4

ABR63119
ID ABR63119 standard; protein; 225 AA.

XX ABR63119;

DT 18-DEC-2003 (first entry)

DE Thermomyces lanuginosus xylanase.

KW xylanase; thermostable; enzyme; feed additive.

XX Thermomyces lanuginosus.

XX Key Location/Qualifiers

PT Peptide 1..30

PT Protein /label= signal_peptide

FT 31..225

XX /label= Mature_protein

XX WO2003062409-A2.

XX 31-JUL-2003.

XX 23-JAN-2003; 2003WO-DK000039.

XX 25-JAN-2002; 2002DK-00000130.

XX (HOPF) ROCHE VITAMINS AG.

XX Wu W, Pettersson D, Fugleang CC;

XX WPI; 2003-731382/69.

XX Composition useful as an animal feed additive comprises at least two

XX thermostable enzymes selected from endoglucanase, xylanase, phytase,

XX protease, galactanase, mannanase, dextranase and alpha-galactosidase.

XX Disclosure; Page 60-61; Opp; English.

XX The present sequence is the protein sequence of a thermostable xylanase

XX of Thermomyces lanuginosus. The xylanase has a melting temperature (Tm)

XX of 75.0 degrees C at pH 7.0. It is preferred for use in a claimed

XX composition of the invention, which comprises at least 2 thermostable

XX enzymes selected from an endoglucanase, xylanase, phytase, protease,

XX galactanase, mannanase, dextranase and alpha-galactosidase. The

XX composition is useful for improving the nutritional value of animal

XX feed, especially those containing soya, wheat, barley, oats and/or rye

XX Sequence 225 AA;

XX Query Match 100.0%; Score 1088; DB 7; Length 225;

XX Best Local Similarity 100.0%; Pred. No. 2.2e-98;

XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 OTTPNSGMDGYYSWSDGGAQATYTNLEGGTYEISWGDGGLVGKGMNPELNARAI 60

Db 32 OTTPNSGMDGYYSWSDGGAQATYTNLEGGTYEISWGDGGLVGKGMNPELNARAI 91

Oy 61 HFEGVYQPNGNSYLA VYGMWRNPLVEYYIENFGTYDPSSGATDLGTVCDGSYIRLGKT 120

Db 92 HFEGVYQPNGNSYLA VYGMWRNPLVEYYIENFGTYDPSSGATDLGTVCDGSYIRLGKT 151

Oy 121 TRVVAPEIDGTQTFDQYWSVRQDKRTSGTYQTGCHFPAMARAAGLVNVDHYQIVATEGY 180

Db 152 TRVVAPEIDGTQTFDQYWSVRQDKRTSGTYQTGCHFPAMARAAGLVNVDHYQIVATEGY 211

Oy 181 FSSGYARITVADVG 194

Db 212 FSSGYARITVADVG 225

RESULT 5

ABE00305
ID ABE00305 standard; protein; 225 AA.

XX ABE00305;

DT 08-SEP-2005 (first entry)

DE xylanase SEQ ID NO:15.

KW enzyme; xylanase; feedstuff; alcohol; fermentation; brewing; filtration.

XX Thermomyces lanuginosus.

XX WO2005059084-A1.

XX 30-JUN-2005.

XX 17-DEC-2004; 2004WO-DK000880.

XX 19-DEC-2003; 2003DK-00001895.

XX (NOVO) NOVOZYMES AS.

XX Feistersen RM, Vilkeoe-Nielsen A, Joergensen CT, Christensen LLH;

XX WPI; 2005-458778/46.

XX Preparation of a mash (having enhanced filterability and/or improved

XX extract yield after filtration) comprises preparing a mash in the

XX presence of enzyme activities comprising xylanase of GH family 10 and

XX filtering to obtain wort.

XX Disclosure; SEQ ID NO 15; 68pp; English.

XX The invention relates to a process for preparing a mash (A) (having

XX enhanced filterability and/or improved extract yield after filtration)

XX which comprises preparing a mash in the presence of enzyme activities

XX (comprising a xylanase of GH family 10 at at least 15% w/w of the total

XX xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a

XX wort. Also described is a composition is useful for reducing the

XX viscosity of an aqueous solution comprising a starch hydrolysate, which

XX is a mash for beer making or a feed composition. The process is useful

XX for the production of an alcoholic beverage, such as beer or whiskey and

XX the composition is useful in the mashing and filtration step in brewing

XX process. The present sequence represents a xylanase used in the mashing

XX process of the invention.

XX Sequence 225 AA;

XX Query Match 100.0%; Score 1088; DB 9; Length 225;

XX Best Local Similarity 100.0%; Pred. No. 2.2e-98;

XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 OTTPNSGMDGYYSWSDGGAQATYTNLEGGTYEISWGDGGLVGKGMNPELNARAI 60

|||||
Db 32 QTPNSEGMDHGYYSWMSDGAQATYTNLEGGTYEISWGGGGLVGGKGMNPGLNARAI 91
Qy 61 HFEVYQPNNGSYLAAYGWTNRNPLVEYYIVENFCTYPPSSGATDLGTVEDCGSIVRLGKT 120
Db 92 HFEVYQPNNGSYLAAYGWTNRNPLVEYYIVENFCTYPPSSGATDLGTVEDCGSIVRLGKT 151
Qy 121 TRVAPSIDGTQTFPDQWYSVRQDKRTSGTVQTGCHFDPMARAGLNVDGHHYQIVATEGY 180
Db 152 TRVAPSIDGTQTFPDQWYSVRQDKRTSGTVQTGCHFDPMARAGLNVDGHHYQIVATEGY 211
Qy 181 FSSGVARITVADVG 194
Db 212 FSSGVARITVADVG 225

RESULT 6

AAB48543

ID AAB48543 standard; protein; 194 AA.

AAB48543;

05-MAR-2001 (first entry)

Thermomyces lanuginosus xylanase.

Bacterial; Bacillus circulans; xylanase; xylanase activity; XA; bleaching agent.

Thermomyces lanuginosus.

WO200068396-A2.

16-NOV-2000.

12-MAY-2000; 2000WO-US013172.

12-MAY-1999; 99US-0133714P.

(XENC-) XENCOR INC.

Benzien JM;

WPI; 2000-679800/66.

Non naturally occurring XA protein with enhanced thermophilicity, algalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.

Disclosure; Fig 16L; 114pp; English.

The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, algalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp

Sequence 194 AA;

Query Match 99.5%; Score 1083; DB 3; Length 194;

Best Local Similarity 100.0%; Pred. No. 5.5e-98;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTPNSEGMHGDYYSWMSDGAQATYTNLEGGTYEISWGGGGLVGGKGMNPGLNARAIH 61
Db 2 TTPNSEGMHGDYYSWMSDGAQATYTNLEGGTYEISWGGGGLVGGKGMNPGLNARAIH 61
Qy 62 FEGYQPNNGSYLAAYGWTNRNPLVEYYIVENFCTYPPSSGATDLGTVEDCGSIVRLGKT 121
Db 62 FEGYQPNNGSYLAAYGWTNRNPLVEYYIVENFCTYPPSSGATDLGTVEDCGSIVRLGKT 121

Qy 122 RVNAPSIDGTQTFPDQWYSVRQDKRTSGTVQTGCHFDPMARAGLNVDGHHYQIVATEGY 181
Db 122 RVNAPSIDGTQTFPDQWYSVRQDKRTSGTVQTGCHFDPMARAGLNVDGHHYQIVATEGY 181
Qy 182 SSGVARITVADVG 194
Db 182 SSGVARITVADVG 194

RESULT 7

AA018649

ID AA018649 standard; protein; 194 AA.

AA018649;

24-OCT-2002 (first entry)

T lanuginosus xylanase.

Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching; liquid clarification; coffee extraction; plant oil extraction; starch extraction; food thickener; animal food additive; mutant; mutein.

Thermomyces lanuginosus.

WO200238746-A2.

16-MAY-2002.

09-NOV-2001; 2001WO-US048018.

10-NOV-2000; 2000US-00710050.

(XENC-) XENCOR INC.

Benzien J, Dahiyat B;

WPI; 2002-608200/65.

Novel xylanase activity protein, useful in bleaching process of pulp and in food and animal feed industry, has enhanced thermostability and algalophilicity.

Disclosure; Fig 16L; 121pp; English.

The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase, where the protein has been modified to exhibit enhanced thermophilicity, algalophilicity, or thermostability relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductor. The present sequence is a xylanase protein described in the exemplification of the invention

Sequence 194 AA;

Query Match 99.5%; Score 1083; DB 5; Length 194;

Best Local Similarity 100.0%; Pred. No. 5.5e-98;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTPNSEGMHGDYYSWMSDGAQATYTNLEGGTYEISWGGGGLVGGKGMNPGLNARAIH 61
Db 2 TTPNSEGMHGDYYSWMSDGAQATYTNLEGGTYEISWGGGGLVGGKGMNPGLNARAIH 61
Qy 62 FEGYQPNNGSYLAAYGWTNRNPLVEYYIVENFCTYPPSSGATDLGTVEDCGSIVRLGKT 121
Db 62 FEGYQPNNGSYLAAYGWTNRNPLVEYYIVENFCTYPPSSGATDLGTVEDCGSIVRLGKT 121

Db 62 FEGYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSGATDLGTECDGSIRLCKTT 121
QY 122 RVNAPSIDGTQTPDQWVSVRQDKRTSGTVGTGCHFPDAMARAGLVNVDHYQIVATEGYF 181
Db 122 RVNAPSIDGTQTPDQWVSVRQDKRTSGTVGTGCHFPDAMARAGLVNVDHYQIVATEGYF 181
QY 182 SSGYARITVADVG 194
Db 182 SSGYARITVADVG 194

RESULT 8
ADI6751
ID ADI6751 standard; protein; 194 AA.
XX ADI6751;
AC
XX
XX 22-APR-2004 (first entry)
XX
XX T. lanuginosus xylanase.
XX
XX Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
XX paper industry; food; animal feed; thermostability; alkaliphilic;
XX hot alkali treatment.
XX
XX Thermomyces lanuginosus.
XX
XX US662923-B1.
XX
XX 27-JAN-2004.
XX
XX 12-MAY-2000; 2000US-00570856.
XX
XX PR 12-MAY-1999; 99US-0133714P.
XX PR 07-JUN-1999; 99US-0138156P.
XX
XX (XENC-) XENCOR.
XX
XX PI Bentzen J, Dahljat BI;
XX
XX WPI; 2004-118575/12.
XX
XX
XX New mutant xylanase (XA) protein comprising at least four amino acid
XX substitutions as compared to Bacillus circulans xylanase, useful for
XX bleaching (paper) pulp, and in the food and animal feed industries.
XX
XX Disclosure; SEQ ID NO 24; 84pp; English.
XX
XX
XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
XX xylanase from Bacillus circulans) protein appearing as ADI6730. Also
XX included is a bleaching agent comprising the XA protein. The non-
XX naturally occurring XA protein comprises at least four amino acid
XX substitutions as compared to Bacillus circulans xylanase ADI6728. The
XX amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
XX 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
XX 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
XX useful for bleaching pulp in the paper and related industries, but is
XX also useful in the food and animal feed industries. The new protein is
XX active at higher pH and temperature ranges than naturally occurring
XX xylanases, simplifying incorporation of the xylanase treatment step into
XX pulp processing, especially where the enzyme is added after hot alkali
XX treatment. The present sequence is a xylanase from another species
XX included for comparison.
XX
XX Sequence 194 AA;
XX
XX
XX Query Match 99.5%; Score 1083; DB 8; Length 194;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-98;
XX Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTNSBGMDHGGYYSWMSDGAQATYTNLEGGTYEISWGDGMLVGKGNPGLNARAIH 61
Db 2 TTNSBGMDHGGYYSWMSDGAQATYTNLEGGTYEISWGDGMLVGKGNPGLNARAIH 61

QY 62 FEGYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSGATDLGTECDGSIRLCKTT 121
Db 62 FEGYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSGATDLGTECDGSIRLCKTT 121
QY 122 RVNAPSIDGTQTPDQWVSVRQDKRTSGTVGTGCHFPDAMARAGLVNVDHYQIVATEGYF 181
Db 122 RVNAPSIDGTQTPDQWVSVRQDKRTSGTVGTGCHFPDAMARAGLVNVDHYQIVATEGYF 181
QY 182 SSGYARITVADVG 194
Db 182 SSGYARITVADVG 194

RESULT 9
AAB48542
ID AAB48542 standard; protein; 194 AA.
XX AAB48542;
AC
XX
XX 05-MAR-2001 (first entry)
XX
XX Paecilomyces variotii
XX
XX Paecilomyces variotii xylanase.
XX
XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
XX bleaching agent.
XX
XX Paecilomyces variotii.
XX
XX WO200068396-A2.
XX
XX 16-NOV-2000.
XX
XX 12-MAY-2000; 2000MO-US013172.
XX
XX PR 12-MAY-1999; 99US-0133714P.
XX
XX (XENC-) XENCOR INC.
XX
XX PI Bentzen JM;
XX
XX WPI; 2000-679800/66.
XX
XX
XX Non naturally occurring XA protein with enhanced thermostability,
XX alkalophilicity or thermostability relative to the naturally occurring
XX Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX Disclosure; Fig 16K; 114pp; English.
XX
XX
XX The present sequence is given in a specification relating to non
XX naturally occurring xylanase activity (XA) proteins. The XA proteins
XX comprise an amino acid sequence less than 97% identical to a naturally
XX occurring Bacillus circulans xylanase. They are modified to exhibit
XX enhanced thermostability, alkalophilicity or thermostability relative
XX to the naturally occurring B. circulans xylanase. They may be used as the
XX active compound in a bleaching agent which is used for bleaching pulp
XX
XX Sequence 194 AA;
XX
XX
XX Query Match 88.7%; Score 965; DB 3; Length 194;
XX Best Local Similarity 87.6%; Pred. No. 2.2e-86;
XX Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 2 TTNSBGMDHGGYYSWMSDGAQATYTNLEGGTYEISWGDGMLVGKGNPGLNARAIH 61
Db 2 TTNSBGMDHGGYYSWMSDGAQATYTNLEGGTYEISWGDGMLVGKGNPGLNARAIH 61
QY 62 FEGYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSGATDLGTECDGSIRLCKTT 121
Db 62 FEGYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSGATDLGTECDGSIRLCKTT 121
QY 122 RVNAPSIDGTQTPDQWVSVRQDKRTSGTVGTGCHFPDAMARAGLVNVDHYQIVATEGYF 181
Db 122 RVNAPSIDGTQTPDQWVSVRQDKRTSGTVGTGCHFPDAMARAGLVNVDHYQIVATEGYF 181

Db 122 RYNAPSIDGTQTFNQYWSVRQDKRSSGTQVOTGCHFDAMASAGLNVGDHYQIVATEGYF 181
Qy 182 SSGYARITVADVG 194
182 SSGYARITVADVG 194

RESULT 10
AAO18648
ID AAO18648 standard; protein; 194 AA.

AAO18648;

24-OCT-2002 (first entry)

P. variotcii xylanase.

Xy lanase activity; enzyme; thermostable; xylanase; pulp bleaching;
liquid clarification; coffee extraction; plant oil extraction;
starch extraction; food thickener; animal food additive; mutant; mutein.
Paecilomyces variotcii.

MO200238746-A2.

16-MAY-2002.

09-NOV-2001; 2001WO-US048018.

10-NOV-2000; 2000US-00710050.

(XENC-) XENCOR INC.

Bentzen J, Dahiyat B;

WPI; 2002-608200/65.

Novel xylanase activity protein, useful in bleaching process of pulp and
in food and animal feed industry, has enhanced thermostability and
alkalophilicity.

Disclosure; Fig 16K; 121pp; English.

The present invention relates to a non-naturally occurring xylanase
activity (XA) protein comprising an amino acid sequence less than 97%
identical to a naturally occurring Bacillus circulans xylanase, where the
protein has been modified to exhibit enhanced thermostability,
alkalophilicity, or thermostability relative to naturally occurring B.
circulans xylanase, and has at least 5 amino acid substitutions. A
bleaching agent comprising a modified xylanase is useful for bleaching
pulp, in the bioconversion of lignocellulosic materials to fuels, for
clarifying juice and wine, extracting coffee, plant oils and starch,
producing food thickeners, altering texture in bakery products, e.g.
improving the quality of dough, helping bread to rise and processing of
wheat and corn for starch production, use as animal food additives to aid
in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductor. The present sequence is a xylanase protein
described in the exemplification of the invention

Sequence 194 AA;

Query Match 88.7%; Score 965; DB 5; Length 194;
Best Local Similarity 87.6%; Pred. No. 2.2e-86;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 2 TTPNSBGMHGGYYSWMSDGAQATYTNLEGGTYEISWGDGNNVGGKGNPGLNARAIH 61
Db 2 TTPNSBGMHGGYYSWMSDGGDSTYNNSGTYEITWGNCGNIVGGKGNPGLNARAIH 61

Qy 62 PEGYVOPNGNSYLAIVGWTNPLVEYIVENFGTYDPSSGATDGLGYECDSIYRLGKTT 121
Db 62 FTGYQPNNGSYLSYVGNTRNPLVEYIVENFGNSPSSGSTIDGLGYSCDSIYTLGOST 121

Qy 122 RYNAPSIDGTQTFNQYWSVRQDKRSSGTQVOTGCHFDAMASAGLNVGDHYQIVATEGYF 181
Db 122 RYNAPSIDGTQTFNQYWSVRQDKRSSGTQVOTGCHFDAMASAGLNVGDHYQIVATEGYF 181
Qy 182 SSGYARITVADVG 194
182 SSGYARITVADVG 194

RESULT 11
ADI66750
ID ADI66750 standard; protein; 194 AA.

ADI66750;

22-APR-2004 (first entry)

P. variotcii xylanase.

Xy lanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
paper industry; food; animal feed; thermostability; alkalophilic;
hot alkali treatment.

Paecilomyces variotcii.

US6682923-B1.

27-JAN-2004.

12-MAY-2000; 2000US-00570856.

12-MAY-1999; 99US-0133714P.

07-JUN-1999; 99US-0138156P.

(XENC-) XENCOR.

Bentzen J, Dahiyat B;

WPI; 2004-118575/12.

New mutant xylanase (XA) protein comprising at least four amino acid
substitutions as compared to Bacillus circulans xylanase, useful for
bleaching (paper) pulp, and in the food and animal feed industries.

Disclosure; SEQ ID NO 23; 84pp; English.

The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
xylanase from Bacillus circulans) protein appearing as ADI66730. Also
included is a bleaching agent comprising the XA protein. The non-
naturally occurring XA protein comprises at least four amino acid
substitutions as compared to Bacillus circulans xylanase ADI66728. The
amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
79, 105, 142, 171, 176, 180 or 182, especially at positions 28, 30,
58, or 144. The non-naturally occurring xylanase activity (XA) protein is
useful for bleaching pulp in the paper and related industries, but is
also useful in the food and animal feed industries. The new protein is
active at higher pH and temperature ranges than naturally occurring
xylanases, simplifying incorporation of the xylanase treatment step into
pulp processing, especially where the enzyme is added after hot alkali
treatment. The present sequence is a xylanase from another species
included for comparison.

Sequence 194 AA;

Query Match 88.7%; Score 965; DB 8; Length 194;
Best Local Similarity 87.6%; Pred. No. 2.2e-86;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 2 TTPNSBGMHGGYYSWMSDGAQATYTNLEGGTYEISWGDGNNVGGKGNPGLNARAIH 61

Db 2 TTPNSBGMHGGYYSWMSDGGDSTYNNSGTYEITWGNCGNIVGGKGNPGLNARAIH 61

Qy 62 PEGYVOPNGNSYLAIVGWTNPLVEYIVENFGTYDPSSGATDGLGYECDSIYRLGKTT 121

Db 62 FTGVQPNSTSYLSVGTWRNPLVEYYIVENFGSSNPSGSDTIGTSCDSTYTLAQST 121
QY 122 RVNAPSIDGTQTFPOVXSVRODKRTSGTQVGCHEFDAMARAGLVNNDHYQIVATGEYF 181
Db 122 RVNAPSIDGTQTFPOVXSVRODKRSSGTQVGCHEFDAMASAGLVNNDHYQIVATGEYF 181
QY 182 SSGYARITVADVG 194
Db 182 SSGYARITVADVG 194

RESULT 12

AA848548
ID AAB48548 standard; protein; 221 AA.

XX AAB48548;

DT 05-MAR-2001 (first entry)

XX Cocchiobolus carbonum xylanase.

XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;

XX bleaching agent.

OS Cocchiobolus carbonum.

XX W0200068396-A2.

XX 16-NOV-2000.

XX 12-MAY-2000; 2000MO-US013172.

XX 12-MAY-1999; 99US-0133714P.

XX (XENC-) XENCOR INC.

XX Benzelen JM;

XX WPI; 2000-679800/66.

XX Non naturally occurring XA protein with enhanced thermostability,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.

XX Disclosure; Fig 160; 114pp; English.

XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermostability, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp

XX Sequence 221 AA:

Query Match 68.2%; Score 742; DB 3; Length 221;
Best Local Similarity 70.0%; Pred. No. 2.2e-64;

Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 1 QTPNBSGWHMDGYYSWSWDGAQATYTNLEGGTYEISWGDGNTLVGKGMNGLNARAI 60
Db 31 QNTPNBSGHTNCGFWSWSDGABARATYTNAGAGSYSVSGGNTLVGKGMNPG-TARTI 89
QY 61 HFEQGVYQPNQNSYLAVYGWTRNPLVEYYIVENFGTYDPSGATDLGTECDGSIYRLGKT 120
Db 90 TYSGTNYNNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSGQSNKGTIVSDGSYKLAQS 149
QY 121 TRNAPSISDGTQTFPOVXSVRODKRTSGTQVGCHEFDAMARAGLVNNDHYQIVATGEY 180
Db 150 TRNAPSISDGTQTFPOVXSVRODKRSSGTQVGCHEFDAMASAGLVNNDHYQIVATGEY 208

QY 181 FSSGYARITV 190
Db 209 FSTGMAQITV 218

RESULT 13

AA018654
ID AAO18654 standard; protein; 221 AA.

XX AAO18654;

DT 24-OCT-2002 (first entry)

XX C carbonum xylanase.

XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;

XX liquid clarification; coffee extraction; plant oil extraction;

XX starch extraction; food thickener; animal food additive; mutant; mutein.

OS Cocchiobolus carbonum.

XX W0200238746-A2.

XX 16-MAY-2002.

XX 09-NOV-2001; 2001MO-US048018.

XX 10-NOV-2000; 2000US-00710050.

XX (XENC-) XENCOR INC.

XX Benzelen J, Dahiyat B;

XX WPI; 2002-608200/65.

XX Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.

XX Disclosure; Fig 160; 121pp; English.

XX The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermostability,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention

XX Sequence 221 AA:

Query Match 68.2%; Score 742; DB 5; Length 221;
Best Local Similarity 70.0%; Pred. No. 2.2e-64;

Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 1 QTPNBSGWHMDGYYSWSWDGAQATYTNLEGGTYEISWGDGNTLVGKGMNGLNARAI 60
Db 31 QNTPNBSGHTNCGFWSWSDGABARATYTNAGAGSYSVSGGNTLVGKGMNPG-TARTI 89
QY 61 HFEQGVYQPNQNSYLAVYGWTRNPLVEYYIVENFGTYDPSGATDLGTECDGSIYRLGKT 120
Db 90 TYSGTNYNNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSGQSNKGTIVSDGSYKLAQS 149
QY 121 TRNAPSISDGTQTFPOVXSVRODKRTSGTQVGCHEFDAMARAGLVNNDHYQIVATGEY 180
Db 150 TRNAPSISDGTQTFPOVXSVRODKRSSGTQVGCHEFDAMASAGLVNNDHYQIVATGEY 208

Db 150 TRTNPSIDGTRTFQYWSVRQNKSSGSVNMKTHFDAMASKGNL-GQHYQIVATEGY 208
QY 181 FSSGYARITV 190
Db 209 FSTGNAQITV 218

RESULT 14
ADI66756
ID ADI66756 standard; protein: 221 AA.
AC ADI66756;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX
DE C. carbonum xylanase.
XX
XX xylanase; XA; EC 3.2.1.8; enzyme; bleaching, bleaching pulp;
KM paper industry; food; animal feed; thermostability; alkaliphilic;
KM hot alkali treatment.
XX
XX Cochllobolus carbonum.
OS
XX US6682923-B1.
PN
XX 27-JAN-2004.
PD
XX 12-MAY-2000; 2000US-00570856.
PF
XX 12-MAY-1999; 99US-0133714P.
PR 07-JUN-1999; 99US-0138156P.
XX
XX (XENC-) XENCOR.
PA
PI Bentzien J, Dahiyat BT;
XX
XX WPI; 2004-118575/12.
DR
XX
XX New mutant xylanase (XA) protein comprising at least four amino acid
PT substitutions as compared to Bacillus circulans xylanase, useful for
PT bleaching (paper) pulp, and in the food and animal feed industries.
PT
XX
XX Disclosure; SEQ ID NO 29; 84pp; English.
PS
XX
XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
CC xylanase, from Bacillus circulans) protein appearing as ADI66730. Also
CC included is a bleaching agent comprising the XA protein. The non-
CC naturally occurring XA protein comprises at least four amino acid
CC substitutions as compared to Bacillus circulans xylanase ADI66728. The
CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
CC useful for bleaching pulp in the paper and related industries, but is
CC also useful in the food and animal feed industries. The new protein is
CC active at higher pH and temperature ranges than naturally occurring
CC xylanases, simplifying incorporation of the xylanase treatment step into
CC pulp processing, especially where the enzyme is added after hot alkali
CC treatment. The present sequence is a xylanase from another species
CC included for comparison.
CC
XX
XX
SQ Sequence 221 AA;
Query Match 68.2%; Score 742; DB 8; Length 221;
Best Local Similarity 70.0%; Pred. No. 2.2e-64;
Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 1 QTTNPSGMDGYYSWMSDGAQATYTNLEGGTYEISWGDGMLVGKGNPNGLNARAI 60
Db 31 QNTNNGEGTHNGCFMSWMSDGAARATYTNNGAGGSYSVSWSGGNLVGKGNPNP- TARTI 89
QY 61 HPEGYOPNGNSYLAIVGWTNRPPLVEYYIVENFGTYDPSGATDGLGTYECGSIYRLGKT 120
Db 90 TYSGYTPNGNSYLAIVGWTNRPPLVEYYIVENFGTYDPSGATDGLGTYECGSIYRLGKT 149

QY 121 TRVNAPSIDGTFQYWSVRQDKRTSGTYQVGCHPDAMARAGLNVDHYYQIVATEGY 180
Db 150 TRTNPSIDGTRTFQYWSVRQNKSSGSVNMKTHFDAMASKGNL-GQHYQIVATEGY 208
QY 181 FSSGYARITV 190
Db 209 FSTGNAQITV 218

RESULT 15
AAW60736
ID AAW60736 standard; protein: 197 AA.
AC AAW60736;
XX
XX
DT 02-SEP-1998 (first entry)
XX
XX
DE xylanase A of Schizophyllum commune.
XX
XX Family 11 xylanase; improve; thermophilicity; alkalophilicity;
KM thermotolerance; bleach; wood pulp; processing; wheat; maize;
KM digestibility-improving animal feed additive; starch production; mutant.
XX
XX Schizophyllum commune.
OS
XX EP828002-A2.
PN
XX 11-MAR-1998.
PD
XX 05-SEP-1997; 97EP-00115412.
PF
XX 09-SEP-1996; 96US-00709912.
PR
XX (CANA) NAT RES COUNCIL CANADA.
PA
PI Sung WL, Yaguchi M, Ishikawa K;
XX
XX WPI; 1998-161100/15.
DR
XX
XX Modified xylanase enzymes - useful for improving wood pulp bleaching,
PT etc.
PT
XX
XX Disclosure; Page 40; 84pp; English.
PS
XX
XX AAW60728-44 represent family 11 xylanases. The specification describes a
CC method for modifying a Family 11 xylanase to improve its thermophilicity,
CC alkalophilicity and or thermotolerance. This method comprises
CC modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase
CC 11 or corresponding aligned amino acids of another Family 11 xylanase,
CC replacement of one or more amino acid sequences in the N-terminal region
CC with corresponding aligned sequences from another Family 11 xylanase to
CC form a chimeric xylanase and/or upstream extension of the N terminus by
CC addition of upto 10 amino acids. The modified xylanases are useful for
CC improving the bleachability of wood pulp by treatment at 55-75 degrees
CC celvius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as
CC digestibility-improving animal feed additives. They might also be useful
CC in the processing of wheat or maize for starch production
CC
XX
XX
SQ Sequence 197 AA;
Query Match 60.9%; Score 663; DB 2; Length 197;
Best Local Similarity 61.3%; Pred. No. 1.1e-56;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 3 TPNSGMDGYYSWMSDGAQATYTNLEGGTYEISWGDGMLVGKGNPNGLNARAIH 61
Db 3 TPNSGMDGYYSWMSDGAQATYTNLEGGTYEISWGDGMLVGKGNPNGLNARAIH 62
QY 62 PEGYOPNGNSYLAIVGWTNRPPLVEYYIVENFGTYDPSGATDGLGTYECGSIYRLGKT 121
Db 63 YSGYTPNGNSYLAIVGWTNRPPLVEYYIVENFGTYDPSGATDGLGTYECGSIYRLGKT 122

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: February 10, 2006, 14:54:33 / Search time 24.0764 Seconds
(without alignments)
775.285 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225

Sequence: 1 QTTPNSEGMHGDGYYSWMSD.....VATEGYSSGVARITVADVG 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 653 | 60.9 | 197 | 1 A44597 | endo-1,4-beta-xylan |
| 2 | 656 | 60.3 | 219 | 2 S71472 | endo-1,4-beta-xylan |
| 3 | 648 | 59.6 | 225 | 1 S57477 | endo-1,4-beta-xylan |
| 4 | 646 | 59.4 | 227 | 2 S43919 | endo-1,4-beta-xylan |
| 5 | 642.5 | 59.1 | 241 | 2 S71473 | endo-1,4-beta-xylan |
| 6 | 636.5 | 58.5 | 190 | 1 A44593 | endo-1,4-beta-xylan |
| 7 | 636.5 | 58.5 | 190 | 1 A44595 | endo-1,4-beta-xylan |
| 8 | 635.5 | 58.4 | 222 | 2 S39154 | endo-1,4-beta-xylan |
| 9 | 635.5 | 58.4 | 223 | 2 S39683 | endo-1,4-beta-xylan |
| 10 | 634.5 | 58.3 | 190 | 1 A44594 | endo-1,4-beta-xylan |
| 11 | 625 | 57.4 | 232 | 2 JC7577 | endo-1,4-beta-xylan |
| 12 | 615 | 56.5 | 221 | 1 S57469 | endo-1,4-beta-xylan |
| 13 | 571.5 | 52.5 | 333 | 1 JS0590 | endo-1,4-beta-xylan |
| 14 | 569.5 | 52.3 | 335 | 2 JS0601 | endo-1,4-beta-xylan |
| 15 | 555.5 | 51.1 | 221 | 2 TC7307 | endo-1,4-beta-xylan |
| 16 | 544 | 50.0 | 240 | 2 T37005 | endo-1,4-beta-xylan |
| 17 | 543.5 | 50.0 | 240 | 1 S47512 | endo-1,4-beta-xylan |
| 18 | 529.5 | 48.7 | 240 | 1 JS0591 | endo-1,4-beta-xylan |
| 19 | 522.5 | 48.0 | 661 | 1 S59633 | endo-1,4-beta-xylan |
| 20 | 509 | 46.8 | 644 | 1 I40712 | endo-1,4-beta-xylan |
| 21 | 503 | 46.1 | 210 | 2 C83762 | endo-1,4-beta-xylan |
| 22 | 491 | 45.1 | 656 | 1 S59631 | endo-1,4-beta-xylan |
| 23 | 470.5 | 43.2 | 213 | 1 I40569 | endo-1,4-beta-xylan |
| 24 | 469.5 | 43.2 | 213 | 1 S48126 | endo-1,4-beta-xylan |
| 25 | 468.5 | 43.1 | 213 | 1 S01734 | endo-1,4-beta-xylan |
| 26 | 451.5 | 41.5 | 354 | 1 S51779 | endo-1,4-beta-xylan |
| 27 | 426.5 | 39.2 | 511 | 1 JQ1935 | endo-1,4-beta-xylan |
| 28 | 395 | 36.3 | 261 | 1 S12745 | endo-1,4-beta-xylan |
| 29 | 393.5 | 36.2 | 228 | 1 WMB5XP | endo-1,4-beta-xylan |

| | | | | | |
|----|-------|------|------|----------|---------------------|
| 30 | 388 | 35.7 | 211 | 1 JC1198 | endo-1,4-beta-xylan |
| 31 | 387 | 35.6 | 211 | 2 S49542 | endo-1,4-beta-xylan |
| 32 | 385 | 35.4 | 211 | 2 S48329 | endo-1,4-beta-xylan |
| 33 | 371 | 34.1 | 954 | 1 S20907 | endo-1,4-beta-xylan |
| 34 | 369.5 | 34.0 | 789 | 2 S58235 | endo-1,4-beta-xylan |
| 35 | 361 | 33.2 | 781 | 2 S51592 | Xyln precursor - R |
| 36 | 353.5 | 32.5 | 802 | 2 A36910 | xylanase, beta(1,3) |
| 37 | 352 | 32.4 | 229 | 2 S39155 | xylanase 2 - fungus |
| 38 | 348.5 | 32.0 | 209 | 2 JC4909 | endo-1,4-beta-xylan |
| 39 | 285.5 | 26.2 | 607 | 2 S49528 | endoxylanase - rum |
| 40 | 280.5 | 25.8 | 607 | 2 S24754 | endo-1,4-beta-xylan |
| 41 | 247.5 | 22.7 | 608 | 2 B53295 | xylanase (EC 3.2.1 |
| 42 | 236.5 | 21.7 | 266 | 1 S48865 | endo-1,4-beta-xylan |
| 43 | 145 | 13.3 | 50 | 2 A61149 | endo-1,4-beta-xylan |
| 44 | 115 | 10.6 | 2817 | 2 B97033 | uncharacterized pr |
| 45 | 113 | 10.4 | 40 | 2 PQ0202 | endo-1,4-beta-xylan |

ALIGNMENTS

RESULT 1
A44597
endo-1,4-beta-xylanase (EC 3.2.1.8) A - bracket fungus (Schizophyllum commune)
N/Alternate names: xylanase A
C/Species: Schizophyllum commune
C/Date: 27-Jun-1994 #sequence revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: A44597; S41411; A05147; S38973
R/Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A/Accession number: A44593
A/Accession: A44597
A/Molecule type: protein
A/Residues: 1197 <YAG>
A/Cross-references: UNIPROT:P35809; UNIPARC:UPI0000034D33
A/Experimental source: strain Delmar ATCC 38548
R/Bray, M.R.; Clarke, A.J.
Eur. J. Biochem. 219, 821-827, 1994
A/Title: Identification of a glutamate residue at the active site of xylanase A from Schu
A/Reference number: S41411; PMID:94155888; PMID:7906649
A/Accession: S41411
A/Status: preliminary
A/Molecule type: protein
A/Residues: 83-123 <BRA>
A/Cross-references: UNIPARC:UPI0000172966
R/Palce, M.G.; Jurasek, L.; Carpenter, M.R.; Smillie, L.B.
Appl. Environ. Microbiol. 36, 802-808, 1978
A/Reference number: A05147; PMID:79102289; PMID:32833
A/Accession: A05147
A/Molecule type: protein
A/Residues: 1-27 <PAI>
A/Cross-references: UNIPARC:UPI0000172967
R/Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Campbell, R.; Yaguchi, M.; Jurasek, L.;
FEB8 Lett. 334, 296-300, 1993
A/Title: Amino acid sequence and thermostability of xylanase A from Schizophyllum commune
A/Reference number: S38973; PMID:94063044; PMID:8243656
A/Accession: S38973
A/Molecule type: protein
A/Residues: 1-197 <OKU>
A/Cross-references: UNIPARC:UPI0000034D33
A/Experimental source: ATCC 38548
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keyword: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:12-197/Domain: endo-1,4-beta-xylanase homology <XYL>
F:87.184/Active site: Glu #status predicted
F:111-160/Disulfide bonds: #status experimental

Query Match 60.9%; Score 663; DB 1; Length 197;
Best Local Similarity 61.3%; Pred. No. 5e-47;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

```

QY 3 PENSEGMDHYGVYWSWSSGGAQATYTNLEGGTYELSW -GDGAINLVGGKMNPLGNARAIH 61
Db 3 TPSSGTGDDGGYIIYHMTDAGADATYQNNGGSSYTLTSGNNGNPLVGGKMPGAASHSIS 62
QY 62 FEGVYQPNGNSYLAAYGWTNRNPLVEYYIVENFGTYDPSSGATDILGTYECDGSIYRLAKTT 121
Db 63 YSGTYQFPNGNSYLAAYGWTNRSLIEYIVESYGSYDPSAASHKGSYTCNGATYDILSTW 122
QY 122 RVNAPSITGCTQTFPDQYVSVYRQDKRT-----SGTYQTGCHFPAMARAGLNVNGDHYIQTIVA 176
Db 123 RVNAPSITGCTQTFEQFQVSVRNPVKAPGGSISGTYDVQCHFPAMAKGLNKLNGISEHNQIQA 182
QY 177 TEGYFSSGARIITVA 190
Db 183 TEGYQSSGTAITTV 196

RESULT 2
S71472
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
N/Alternate names: xylanase A
C/Species: Chaetomium gracile
C/Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
A/Accession: S71472; S78206
R/Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
A/Rfile: Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus
A/Reference number: S71472; MUID:96118924; PMID:8595661
A/Accession: S71472
A/Molecule type: DNA
A/Residues: 1-219 <YOS>
A/Cross-references: UNIPROT:Q12579; UNIPARC:UPI00000421A6; EMBL:D49850; NID:g1339857; PIR:
A/Molecule type: protein
A/Residues: 31-45;82-94;152-160 <YOH>
A/Cross-references: UNIPARC:UPI0000175A79; UNIPARC:UPI0000175A82; UNIPARC:UPI0000175A83
C/Genetics:
A/Introns: 81/2
C/Function:
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F.1-30/Domain: signal sequence #status predicted <SIG>
F.31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F.412-219/Domain: endo-1,4-beta-xylanase homology <XTL>
F.415,206/Active site: Glu #status predicted

Query Match 60.3%; Score 656; DB 2; Length 219;
Best Local Similarity 61.9%; Pred. NO. 2.1e-46;
Matches 117; Conservative 28; Mismatches 42; Indels 2; Gaps 2;

QY 3 TPNSGMDHYGVYWSWSSGGAQATYTNLEGGTYELSWGDDGNLVGGKMNPLGNARAIH 62
Db 3 TPSSGTGNNGYFYSFWTGGGTGVNQNAGAGGSYSYQMNCGNPFVGGKMNPGA-ARTINF 91
QY 63 EGVYQPNGNSYLAAYGWTNRNPLVEYYIVENFGTYDPSSGATDILGTYECDGSIYRLAKTT 122
Db 92 SGTFSPQNGYIATLGWTONPLVEYIVESFCTDIPSSQASFGFTIQDDGSTYIAKTR 151
QY 123 VNAPSIDGCTQTFPDQYVSVYRQDKRTSGTYQTGCHFPAMARAGLNVNGDHYIQTIVA 182
Db 152 VNQPSITEGISTFDQVSWVRQNRSSGSSVVAHAFAMAGLKL-GSNHYQIVATEGYQS 210
QY 183 SGYARITVA 191
Db 211 SSSSSITVS 219

RESULT 3
S57477
endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - Emericella nidulans
N/Alternate names: xylanase 1

```

CtSpecies: Emericella nidulans, Aspergillus nidulans
CtDate: 10-Oct-1995 #sequence_revision 22-Nov-1996 #ext_change 09-Jul-2004
CtAccession: S57477
Riperez-Gonzalez, J.A.
Submitted to the EMBL Data Library, June 1995
A>Description: Expression in Saccharomyces cerevisiae of two xylanase encoding genes from A.Reference number: S57469

A:Accession: S57477
A:Molecule type: DNA
A:Residues: 1-225 <PER>
A:Cross-references: UNIPROT:P55332; UNIPARC:UPI0000139073; EMBL:Z49892; NID:g505260; PIDD C:Genetics:

A:Introns: 93/2
C:Function:
A>Description: catalyzes the hydrolysis of 1,4-beta-xylonic bonds in xylnas
C:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domaln: signal sequence #status predicted <SIG>
F:20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
F:48-225/Domaln: endo-1,4-beta-xylanase homology <XYL>
F:121,212/Active site: Glu #status predicted

Query Match 59.6%; Score 648; DB 1; Length 225;
Best Local Similarity 61.1%; Pred. No. 9.6e+46;
Matches 116; Conservative 27; Mismatches 45; Indels 2; Gaps 2;

OY 1 OTTPSEGMDHYVYSWNSDGAQATYTNLBGTVEISNGDGSLVGKGMNFGLNARAI 60
 :|::||:||||:||:||||:||||:||||:||||:||||:||||:||||:|
DB 37 RSTPSTGMSNXXYYSPMTDDGGDYTYTNAGAGSYLVQMNSNVGNPFVGGKMFPQ-STRTI 95
OY 61 HFEVGYOPNGSNLYAVGWTRNPVLVEYTVENPGTYPDSGATDLCTVEDCSITRLGKT 120
 ::||:||||:||||:||||:||||:||||:||||:||||:||||:|
DB 96 NYGSFFNPSGNGYLAVGVWTQNPLIEYIVESYGVTNPPSGQHRTVSVDGATYDIYTA 155
OY 121 TRYNAPSIDGTQTFPOVWSVRDCKRTSGTVNQCGHPDMARAGLANNDHYYOI VATEGY 180
 |||:||||:||||:||||:||||:||||:||||:||||:||||:|
DB 156 TRYNPSSLEGTAPEQFMFSVKRSKRGTGTATTANFNMAALGLMRL-GTHNYQLVAITEGY 214
OY 181 FSSGYARTIV 190
 |||:||||
DB 215 QSSGSASITV 224

RESULT 4
S43919
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (*Humicola insolens*)
CtSpecies: Humicola insolens
CtDate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #ext_change 09-Jul-2004
CtAccession: S43919
R.Dalbooge, H.; Heldt-Hansen, H.P.
MOL. Gen. Genet. 243, 253-260, 1994
A>Title: A novel method for efficient expression cloning of fungal enzyme genes.
A:Reference number: S43919; MID:94247364; PMID:8190078
A:Accession: S43919
A:Molecule type: mRNA
A:Residues: 1-227 <DAL>
A:Cross-references: UNIPROT:P55334; UNIPARC:UIP0000421A4; EMBL:X76047; NID:g505260; PID C:Genetics:
A:Gene: XYL1
C:Function:
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domaln: signal sequence #status predicted <SIG>
F:20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>
F:48-225/Domaln: endo-1,4-beta-xylanase homology <XYL>
F:112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
F:121,212/Active site: Glu #status predicted

Query Match 59.4%; Score 646; DB 2; Length 227;
Best Local Similarity 59.5%; Pred. No. 1.4e+45;
Matches 113; Conservative 27; Mismatches 48; Indels 2; Gaps 2;

QY 1 QTPNBSGMDGYYSWMSDGAQATYTNLEGGTYEISMGDGNLVGKGMNPGLNARAI 60
D 37 QVTPNBSGMDGYYSWMSDGAQATYTNLEGGTYEISMGDGNLVGKGMNPGLNARAI 95
QY 61 HFBGVYOPNGNSYLAIVGWTNPLVEYYIYENFGTIDPSSGATDLCGVECDGSITRLGKT 120
D 96 NYGGYFNPQNGYLAIVGWTNPLVEYYIYENFGTIDPSSGATDLCGVECDGSITRLGKT 155
QY 121 TRVNAISIDGTQTFDQYWSVRQDKRTSGVTQTCGHPDAMARAGLVNNGDHYQIVATEGY 180
D 156 TRVNAISIDGTQTFDQYWSVRQDKRTSGVTQTCGHPDAMARAGLVNNGDHYQIVATEGY 214
QY 181 FSSGVARITV 190
D 215 QSSGESDITV 224

RESULT 5
S71473
C/Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
C/Accession: S71473; S78207
R/Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
C/Title: Two family G xylanase genes from Chaetomium gracile and their expression in Aef
A/Reference number: S71472; MUID:96118924; PMID:8595661
A/Molecule type: DNA
A/Accession: S71473
A/Residues: 1-241 <YOS>
A/Cross-references: UNIPROT:Q12580; UNIPARC:UPI00000421AB; EMBL:D49851; NID:gl339855; PI
A/Accession: S78207
A/Molecule type: protein
A/Residues: 38-44; 89-91; 153-161 <YOH>
A/Cross-references: UNIPARC:UPI0000175A77; UNIPARC:UPI0000175A78; UNIPARC:UPI0000175A79
C/Genetics:
A/Insertions: 88/2
A/Function:
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/1-30/Domain: signal sequence #status predicted <SIG>
F/31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>
F/43-220/Domain: endo-1,4-beta-xylanase homology <XYL>
F/116-/Active site: Glu #status predicted

Query Match 59.1%; Score 642.5; DB 2; Length 241;
Best Local Similarity 61.8%; Pred. No. 2,9e-45;
Matches 116; Conservative 27; Mismatches 43; Indels 3; Gaps 3;

QY 1 QTPNBSGMDGYYSWMSDGAQATYTNLEGGTYEISMGDGNLVGKGMNPGLNARAI 59
D 31 QVTPNBSGMDGYYSWMSDGAQATYTNLEGGTYEISMGDGNLVGKGMNPGLNARAI 89
QY 60 IHFBGVYOPNGNSYLAIVGWTNPLVEYYIYENFGTIDPSSGATDLCGVECDGSITRLGKT 119
D 90 INYVNAISIDGTQTFDQYWSVRQDKRTSGVTQTCGHPDAMARAGLVNNGDHYQIVATEGY 149
QY 120 TRVNAISIDGTQTFDQYWSVRQDKRTSGVTQTCGHPDAMARAGLVNNGDHYQIVATEGY 179
D 150 TRVNAISIDGTQTFDQYWSVRQDKRTSGVTQTCGHPDAMARAGLVNNGDHYQIVATEGY 208
QY 180 FSSGVARITV 190
D 209 YSSGSATVNV 219

RESULT 6
A44593
C/Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
C/Accession: A44593
R/Yaguchi, M.
C/Title: The protein sequence database, March 1994
A/Reference number: A44593
A/Accession: A44593
A/Molecule type: protein
A/Residues: 1-190 <YAG>
A/Cross-references: UNIPARC:UPI00000493CB
A/Experimental source: Strain B58
R/Campbell, R.L.; Rose, D.R.
C/Title: The Brookhaven Protein Data Bank, June 1994
A/Reference number: A52868; PDB:1XND
A/Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, A'48-190
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xyloisidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F/86-/Active site: Glu #status predicted
F/126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted
F/129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 58.5%; Score 636.5; DB 1; Length 190;
Best Local Similarity 60.2%; Pred. No. 6,9e-45;
Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;

QY 1 QTPNBSGMDGYYSWMSDGAQATYTNLEGGTYEISMGDGNLVGKGMNPGLNARAI 60

C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
C/Accession: A44593
R/Yaguchi, M.
C/Title: The protein sequence database, March 1994
A/Reference number: A44593
A/Accession: A44593
A/Molecule type: protein
A/Residues: 1-190 <YAG>
A/Cross-references: UNIPARC:UPI00000493CB
A/Experimental source: Strain B58
R/Campbell, R.L.; Rose, D.R.
C/Title: The Brookhaven Protein Data Bank, June 1994
A/Reference number: A52868; PDB:1XND
A/Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, A'48-190
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xyloisidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F/86-/Active site: Glu #status predicted
F/126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted
F/129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 58.5%; Score 636.5; DB 1; Length 190;
Best Local Similarity 60.2%; Pred. No. 6,9e-45;
Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;

QY 1 QTPNBSGMDGYYSWMSDGAQATYTNLEGGTYEISMGDGNLVGKGMNPGLNARAI 60

RESULT 7
A44595
C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: A44595
R/Yaguchi, M.
C/Title: The protein sequence database, March 1994
A/Reference number: A44595
A/Accession: A44595
A/Molecule type: protein
A/Residues: 1-190 <YAG>
A/Cross-references: UNIPROT:Q7W520; UNIPARC:UPI0000172968
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xyloisidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F/86-/Active site: Glu #status predicted
F/126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted
F/129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 58.5%; Score 636.5; DB 1; Length 190;
Best Local Similarity 60.2%; Pred. No. 6,9e-45;
Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;

QY 1 QTPNBSGMDGYYSWMSDGAQATYTNLEGGTYEISMGDGNLVGKGMNPGLNARAI 60

[illegible]

```

RESULT 8
S39154
Xylanase 1 - fungus (Trichoderma reesei)
C|Species: Trichoderma reesei
C|Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C|Accession: S39154
R|ToCorrName, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A.; Kubitz
Biotechnology 10, 1461-1465, 1992
A|Title: The two major xylanases from trichoderma reesei: characterization of both enzymes
A|Reference number: S39154
A|Accession: S39154
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-222 <T05>
A|Cross-references: UNIPROT:P36217; UNIPARC:UPI00000421A9; EMBL:X69573; NID:g396563; PIR
C|Gene: xyn1
A|Gene: xyn1
A|Intons: 90/2
C|Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
/144-222|Domain: endo-1,4-beta-xylanase homology <X1>

```

| Query Match | 58.4% | Score 635.5 | DB 2 | Length 222 |
|-----------------------|-----------------|--|----------|------------|
| Best Local Similarity | 60.2% | Pred. No. 9 | 9e-45 | |
| Matches 115 | Conservative 28 | Mismatches 47 | Indels 1 | Gaps 1 |
| QY | 1 | QTPNSGCHDQYYSWMSDGAQATYTNLBCGYEISWGDGNNLVGKGMPGLNARAI | 60 | |
| Db | 33 | OTIQPGTGNNGYFPFSYMNDDHGGLTYTNGPGGQFSVMNSNSGNFVGKGMPGTNKVY | 92 | |
| QY | 61 | HPEGYQPNNGNSYLLVWGTRNPLVEYYIVENFGYTPDSSGATDIDGVEKDSIRLGT | 120 | |
| Db | 93 | NFSGSYNPNNGNSYLLVWGSRNPLLEYYIVENFGYTNPSGTAKDGEVTSDDSVYDIYK | 152 | |
| QY | 121 | TRVNAPSIDGQTFQDQYWSVRDKEKTSQVQTGCHFDAMARAGLVNNGDHYQIYATBEG | 180 | |
| Db | 153 | QRVNGPSIIGTATFYQYMSVRNRHSSSGSVTANFHNMAAQGLTL-GTMDYQIVAVEGY | 211 | |
| QY | 181 | FSSGYARTITVA | 191 | |
| Db | 212 | FSSGSASITVS | 222 | |

RESULT 9
S39883
endo-1,4-beta-xylosylase (EC 3.2.1.8) II precursor - fungus (*Trichoderma reesei*)
N.Alternate names: endoxylosylase II
C.Species: *Trichoderma reesei*
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C.Accession: S39883; S39884
R.Saarelainen, R.; Palohelmo, M.; Pajetstroem, R.; Suominen, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A.Title: Cloning, sequencing and enhanced expression of the *Trichoderma reesei* endoxylosylase
A.Reference number: S39883; MUID:94088442; PMID:8264524
A.Accession: S39883
A.Molecule type: DNA
A.Residues: 1-223 <SAA>
A.Cross-references: UNIPROT:002244; UNIPARC:UPI00000421A8; EMBL:S67387; NID:q455906; PIR

A:Experimental source: strain QM6a
A:Accession: S39884
A:Molecule type: protein
A:Residues: 34-43;49-57;121-151;178-191 <SAF>
A:Cross-references: UNIPARC:UP10000175A7C; UNIPARC:UP10000175A7D; UNIPARC:UP10000175A7E
C:Genetics
A:Gene: xln2
A:Introns: 91/2
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylane
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
P:1-19/Domain: signal sequence #status predicted <IG>
P:20-33/Domain: propeptide #status predicted <PO>
P:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MT>
F:45-223/Domain: endo-1,4-beta-xylanase homology <YL>
F:71;94/Binding site: carbohydrate (Asn) (covariant) #status predicted
F:110;121/Binding site: substrate (Tyr) #status predicted
F:119;210/Active site: Glu #status predicted

| | | |
|----|--|---|
| | Query Match | 58.4%; Score 635.5; DB 2; Length 223; |
| | Best Local Similarity | 60.2%; Pred. No. 1e-44; |
| | Matches | 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1 |
| QY | 1 QTTNSBGMHDGYIYSWSDGQAQTYYNLHCGTIEISWDGGNLYVGKGNPGLNAAI | 60 |
| | : | |
| DB | 34 QTIOPTGTNGXGFYSYNNDDHGVTYNGGQGPVSVMSSNGNFVGGKMGPGTKNYI | 93 |
| QY | 61 HPEGYOBNGSYLAVYGMTNRPLVEYYIVENFGYDPPSSGATDGTGECSGIYRLAKT | 120 |
| | : | |
| DB | 94 NPSGSYNPNNGSYLSYIGMSRNPFLIEYIVENFPGYNSTGATLGEFTSIDSQSVDIRT | 153 |
| QY | 121 TRVANPSIDGTOTPDQYWSVRQDKRTSGTYOQCHPAMARAGLVNNDHYIQIYAEGY | 180 |
| | : ~ | |
| DB | 154 QRVNQPSTIGTATFYQYWSVRNHRSSGVNTAHFNMAAOQGLTL~GTMDYQIVAIVEGY | 212 |
| QY | 181 FSSGGARTVA 191 | |
| | : ~ | |
| DB | 213 FSSGSASTIVS 223 | |

```

RESULT 10
A44594
    endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
N:Alternate names: xylanase IIA
C:Species: Trichoderma viride
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #ext_change 05-Jul-2004
C:Accession: A44594
R:Yaguchi, M.
    submitted to the Protein Sequence Database, March 1994
A:Reference number: A44593
A:Accession: A44594
A:Molecule type: protein
A:Residues: 1-190 <YAG>
A:Cross-references: UNIPROT:Q7M513; UNIPARC:UPI0000034D34
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:12-190/Domain: endo-1,4-beta-xylanase homology <XY>
F:77,88/Binding site: substrate (Tyr) #status predicted
F:86,177/Active site: Glu #status predicted

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Query Match 35: Score 634.5; DB 1; Length 190;
      Local Similarity 60.2%; Pred. No. 1e-44;
Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;

QY      1 OTTPNSBEMHGGYYTYSWSDGAGATYTNLEGGTYEISWEGGDLVGGKGNIPGLNAPAI 60
      1 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db      1 QTIGGTEGNGFYFSYNNDDHGATYTNNGGGGQPSVWNSGNGFVGGKGGQPGIKNKYI 60

```

3 TPNSEGWHDCYYYSWWSDCGAQATYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHF 62

3 TPNSEGWHDCYYYSWWSDCGAQATYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHF 62

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 14:49:37 ; Search time 195.852 Seconds

(without alignments)
698.857 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225

Sequence: 1 QTPNSEGMDGYGWSMD.....VATEGYSSGARITVADVG 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------|
| 1 | 1088 | 100.0 | 225 | 1 | XYNA_THELA |
| 2 | 965 | 88.7 | 194 | 1 | XYNA_PABVA |
| 3 | 758 | 69.7 | 227 | 2 | Q9UJZ3_9PLEO |
| 4 | 750 | 68.9 | 225 | 2 | Q9CIR2_FUSOX |
| 5 | 742 | 68.2 | 221 | 1 | XYN1_COCOA |
| 6 | 721 | 66.3 | 227 | 2 | Q00263_9PEZI |
| 7 | 705 | 64.8 | 204 | 2 | Q518A1_MAGGR |
| 8 | 705 | 64.8 | 231 | 2 | Q92245_MAGGR |
| 9 | 665 | 61.1 | 225 | 2 | Q766V1_9ASCO |
| 10 | 663 | 60.9 | 197 | 1 | XYNA_SCHCO |
| 11 | 656 | 60.3 | 219 | 2 | Q12579_9PEZI |
| 12 | 656 | 60.3 | 211 | 2 | Q13447_COCOA |
| 13 | 654 | 60.1 | 231 | 2 | Q70T28_9PLEO |
| 14 | 651 | 59.8 | 220 | 2 | Q7SD01_NEUCR |
| 15 | 651 | 59.8 | 228 | 2 | Q4WGL1_ASFPU |
| 16 | 650 | 59.7 | 223 | 2 | Q871E8_NEUCR |
| 17 | 648 | 59.6 | 225 | 1 | XYNA_EMENT |
| 18 | 648 | 59.6 | 225 | 2 | Q5B767_EMENT |
| 19 | 648 | 59.6 | 231 | 2 | Q00350_COCOA |
| 20 | 647 | 59.5 | 227 | 2 | Q9HGE1_HUMGT |
| 21 | 646 | 59.4 | 227 | 1 | XYN1_HUMIN |
| 22 | 642.5 | 59.1 | 241 | 2 | Q12580_9PEZI |
| 23 | 637.5 | 58.6 | 221 | 2 | Q8UJY6_9PEZI |
| 24 | 636.5 | 58.5 | 190 | 2 | Q7M520_TRIYI |
| 25 | 635.5 | 58.4 | 222 | 1 | XYN2_TRIRE |
| 26 | 635.5 | 58.4 | 223 | 2 | Q02244_TRIRE |
| 27 | 634.5 | 58.3 | 190 | 2 | Q7M519_TRIYI |
| 28 | 634 | 58.3 | 220 | 2 | Q8UJY5_9PEZI |
| 29 | 631.5 | 58.0 | 267 | 2 | Q6UN40_9PEZI |
| 30 | 630.5 | 58.0 | 190 | 1 | XYN TRIHA |
| 31 | 630 | 57.9 | 221 | 2 | Q4WLV2_ASFPU |

| | | | | | | |
|----|-------|------|-----|---|--------------|--------------------|
| 32 | 629.5 | 57.9 | 220 | 2 | Q8J0T4_9HYPO | Q8J0T4 trichoderma |
| 33 | 627.5 | 57.7 | 223 | 2 | Q728Q3_TRIYI | Q728Q3 trichoderma |
| 34 | 625 | 57.4 | 232 | 2 | Q9HFA4_ASFPU | Q9HFA4 aspergillus |
| 35 | 623.5 | 57.3 | 223 | 2 | Q99015_TRIRE | Q99015 trichoderma |
| 36 | 621 | 57.1 | 225 | 1 | XYNB_ASFKA | P48824 aspergillus |
| 37 | 620 | 57.0 | 221 | 2 | Q5AQR5_EMENT | Q5AQR5 aspergillus |
| 38 | 619 | 56.9 | 231 | 2 | Q4HYK9_GIBZE | Q4HYK9 gibberella |
| 39 | 619 | 56.9 | 231 | 2 | Q7ZA57_GIBZE | Q7ZA57 gibberella |
| 40 | 617 | 56.7 | 225 | 2 | Q8TG22_ASFPU | Q8TG22 aspergillus |
| 41 | 617 | 56.7 | 225 | 2 | Q6QAZ1_9PLEO | Q6QAZ1 aspergillus |
| 42 | 617 | 56.7 | 231 | 2 | Q9CIR1_FUSOX | Q9CIR1 fusarium ox |
| 43 | 616 | 56.6 | 225 | 1 | XYNB_ASFNG | P55330 aspergillus |
| 44 | 615 | 56.5 | 221 | 1 | XYNB_EMENT | P55333 emeritella |
| 45 | 609 | 56.0 | 223 | 1 | XYN2_MAGGR | P55335 magnaporthe |

ALIGNMENTS

RESULT 1
XYNA_THELA STANDARD; PRT; 225 AA.
ID XYNA_THELA
AC Q43097;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, last sequence update)
DT 13-SEP-2005 (Rel. 48, last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan xylanohydrolase).
GN Name=XYNA;
OS Thermomyces lanuginosus (Humicola lanuginosa).
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
OX NCBI_TaxId=5541;
RN [1]
RP NOCLOTIDE SEQUENCE.
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=97033440; PubMed=8879171; DOI=10.1016/0168-1656(96)01516-7;
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;
RT "Cloning and characterization of the gene for the thermostable
RT xylanase Xyna from Thermomyces lanuginosus";
RL J. Biotechnol. 49:211-218(1996).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=98426042; PubMed=9753433; DOI=10.1021/bi9808641;
RA Gruber K., Klintschar G., Hayn M., Schlacher A., Steiner W.,
RA Kratky C.;
RT "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution
RT X-ray structure and modeling studies";
RL Biochemistry 37:13475-13485(1998).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic
CC linkages in xylans.
CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
CC Temperature dependence:
CC Thermostable;
CC -1- PATHWAY: Xylan degradation.
CC -1- FAMILY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U5436; AAB94633.1; -; Genomic_DNA.
CC PDB; 1YNA; X-ray; @=32-225.
CC InterPro: IPR001137; Glyco_hydro_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLYDRLASE11.
CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC 3D-structure; Glycosidase; Hydrolase; Pyroglutamate carboxylic acid;
CC Signal; Xylan degradation.

FT SIGNAL 1 31
FT CHAIN 32 225
FT ACT_SITE 117 117
FT ACT_SITE 209 209
FT MOD_RES 32 32
FT DISULFID 141 185
FT STRAND 33 33
FT TURB 37 41
FT STRAND 42 43
FT STRAND 44 50
FT STRAND 56 60
FT TURB 63 64
FT STRAND 65 70
FT STRAND 82 82
FT STRAND 90 100
FT STRAND 103 112
FT TURB 113 115
FT STRAND 116 124
FT TURB 129 132
FT STRAND 134 141
FT TURB 142 143
FT STRAND 144 158
FT TURB 159 160
FT STRAND 161 172
FT STRAND 179 182
FT HELIX 183 192
FT TURB 193 194
FT STRAND 200 211
FT STRAND 214 223
SQ SEQUENCE 225 AA; 24356 MW; FAA79A914C5C676C CRC64;

Query Match 100.0%; Score 1088; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 7.3e-87;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTTNSGMDHGYYSWSDGGAQATTNLEGGTYEISMGDGNLVGGKGNPGLNARAI 60
DB 32 QTTNSGMDHGYYSWSDGGAQATTNLEGGTYEISMGDGNLVGGKGNPGLNARAI 91
QY 61 HFEVYQPNNGSYLAIVYGWTRNPLVEYYIVENFGTYPPSSGATDLGTYECDSIYRLGKT 120
DB 92 HFEVYQPNNGSYLAIVYGWTRNPLVEYYIVENFGTYPPSSGATDLGTYECDSIYRLGKT 151
QY 121 TRVAPSIDGTOTPDQWYSVRQDKRTSGTVGTGCHFPAMARAGLVNGDHYQIVATEGY 180
DB 152 TRVAPSIDGTOTPDQWYSVRQDKRTSGTVGTGCHFPAMARAGLVNGDHYQIVATEGY 211
QY 181 FSSGYARTTVADVG 194
DB 212 FSSGYARTTVADVG 225

RESULT 2
XNA_PAEVA STANDARD; PRT; 194 AA.
ID XNA_PAEVA
AC P81536;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylosidase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
DE xylanohydrolase) (PVX).
OS Paecilomyces variotii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
NCBI_TaxID=45996;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (1.59 ANGSTROMS), AND PROTEIN SEQUENCE OF 50-58
RP AND 123-128.
RC STRAIN=Bainier;
RX MEDLINE=20090955; PubMed=10623548; DOI=10.1006/jmbi.1999.3348;
RA Kumar P.R., Bswamoorthy S., Vithayachil P.J., Vismaitra M.A.;
RT "The tertiary structure at 1.59 A resolution and the proposed amino
RT acid sequence of a family-11 xylanase from the thermophilic fungus

RT Paecilomyces variotii bainier.";
RL J. Mol. Biol. 295:581-593(2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- BIOPHYSICO-CHEMICAL PROPERTIES:
CC Temperature dependence:
CC Thermotable;
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
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CC removed.
CC -----
DR PDB; 1PVX; X-ray; A=1.194.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW 3D-structure; Acetylation; Direct protein sequencing; Glycosidase;
KW Hydrolase; Xylan degradation.
FT ACT_SITE 86 86 Nucleophile (By similarity).
FT ACT_SITE 178 178 Proton donor (By similarity).
FT MOD_RES 1 1 N-acetylglutamine.
FT DISULFID 110 154
SQ SEQUENCE 194 AA; 20947 MW; 1D5C50AA4FEBDB90 CRC64;

Query Match 88.7%; Score 965; DB 1; Length 194;
Best Local Similarity 87.6%; Pred. No. 3.3e-76;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 2 TTNSGMDHGYYSWSDGGAQATTNLEGGTYEISMGDGNLVGGKGNPGLNARAI 61
DB 2 TTNSGMDHGYYSWSDGGAQATTNLEGGTYEISMGDGNLVGGKGNPGLNARAI 61
QY 62 HFEVYQPNNGSYLAIVYGWTRNPLVEYYIVENFGTYPPSSGATDLGTYECDSIYRLGKT 121
DB 62 HFEVYQPNNGSYLAIVYGWTRNPLVEYYIVENFGTYPPSSGATDLGTYECDSIYRLGKT 121
QY 122 RVNAPSIDGTOTPDQWYSVRQDKRTSGTVGTGCHFPAMARAGLVNGDHYQIVATEGY 181
DB 122 RVNAPSIDGTOTPDQWYSVRQDKRTSGTVGTGCHFPAMARAGLVNGDHYQIVATEGY 181
QY 182 SSGYARTTVADVG 194
DB 182 SSGYARTTVADVG 194

RESULT 3
Q9UVZ3_PLEO PRELIMINARY; PRT; 227 AA.
ID Q9UVZ3_PLEO
AC Q9UVZ3;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Xylanase precursor.
GN Name=Xyl1;
OS Setosphaeria tuscia.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
NCBI_TaxID=93612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H2;
RA Degefu Y., Paulin L., Lubbeck P.S.;
RT "Cloning, sequencing and expression of a xylanase gene from the maize
RT pathogen Helminthosporium turcicum Paas.";
RL Eur. J. Plant Pathol. 107:457-465(2001).
DB EMBL; AJ238895; CAB52417.1; -; genomic_DNA.

DR HSP; 043097; 1YNA.
 DR SMR; 090V23; 37-224.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0045493; P:xylen catabolism; IEA.
 DR InterPro; IP001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Signal; Xylan degradation.
 FT SIGNAL 1
 FT CHAIN 20 227
 SQ SEQUENCE 227 AA; 24123 MM; BA86FC075EE5306E CRC64;

Query Match 69.7%; Score 758; DB 2; Length 227;
 Best Local Similarity 71.6%; Pred. No. 4,7e-58;
 Matches 136; Conservative 20; Mismatches 32; Indels 2; Gaps 2;

QY 1 QTPNSGWHHDGYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGMNPLNARAI 60
 DB 37 QSTPNEGCTHNGCYTWSWSDGAPATYTNAGSGSYSWGTGNTLVGKGMNPE-TARTI 95
 QY 61 HFGVYQPNNSYLAIVGWTNPLVEYYIVENFGTYDPPSGATDLAGTECDGSIYRLGKT 120
 DB 96 TYGGQVYVNGNSYLAIVGWTNPLVEYYIVENFGTYDPPSGAQKGTSTDSGSEYKLAQS 155
 QY 121 TRNAPSIDGTQTFPDQVSVRODKRTSGTYQVQGHFPMARAGLVNNGDHYQIVATEGY 180
 DB 156 TRNQPISIDGTQTFQOQVSVRQNRSGSVNMTKTHFDAMASKMNL-GSHYQIVATEGY 214
 QY 181 FSSGVARTIV 190
 DB 215 FSSGSASITIV 224

RESULT 4

09CIR2_FUSOX PRELIMINARY; PRT; 295 AA.
 AC 09CIR2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Xylanase 5 protein.
 GN Name=xy15;
 OS Fusarium oxysporum f. sp. lycopersici.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 OC Fusarium oxysporum complex.
 OX NCBI_TaxId=59765;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=1654148; PubMed=11795847; DOI=10.1007/s00294-001-0260-0;
 RA Gomez-Gomez E., Roncero M.I.G., Di Pietro A., Hera C.;
 RT "Molecular characterization of a novel endo-beta-1,4-xylanase gene
 from the vascular wilt fungus Fusarium oxysporum.";
 RL Curr. Genet. 40:268-275(2001).
 DR EMBL; AF246830; AAK27974.1; -; Genomic_DNA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0045493; P:xylen catabolism; IEA.
 DR InterPro; IP001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation.
 SQ SEQUENCE 295 AA; 30858 MM; CA44056DCD3C104 CRC64;

Query Match 68.9%; Score 750; DB 2; Length 295;
 Best Local Similarity 70.5%; Pred. No. 3.2e-57;
 Matches 134; Conservative 25; Mismatches 29; Indels 2; Gaps 2;

QY 3 TPNSGWHHDGYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGMNPLNARAIHF 62
 DB 36 TPNSGWHHDGYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGMNPE-KARTISY 94
 QY 63 EGVYQPNNSYLAIVGWTNPLVEYYIVENFGTYDPPSGATDLAGTECDGSIYRLGKTTR 122
 DB 95 EGVYQPNNSYLAIVGWTNPLVEYYIVENFGTYDPPSGATDLAGTECDGSIYRLGKTTR 154
 QY 123 VNPASIDGTQTFPDQVSVRODKRTSGTYQVQGHFPMARAGLVNNGDHYQIVATEGYFS 182
 DB 155 VNPASIDGTQTFQOQVSVRQNRSGSVNMTKTHFDAMASKMNL-GTHDYQIVATEGYFS 213
 QY 183 SGYARTIVAD 192
 DB 214 SGSSHRTVSE 223

RESULT 5

XYN1 COCCA
 ID XYN1 COCCA
 AC 006562; STANDARD; PRT; 221 AA.
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Bodo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I) (1,4-beta-D-xyloxy xylanohydrolase 1).
 GN Name=XYN1;
 OS Cochliobolus carbonum (Bipolaris zeicola).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; Cochliobolus.
 OX NCBI_TaxId=5017;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Race 1 / Isolate SB11;
 RX MEDLINE=94003417; PubMed=8400376;
 RA Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
 RT "Cloning and targeted gene disruption of XYN1, a beta 1,4-xylanase
 gene from the maize pathogen Cochliobolus carbonum.";
 RL Mol. Plant Microbe Interact. 6:467-473(1993).
 RN [2]
 RP PARTIAL PROTEIN SEQUENCE.
 RA Holden F.R., Walton J.D.;
 RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum.";
 RL Physiol. Mol. Plant Pathol. 40:39-47(1992). Contributes to the
 CC -1- FUNCTION: Major xylan-degrading enzyme. Contributes to the
 CC hydrolysis of arabinoxylan, the major component of maize cell-
 CC walls.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xyans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PFM: The N-terminus is blocked.
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
 CC family.
 CC -----
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 CC removed.
 CC -----
 DR EMBL; L13596; AAA33024.1; -; Genomic_DNA.
 DR HSP; 043097; 1YNA.
 DR SMR; 006562; 31-218.
 DR InterPro; IP001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Direct protein sequencing; Glycosidase; Hydrolyase; Signal;
 KW Xylan degradation.
 FT SIGNAL 1 30 Potential.

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FT CHAIN 31 221 Endo-1,4-beta-xylanase I.
FT ACT_SITE 115 115 Nucleophile (By similarity).
FT ACT_SITE 206 206 Proton donor (By similarity).
FT CONFLICT 81 81 W -> I (in Ref. 2).
FT CONFLICT 107 107 G -> A (in Ref. 2).
FT CONFLICT 131 131 S -> W (in Ref. 2).
SQ SEQUENCE 221 AA; 23728 MW; 59DBD983FC5B08C CRC64;

Query March 68.2%; Score 742; DB 1; Length 221;
Best Local Similarity 70.0%; Pred. No. 1,1e-56;
Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 1 QTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYSISWGDGGLVGKGMNPLNARAI 60
DB 31 QNTNGSGTHNGCFWMSWSDGADATYTNAGAGSYSVSGGNTLVGKGMNPG-TARTI 89
QY 61 HPEBVYQPNNGNSYLAAYGWTNRNPLVEYYIVENFGTYPPSSATDLGTVECDGSIYRLGKT 120
DB 90 TYSGTYYNNGNSYLAAYGWTNRNPLVEYYIVENFGTYPPSSQSKGTVTSDSSSYKLAQS 149
QY 121 TRVNAPSIDGTQTPDOYWSVRQDKRTSGTVQTCGFPMAPARAGLNVNGDHYQIVATEGY 180
DB 150 TRTNQPSIDGTTRTQQTWRSVRQDKRTSGTVQTCGFPMAPARAGLNVNGDHYQIVATEGY 208
QY 181 FSSGVARITV 190
DB 209 FSTGNAQITV 218

RESULT 6
Q00263_9PEZI PRELIMINARY; PRT; 227 AA.
ID Q00263_9PEZI PRELIMINARY; PRT; 227 AA.
AC Q00263;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endo-1,4-beta-xylanase precursor.
OS Ascochyta blati.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC mitosporic Pezizomycotina; Ascochyta.
OX NCBI_TaxID=47971;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lubbeck P.S., Paulin L., Degefu Y., Lubbeck M., Collinge D.;
RT "Molecular cloning and DNA sequencing of a xylanase gene from the
RT phytopathogenic fungus Ascochyta blati lib. ";
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; Z68891; CA93120.1; -; Genomic_DNA.
DR HSSP; O43097; 1YNA.
DR SMK; Q00263; 39-224.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal, xylan degradation.
FT SIGNAL 1 19 Potential.
FT CHAIN 1 227 Potential.
SQ SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0F CRC64;

Query March 66.3%; Score 721; DB 2; Length 227;
Best Local Similarity 69.1%; Pred. No. 7.9e-55;
Matches 130; Conservative 22; Mismatches 34; Indels 2; Gaps 2;

QY 3 TPNSBGMHDGYYYSWMSDGAQATYTNLEGTYSISWGDGGLVGKGMNPLNARAIHF 62
DB 39 TPSSGTHNGCFWMSWSDGADATYTNAGAGSYSVNMKTGNTLVGKGMNPG-AKITTY 97
QY 63 EGVYQPNNGNSYLAAYGWTNRNPLVEYYIVENFGTYPPSSGATDLGTVECDGSIYRLGKTTR 122
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DB 98 SGTYSSGNSYLAAYGWTNRNPLVEYYIVENFGTYPPSSGATDLGTVECDGSIYRLGKTTR 157
QY 123 VNAPSIDGTQTPDOYWSVRQDKRTSGTVQTCGFPMAPARAGLNVNGDHYQIVATEGYFS 182
DB 158 TNPSPIDGTQTPDOYWSVRQDKRTSGTVQTCGFPMAPARAGLNVNGDHYQIVATEGYFS 216
QY 183 SSVARITV 190
DB 217 SSGAQTIV 224

RESULT 7
Q01SAL1_MAGGR PRELIMINARY; PRT; 204 AA.
ID Q01SAL1_MAGGR PRELIMINARY; PRT; 204 AA.
AC Q01SAL1;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Hypothetical protein.
DE ORFNames=MG08424.4;
OS Magnaporthe oryzae 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Al-Zahr M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Biltshstein B., Bloom T., Blye J., Boguslavsky L.,
RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshtang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corn B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorris J., Dorris L., Duffey N., Dupes A., Elkins I., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geary G., Gierke S.,
RA Gierke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Hueb E., Iliev I.,
RA Jarfe D., Jones C., Kamal M., Kamet A., Kamyseleis M., Karlsson E.,
RA Kells C., Kieu A., Kisher P., Kodira S., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokytang T., Lokytang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., MacDonald J., Mclellan C., Major J.,
RA Manning J., Maraballa R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Mellem T., Menes L.,
RA Mesirov J., Mihalov A., Mihova T., Mikkelson T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoswo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phukhang P., Pigani B.,
RA Parcell S., Rachupka T., Ramasamy U., Ramau R., Ray V., Raymond C.,
RA Ratta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov N., Smith C., Souguez C.,
RA Spencer B., Stalker J., Stange-chomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoutateng Y., Topham K.,
RA Towey S., Tsamta T., Tsomo N., Vallee D., Vassilev H.,
RA Venkataraman V., Vaseon J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee B., Young G., Zainoun J., Zembek L.,
RA Zimmer A., Zody M., Zander E.,
RT "The genome sequence of Magnaporthe oryzae.",
RL Submitted (OCT-2003) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.,
RL Submitted (OCT-2003) to the EMBL/Genbank/DBJ databases.
RN [3]
```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACU01001255; EAA49509.1; -; Genomic_DNA.
DR InterPro: IPR002453; Beta_tubulin.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00716; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE: PS00228; TUBULIN_E_AUTOREG; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 204 AA; 22624 MW; 2396D83ED2B92260 CRC64;

Query Match 64.8%; Score 705; DB 2; Length 204;
Best Local Similarity 66.5%; Pred. No. 1.7e-53;
Matches 125; Conservative 25; Mismatches 36; Indels 2; Gaps 2;

QY 3 TPNSGMDGYYSWNSDGAQATYTNLEGTYEISWGDGNI.VGKGNNPGLNARAIHF 62
DB 17 TPSTSTGHDGFYSMTWDNGAQATYTNMAGGSYSITWSGNGNLVGKGNP-G-SARIVTY 75
QY 63 EGYVQNGNSYLA.VGWTNPLVEYYIVENFGTYDPSGATDGTVECDGSIYRLKTTT 122
DB 76 SANVRPNNGNSYLSVGVWTRNPLVEYYIVENFGTYDPSQASRKGTINVDGATYQVAQSTR 135
QY 123 VNAPSIDGTOTFPQYWSVRQDKRTSGTVQTGCHFDMAARAGLNVNGDHYQIYATGEGYS 182
DB 136 TNPQSIDGTITFTFOQYWSVRQDKRSSGTVDMKKHFDAMASGMKL-GTHDYQIYATGEGYS 194
QY 183 SGYARITV 190
DB 195 SGSSITVTI 202

RESULT 8
Q92245 MAGGR PRELIMINARY; PRT; 231 AA.
AC 092245;
DT 01-FEB-1997 (TEMBLrel. 02, Created)
DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 02, Last annotation update)
DE Endo-beta-1,4-D-xylosidase.
GN Name=xy14;
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Mycelium;
RA Wu S.-C., Darvill A.G., Alberheim P.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY144349; AAB06573.2; -; Genomic_DNA.
DR HSP; O43097; 1YNA.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0045493; P:xylian catabolism; IEA.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation.
SQ SEQUENCE 231 AA; 25305 MW; CECF024A9D5A795B CRC64;

Query Match 64.8%; Score 705; DB 2; Length 231;
Best Local Similarity 66.5%; Pred. No. 2e-53;
Matches 125; Conservative 25; Mismatches 36; Indels 2; Gaps 2;

QY 3 TPNSGMDGYYSWNSDGAQATYTNLEGTYEISWGDGNI.VGKGNNPGLNARAIHF 62
DB 44 TPSTSTGHDGFYSMTWDNGAQATYTNMAGGSYSITWSGNGNLVGKGNP-G-SARIVTY 102
QY 63 EGYVQNGNSYLA.VGWTNPLVEYYIVENFGTYDPSGATDGTVECDGSIYRLKTTT 122
DB 103 SANVRPNNGNSYLSVGVWTRNPLVEYYIVENFGTYDPSQASRKGTINVDGATYQVAQSTR 162
QY 123 VNAPSIDGTOTFPQYWSVRQDKRTSGTVQTGCHFDMAARAGLNVNGDHYQIYATGEGYS 182
DB 163 TNPQSIDGTITFTFOQYWSVRQDKRSSGTVDMKKHFDAMASGMKL-GTHDYQIYATGEGYS 221
QY 183 SGYARITV 190
DB 222 SGSSITVTI 229

RESULT 9
Q766V1_GASCO PRELIMINARY; PRT; 235 AA.
AC Q766V1;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE G/11 family xylosidase.
GN Name=xy11;
OS Scytalidium thermophilum.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Scytalidium.
OX NCBI_TaxID=85995;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af101-3;
RA Morinaga T., Boonjue S., Aimi T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB114442; BAD07040.1; -; Genomic_DNA.
DR HSP; P09850; 1BCX.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0045493; P:xylian catabolism; IEA.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation.
SQ SEQUENCE 235 AA; 25526 MW; C929BE7FD73682CA CRC64;

Query Match 61.1%; Score 665; DB 2; Length 235;
Best Local Similarity 63.8%; Pred. No. 6.4e-50;
Matches 120; Conservative 24; Mismatches 42; Indels 2; Gaps 2;

QY 3 TPNSGMDGYYSWNSDGAQATYTNLEGTYEISWGDGNI.VGKGNNPGLNARAIHF 62
DB 49 TPSTSTGHDGFYSMTWDNGAEVYNNVNNNGNNGVNMWRCNFGVKGWPKGA-AKTINY 107
QY 63 EGYVQNGNSYLA.VGWTNPLVEYYIVENFGTYDPSGATDGTVECDGSIYRLKTTT 122
DB 108 SGTENPSGNGYLAIVGWTNPLVEYYIVENFGTYDPSQASRKGTINVDGATYQVAQSTR 167
QY 123 VNAPSIDGTOTFPQYWSVRQDKRTSGTVQTGCHFDMAARAGLNVNGDHYQIYATGEGYS 182
DB 168 TNPQSIDGTITFTFOQYWSVRQDKRSSGTVDMKKHFDAMAGRLNV-GNHDYQIYATGEGYS 226
QY 183 SGYARITV 190
DB 227 SGSSITVTI 234

RESULT 10
XNNA_SCHCO STANDARD; PRT; 197 AA.
AC XNNA_SCHCO
ID XNNA_SCHCO
AC P35809;

DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
DE xylanohydrolase A).
GN Name=xYNA;
OS Schizopyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizopyllum.
NCBI_TaxID=5334;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ATCC 38548 / Delmar;
RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.,
RL (in) Vliesser J., Beidman G., Kusters-van Someren M.A., Voragen A.G.J.
RL (eds.),
RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
RN [2]
RP PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RC STRAIN=ATCC 38548 / Delmar;
RX MEDLINE=94063044; PubMed=8243636; DOI=10.1016/0014-5793(93)80698-T;
RA Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
RA Urasek L., Palce M.G.,
RT "Amino acid sequence and thermostability of xylanase A from
RT Schizopyllum commune.";
RL FEBS Lett. 334:296-300(1993).
RN [3]
RP PARTIAL PROTEIN SEQUENCE, AND ACTIVE SITE GLU-87.
RC STRAIN=ATCC 38548 / Delmar;
RX MEDLINE=94155888; PubMed=7906649;
RA Bray M.R., Clarke A.J.,
RT "Identification of a glutamate residue at the active site of xylanase
RT A from Schizopyllum commune.";
RL Bur. J. Biochem. 219:821-827(1994).
CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
CC pH dependence:
CC Active over a very broad pH range;
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR: A44597; A44597.
DR HSP: P81536; 1PVX.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Direct protein sequencing; Glycosidase; Hydrolase; Xylan degradation.
FT ACT_SITE 87 Nucleophile (Probable).
FT ACT_SITE 184 Proton donor (By similarity).
FT DISULFID 111 160
SQ SEQUENCE 197 AA; 20979 MW; 42C8074B67C1FB8 CRC64;
Query Match 60.9%; Score 663; DB 1; Length 197;
Best Local Similarity 61.3%; Pred. No. 7.7e-50;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;
QY 3 TPNSGMDGYVYVWMSDGAQATYTNLEGGTYEISW-GDGGNIVGKGMNPGLNARAIH 61
DB 3 TPSSGTGDDGTYVWMSDGAQATYTNLEGGTYEISW-GDGGNIVGKGMNPGLNARAIH 62
QY 62 PEGYQPNNGSYLAIVYGTWTRNPLVEYYIVENFGTYDPSSGATDGTVECDGSIYRLGKTT 121

DB 63 YSGTYQPNNGSYLAIVYGTWTRNPLVEYYIVENFGTYDPSSGATDGTVECDGSIYRLGKTT 122
QY 122 RVNAPSIDGTQTFDDQVWSYRQDKRT-----SGVQVGCDFPDAMARAGLNVNGHYQIYA 176
DB 123 RVNAPSIDGTQTFDDQVWSYRQDKRT-----SGVQVGCDFPDAMARAGLNVNGHYQIYA 182
QY 177 TEGYFSSGYARITV 190
DB 183 TEGYQSSGATITV 196
RESULT 11
Q12579_9PEZI
ID Q12579_9PEZI PRELIMINARY; PRT; 219 AA.
AC 012579;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Endo-beta-1,4-xylanase A (EC 3.2.1.8).
GN Name=cgXA;
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.
NCBI_TaxID=47794;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118924; PubMed=8595661; DOI=10.1007/BF00313196;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.,
RT "Two family G xylanase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans.";
RL Curr. Genet. 29:73-80(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tsukagoshi N.,
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: D49850; BAA08649.1; -; Genomic_DNA.
DR PIR: S71472; S71472.
DR HSP: P36217; 1XVO.
DR GO: GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0045493; P:xylan catabolism; IEA.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 219 AA; 23325 MW; 4729299E08FD9FBA CRC64;
Query Match 60.3%; Score 656; DB 2; Length 219;
Best Local Similarity 61.9%; Pred. No. 3.6e-49;
Matches 117; Conservative 28; Mismatches 42; Indels 2; Gaps 2;
QY 3 TPNSGMDGYVYVWMSDGAQATYTNLEGGTYEISW-GDGGNIVGKGMNPGLNARAIH 62
DB 3 TPSSGTGDDGTYVWMSDGAQATYTNLEGGTYEISW-GDGGNIVGKGMNPGLNARAIH 62
QY 33 TPSSGTGDDGTYVWMSDGAQATYTNLEGGTYEISW-GDGGNIVGKGMNPGLNARAIH 91
DB 33 TPSSGTGDDGTYVWMSDGAQATYTNLEGGTYEISW-GDGGNIVGKGMNPGLNARAIH 91
QY 63 EGYVQPNNGSYLAIVYGTWTRNPLVEYYIVENFGTYDPSSGATDGTVECDGSIYRLGKTT 122
DB 92 SGTFPSQNGSYLAIVYGTWTRNPLVEYYIVENFGTYDPSSGATDGTVECDGSIYRLGKTT 151
QY 123 VNAPSIDGTQTFDDQVWSYRQDKRTSGVQVGCDFPDAMARAGLNVNGHYQIYATGEGYS 182
DB 152 VNAPSIDGTQTFDDQVWSYRQDKRTSGVQVGCDFPDAMARAGLNVNGHYQIYATGEGYS 210
QY 183 SGYARITVA 191
DB 211 SGSSSITVS 219
RESULT 12
013447_COCXA

ID 013447 COCSA PRELIMINARY; PRT; 231 AA.
AC 013447;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-1,4-xylosanase.
GN Nameexyl2;
OS Cochliobolus sativus (Bipolaris sorokiniana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=45130;
RN NUCLEOTIDE SEQUENCE.
RP Emani K., Hack B.;
RA "Characterization of a xylosanase gene from Cochliobolus sativus and its
RT expression.";
RL MYCOL. Res. 105:352-359(2001).
DR HSP; 081116; 1H1A.
DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0045493; P:xylosan catabolism; IEA.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation.
SQ SEQUENCE 231 AA; 25577 MW; 333BEDD1F065A6BF CRC64;

Query Match 60.3%; Score 656; DB 2; Length 231;
Best Local Similarity 61.1%; Pred. No. 3.8e-49;
Matches 116; Conservative 27; Mismatches 45; Indels 2; Gaps 2;

QY 1 QTPNSEGMHGDYGYYSWSDGGAQATYTNLEGTYSISWGDGNTLVGKGMNPGLNARAI 60
DB 41 QSTPSEBGHNGYFYFWMTDGGSAQYTMGEGSKYVTWNTGNTFVGKGMNPG-NGRTI 99
QY 61 HFEGVYQPNNGSYLAVYGMTNPLVEYIYVENFTYDPSGATDLGTECDGSIYRLGKT 120
DB 100 NYGAFNPGNGYLAAYVGMTNPLVEYIYVESYGTVPSSGAQYKGSFOTDGGTYNVAVS 159
QY 121 TRVNASIDGTOTFDQYWSVRQDKRTSGYQTCGHPAMARAGLVNAGDHYQIVATGEY 180
DB 160 TRYNQPSIDGTRFQYQYWSVRQDKRVGGSVNMGNHFNMSRYGLNL-GHYIYQIVATGEY 218
QY 181 FSSGYARTY 190
DB 219 QSSGSSDIYV 228

RESULT 13
Q70728_9PLEO PRELIMINARY; PRT; 231 AA.
ID Q70728_9PLEO PRELIMINARY;
AC Q70728;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Xylanase precursor.
GN Nameexyl2;
OS Setosphaeria turcica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Setosphaeria.
OX NCBI_TaxID=93612;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15016446; DOI=10.1016/j.biochi.2004.01.001;
RA Degdeli Y., Iohender K., Paulin B.G.;
RT "Expression patterns and phylogenetic analysis of two xylanase genes
RT (hxy1 1 and hxy1 2) from Helminthosporium turcicum, the cause of
RL Blotchmle 86:83-90(2004).
EMBL; AJ548879; CAD70174.1; -, Genomic_DNA.

DR HSP; P09850; 1BCX.
DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0045493; P:xylosan catabolism; IEA.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Signal; Xylan degradation.
FT SIGNAL 1 19 Potential1.
FT CHAIN 20 231 xy12.
SQ SEQUENCE 231 AA; 25611 MW; 44078D5B52BAF15 CRC64;

Query Match 60.1%; Score 654; DB 2; Length 231;
Best Local Similarity 60.5%; Pred. No. 5.7e-49;
Matches 115; Conservative 28; Mismatches 45; Indels 2; Gaps 2;

QY 1 QTPNSEGMHGDYGYYSWSDGGAQATYTNLEGTYSISWGDGNTLVGKGMNPGLNARAI 60
DB 41 QSTPSEBGHNGYFYFWMTDGGSAQYTMGEGSKYVTWNTGNTFVGKGMNPG-NGRTI 99
QY 61 HFEGVYQPNNGSYLAVYGMTNPLVEYIYVENFTYDPSGATDLGTECDGSIYRLGKT 120
DB 100 NYGAFNPGNGYLAAYVGMTNPLVEYIYVESYGTVPSSGAQYKGSFOTDGGTYNVAVS 159
QY 121 TRVNASIDGTOTFDQYWSVRQDKRTSGYQTCGHPAMARAGLVNAGDHYQIVATGEY 180
DB 160 TRYNQPSIDGTRFQYQYWSVRQDKRVGGSVNMGNHFNMSRYGLNL-GHYIYQIVATGEY 218
QY 181 FSSGYARTY 190
DB 219 QSSGSSDIYV 228

RESULT 14
Q7SD01_NEUCR PRELIMINARY; PRT; 220 AA.
ID Q7SD01_NEUCR PRELIMINARY;
AC Q7SD01;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothesized protein (Probable endo-1, 4-beta-xylosanase A).
GN Name=NC002855.1; Synonyms=B10D6.120;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=OR74A;
RC Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Maeburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte B., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Krysstofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Carlsbeide D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Selter S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Manhaupt G., Ebbold D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Bitren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
RN NUCLEOTIDE SEQUENCE.
RP Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Manhaupt G.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.
 RA German Neurospora genome project;
 RU Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX01000046; EAA34909.1; -; Genomic DNA.
 DR EMBL; BX842624; CAE76228.1; -; Genomic DNA.
 DR HSP; Q8116; 1H1A.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0045493; P:xylian catabolism; IEA.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Hypothetical protein; Xylan degradation.
 SQ SEQUENCE 220 AA; 23848 MW; D2EEC2D31553E0B CRC64;

Query Match 59.8%; Score 651; DB 2; Length 220;
 Best Local Similarity 62.8%; Pred. No. 9.8e-48;
 Matches 118; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 3 TPNSGMDGYYSWMSDGAQATYTNLEGGTYEISWGDGGLVGGKMPGLNARAIFH 62
 DB 33 TPSTGTGNNFYYSFWTDGNGNVVYANGAGSGYSVMNNGNPFVAGKMPG-SARTITY 91
 QY 63 EGYQNGNSYLAIVGWTNPVLEYIYVENFGTYDPSSGATDGTVECDGSIYRLGKTR 122
 DB 92 SGNRPSPGNGYLAIVGWTNPVLEYIYVENFGSYNPSGQRLDSVYTDSTVDIYKTR 151
 QY 123 VNAPSIDGTQTFPDQYMSVRQDKRTSGTVQGCHPDAMARAGLVNNGDHYQIVATGEGYS 182
 DB 152 YNPSIDGTITFQYMSVRQDKRTGTVTMANHFMAKAGLH-GTHNQIVATGEGYS 210
 QY 183 SGYARITV 190
 DB 211 SGSAQITV 218

RESULT 15
 Q4MG11 ASPFU PRELIMINARY; PRT; 228 AA.
 ID Q4MG11 ASPFU PRELIMINARY; PRT; 228 AA.
 AC Q4MG11
 DT 13-SEP-2005 (TrEMBLrel. 31, Last Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Endo-1,4-beta-xylosidase (XlnA), putative.
 GN ORFNames=Afu3900320;
 OS Aspergillus fumigatus Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillu.
 OC NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Af293.
 RA Niernan W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley J.,
 RA Atrova J., Bertrman M., Abe K., Archer D.B., Berneto C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Fobker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
 RA Haas H., Harris D., Horluchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Kouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafon A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Maizoro W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
 RA Penava M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,

RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrrell B., Denning D.W.,
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT Aspergillus fumigatus";
 RU Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX01000010; EAL86316.1; -; Genomic DNA.
 DR Xylan degradation.
 SQ SEQUENCE 228 AA; 24494 MW; 7DBED47138DA238F CRC64;

Query Match 59.8%; Score 651; DB 2; Length 228;
 Best Local Similarity 61.7%; Pred. No. 1e-48;
 Matches 116; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 3 TPNSGMDGYYSWMSDGAQATYTNLEGGTYEISWGDGGLVGGKMPGLNARAIFH 62
 DB 42 TPSTGTGNNFYYSFWTDGNGVDVYTNAGAGSGYSVMNNGNPFVAGKMPG-SARTINY 100
 QY 63 EGYQNGNSYLAIVGWTNPVLEYIYVENFGTYDPSSGATDGTVECDGSIYRLGKTR 122
 DB 101 GGSFNPSPGNGYLAIVGWTNPVLEYIYVENFGSYNPSGQRLDSVYTDSTVDIYKTR 160
 QY 123 VNAPSIDGTQTFPDQYMSVRQDKRTSGTVQGCHPDAMARAGLVNNGDHYQIVATGEGYS 182
 DB 161 YNAPSIDGTITFQYMSVRQDKRTGTVTMANHFMAKAGLH-GTHNQIVATGEGYS 219
 QY 183 SGYARITV 190
 DB 220 SGSAQITV 227

Search completed: February 10, 2006, 15:01:23
 Job time : 196.852 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 15:01:51 ; Search time 32.8735 Seconds

(without alignments)
487.903 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225

Perfect score: 1088
Sequence: 1 QTPNSEGMDGYYSWMSD.....VATGYPSSGYARITVADVG 194

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 8265679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 1088 | 100.0 | 225 | 1 | US-08-886-765-2 |
| 2 | 1088 | 100.0 | 225 | 2 | US-09-115-660-2 |
| 3 | 1083 | 99.5 | 194 | 2 | US-09-570-856B-24 |
| 4 | 965 | 88.7 | 194 | 2 | US-09-570-856B-23 |
| 5 | 742 | 68.2 | 221 | 2 | US-09-570-856B-29 |
| 6 | 663 | 60.9 | 197 | 1 | US-08-044-621D-29 |
| 7 | 663 | 60.9 | 197 | 1 | US-08-709-912-9 |
| 8 | 663 | 60.9 | 197 | 1 | US-09-047-370-9 |
| 9 | 663 | 60.9 | 197 | 2 | US-09-570-856B-18 |
| 10 | 645 | 59.3 | 227 | 1 | US-08-458-023B-4 |
| 11 | 638.5 | 58.7 | 223 | 2 | US-09-254-733-7 |
| 12 | 637.5 | 58.6 | 261 | 2 | US-08-768-373-2 |
| 13 | 637.5 | 58.6 | 261 | 2 | US-09-849-242A-2 |
| 14 | 636.5 | 58.5 | 190 | 1 | US-08-044-621D-28 |
| 15 | 636.5 | 58.5 | 190 | 1 | US-08-709-912-14 |
| 16 | 636.5 | 58.5 | 190 | 1 | US-09-047-370-14 |
| 17 | 635.5 | 58.4 | 190 | 1 | US-08-044-621D-26 |
| 18 | 635.5 | 58.4 | 190 | 1 | US-08-709-912-6 |
| 19 | 635.5 | 58.4 | 190 | 1 | US-09-047-370-16 |
| 20 | 635.5 | 58.4 | 223 | 1 | US-08-121-436A-2 |
| 21 | 634.5 | 58.3 | 190 | 1 | US-08-044-621D-27 |
| 22 | 634.5 | 58.3 | 190 | 2 | US-09-570-856B-19 |
| 23 | 634 | 58.3 | 230 | 2 | US-08-768-373-4 |
| 24 | 634 | 58.3 | 230 | 2 | US-09-849-242A-4 |
| 25 | 632.5 | 58.1 | 190 | 1 | US-08-709-912-17 |
| 26 | 632.5 | 58.1 | 190 | 1 | US-09-047-370-17 |
| 27 | 630.5 | 58.0 | 190 | 2 | US-09-570-856B-20 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 630.5 | 58.0 | 190 | 2 | US-09-570-856B-22 | Sequence 22, Appl |
| 29 | 621 | 57.1 | 225 | 1 | US-09-570-856B-26 | Sequence 26, Appl |
| 30 | 617 | 56.7 | 225 | 2 | US-08-290-979A-8 | Sequence 8, Appl |
| 31 | 586.5 | 53.9 | 226 | 2 | US-09-357-891A-2 | Sequence 2, Appl |
| 32 | 576 | 52.9 | 223 | 2 | US-09-462-246-2 | Sequence 2, Appl |
| 33 | 574.5 | 52.8 | 296 | 1 | US-08-507-431-6 | Sequence 6, Appl |
| 34 | 574.5 | 52.8 | 296 | 2 | US-09-116-622-6 | Sequence 6, Appl |
| 35 | 574.5 | 52.8 | 296 | 2 | US-09-219-277-6 | Sequence 6, Appl |
| 36 | 574.5 | 52.8 | 296 | 2 | US-09-599-661-6 | Sequence 6, Appl |
| 37 | 572.5 | 52.6 | 231 | 1 | US-08-902-655A-6 | Sequence 6, Appl |
| 38 | 571.5 | 52.5 | 215 | 1 | US-08-044-621D-34 | Sequence 34, Appl |
| 39 | 571.5 | 52.5 | 335 | 2 | US-09-570-856B-15 | Sequence 15, Appl |
| 40 | 568 | 52.2 | 189 | 1 | US-08-709-912-13 | Sequence 13, Appl |
| 41 | 568 | 52.2 | 189 | 1 | US-09-047-370-13 | Sequence 13, Appl |
| 42 | 566.5 | 52.1 | 206 | 1 | US-08-315-695-19 | Sequence 19, Appl |
| 43 | 562.5 | 51.7 | 191 | 1 | US-08-709-912-10 | Sequence 10, Appl |
| 44 | 562.5 | 51.7 | 191 | 1 | US-09-047-370-10 | Sequence 10, Appl |
| 45 | 559 | 51.4 | 344 | 1 | US-08-468-812-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-886-765-2
Sequence 2, Application US/08866765
Patent No. 5817500
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSER: No. 58175000 No. 5817500disk of No. 5817500th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-886-765-2

Query Match 100.0%; Score 1088; DB 1; Length 225;

Best Local Similarity 100.0%; Pred. No. 4e-97; Mismatches 0; Indels 0; Gaps 0;

Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QTPNSEGMDGYYSWSDGGAQATYTNLEGTYEISWEDGNTVGKGMNPLNRAI 60
DB 32 QTPNSEGMDGYYSWSDGGAQATYTNLEGTYEISWEDGNTVGKGMNPLNRAI 91

Qy 61 HFEVYQPNNGNSYLA VGMTRNPLVEYYIVENFGTYDSSGATDLGTVECDSIYRLGKT 120
Db 92 HFEVYQPNNGNSYLA VGMTRNPLVEYYIVENFGTYDSSGATDLGTVECDSIYRLGKT 151
Qy 121 TRVNAPSIDGQTQFDQYWSVRQDKRTSGTVQTCGFDMARAGLNVNDHYQIVATEGY 180
Db 152 TRVNAPSIDGQTQFDQYWSVRQDKRTSGTVQTCGFDMARAGLNVNDHYQIVATEGY 211
Qy 181 FSSGYARITVADV 194
Db 212 FSSGYARITVADV 225

RESULT 2
US-09-115-660-2
Sequence 2, Application US/09115660
Patent No. 6245546
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knop, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No. 62455460 No. 6245546disk of No. 6245546th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PaeSeQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,660
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambirth, Bllae J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-115-660-2

Query Match 100.0%; Score 1088; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QTPNSEGMHDGYYSWMSDGAQATYTNLEGGTYEISMGGCNLVGKGNPGLNARAI 60
Db 32 QTPNSEGMHDGYYSWMSDGAQATYTNLEGGTYEISMGGCNLVGKGNPGLNARAI 91
Qy 61 HFEVYQPNNGNSYLA VGMTRNPLVEYYIVENFGTYDSSGATDLGTVECDSIYRLGKT 120
Db 92 HFEVYQPNNGNSYLA VGMTRNPLVEYYIVENFGTYDSSGATDLGTVECDSIYRLGKT 151
Qy 121 TRVNAPSIDGQTQFDQYWSVRQDKRTSGTVQTCGFDMARAGLNVNDHYQIVATEGY 180
Db 152 TRVNAPSIDGQTQFDQYWSVRQDKRTSGTVQTCGFDMARAGLNVNDHYQIVATEGY 211

Qy 181 FSSGYARITVADV 194
Db 212 FSSGYARITVADV 225

RESULT 3
US-09-570-856B-24
Sequence 24, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiya, Basall I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 194
TYPE: PRT
ORGANISM: Thermomyces lanuginosus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(1)
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3+"
US-09-570-856B-24

Query Match 99.5%; Score 1083; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 1e-96;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TTPNSEGMHDGYYSWMSDGAQATYTNLEGGTYEISMGGCNLVGKGNPGLNARAI 61
Db 2 TTPNSEGMHDGYYSWMSDGAQATYTNLEGGTYEISMGGCNLVGKGNPGLNARAI 61
Qy 62 HFEVYQPNNGNSYLA VGMTRNPLVEYYIVENFGTYDSSGATDLGTVECDSIYRLGKT 121
Db 62 HFEVYQPNNGNSYLA VGMTRNPLVEYYIVENFGTYDSSGATDLGTVECDSIYRLGKT 121
Qy 122 RVNAPSIDGQTQFDQYWSVRQDKRTSGTVQTCGFDMARAGLNVNDHYQIVATEGY 181
Db 122 RVNAPSIDGQTQFDQYWSVRQDKRTSGTVQTCGFDMARAGLNVNDHYQIVATEGY 181
Qy 182 SSGYARITVADV 194
Db 182 SSGYARITVADV 194

RESULT 4
US-09-570-856B-23
Sequence 23, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiya, Basall I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 194
TYPE: PRT
ORGANISM: Paecilomyces variotii
US-09-570-856B-23

Query Match 88.7%; Score 965; DB 2; Length 194;
Best Local Similarity 87.6%; Pred. No. 2,4e-85;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 2 TTNSGMDHGYYSWSDGGAQATYTNLEGGTYEISWGGGMLVGGKGNPGLNARAIH 61
DB 2 TTNSGMDHGYYSWSDGGAQATYTNLEGGTYEISWGGGMLVGGKGNPGLNARAIH 61

QY 62 FEGVQPNNGSYLAAYGWTNRNPLVEYYIVENFGTYDPSGATDLGTVECDGSIYRLGKT 121
DB 62 FEGVQPNNGSYLAAYGWTNRNPLVEYYIVENFGTYDPSGATDLGTVECDGSIYRLGKT 121

QY 122 RVNAPSIDGTQTFDQYVSWAQDKRTSGTYGCHFDAMARAGLNVGDHYQIVATEGYF 181
DB 122 RVNAPSIDGTQTFDQYVSWAQDKRTSGTYGCHFDAMARAGLNVGDHYQIVATEGYF 181

QY 182 SSGYARITVADVG 194
DB 182 SSGYARITVADVG 194

RESULT 5
US-09-570-856B-29
Sequence 29, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Benzien, Joerg M
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RTT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570, 856B
PRIOR FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 221
TYPE: PRT
ORGANISM: Cochliobolus carbonum
US-09-570-856B-29

Query Match 68.2%; Score 742; DB 2; Length 221;
Best Local Similarity 70.0%; Pred. No. 9,6e-64;
Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 1 QTTPNSEGMHDGYYSWSDGGAQATYTNLEGGTYEISWGGGMLVGGKGNPGLNARAI 60
DB 31 QTTPNSEGMHDGYYSWSDGGAQATYTNLEGGTYEISWGGGMLVGGKGNPGLNARAI 60

QY 61 HFEQVYQPNNGSYLAAYGWTNRNPLVEYYIVENFGTYDPSGATDLGTVECDGSIYRLGKT 120
DB 90 HFEQVYQPNNGSYLAAYGWTNRNPLVEYYIVENFGTYDPSGATDLGTVECDGSIYRLGKT 120

QY 121 TRVNASPIDGTQTFDQYVSWAQDKRTSGTYGCHFDAMARAGLNVGDHYQIVATEGY 180
DB 150 TRVNASPIDGTQTFDQYVSWAQDKRTSGTYGCHFDAMARAGLNVGDHYQIVATEGY 180

QY 181 FSSGYARITV 190
DB 209 FSSGYARITV 190

RESULT 6
US-08-044-621D-29
Sequence 29, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose

TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: Gowling, Strachy & Henderson
STREET: Suite 2600, 160 Bighin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Bratc
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 197
TYPE: Amino Acid
STRANDEDNESS: No, 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHEICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Schizophyllum commune
STRAIN: Schizophyllum commune, Xylanase A
IMMEDIATE SOURCE:
PUBLICATION INFORMATION:
AUTHORS: Oku T., Yaguchi M., Paice M., & Jurssek
TITL: L.
JOURNAL: Canadian Fed. Biol. Soc. Annu. Meet.
VOLUME:
ISSUE:
PAGES: Abstract 676
DATE: 1988
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-29

Query Match 60.9%; Score 663; DB 1; Length 197;
Best Local Similarity 61.3%; Pred. No. 3,4e-56;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 3 TTNSGMDHGYYSWSDGGAQATYTNLEGGTYEISWGGGMLVGGKGNPGLNARAIH 61
DB 3 TTNSGMDHGYYSWSDGGAQATYTNLEGGTYEISWGGGMLVGGKGNPGLNARAIH 61

QY 62 FEGVQPNNGSYLAAYGWTNRNPLVEYYIVENFGTYDPSGATDLGTVECDGSIYRLGKT 121
DB 62 FEGVQPNNGSYLAAYGWTNRNPLVEYYIVENFGTYDPSGATDLGTVECDGSIYRLGKT 121

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QY      122  RWAPASIDTGTQTEPDXYMSVRKODKRT-----SGTYQTGCHFPAMAKAALNVNGDHYOIVA 176
        ||| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db       123  RWAPASIDTGTQTEPDXYMSVRNPKKAPAGGSISGTVDOVCHFPAKGLGNLGSSENNYOIVA 182
        ||| | | | | | | | | | | | | | | | | | | | | | : | | | | |

QY      177  TEGYFSSGVARITV 190
        ||| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db       183  TEGYOSSGRATITV 196
        ||| | | | | | | | | | | | | | | | | | | | | | : | | | | |

RESULT 7
US-08-709-912-9
; Sequence 9, Application US/08709912
; Patent No. 5759840
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Ming L
; APPLICANT: Yaguchi Dr., Makoto
; TITLE OF INVENTION: Modification of xylanase to improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,912
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olesen Mr, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Schizosaccharomyces commune
; STRAIN: Xylanase A
; PUBLICATION INFORMATION:
; AUTHORS: Oku, T
; AUTHORS: Yaguchi, M
; AUTHORS: Parsee, M
; AUTHORS: Juraszek, L
; JOURNAL: Canadian Fed. Biol. Soc. annual meeting
; PAGES: Abstract #676
; DATE: 1988
; US-08-709-912-9

```

| | | | | |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 60.9% | Score 663; | DB 1; | Length 197; |
| Best Local Similarity | 61.3% | Pred. No. 3.4e-56; | | |
| Matches 119; | Conservative 26; | Mismatches 43; | Indels 6; | Gaps 2. |

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Db      3  TPSSGTGTGGYITYSMTWTDGAGDATTQNNGGSSYTLTSSANNNGLVGGKGNPAAARSSIS 62
QY      62  FEGVYQPNGNSYLAAYGWTTRNPLVEYYIYVENFGTYDPSSGATDGTVECDGSITRLGKTT 121
Db      63  YSGTYQPNGNSTLYVGMWTRRSLEIYIYVESYSDPSAASHKGSVTCNGATYDILSTW 122
QY      122  RVNAPSISGTGTFFDQYMSVRQDKRT-----SGTVQTGCFPDMAKAGLVNNGHYQIVA 176
Db      123  RVNAPSISGTGTFFDQYMSVRNPKKAPGGSISGTVDVQCFPDAMKGLGNMGSEHNYQIVA 182
QY      177  TEGYFSSGVARTIV 190
Db      183  TEGYQSSGTATITV 196

RESULT 8
US-09-047-370-9
; Sequence 9, Application US/09047370
; Patent No. 5866408
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Iehikawa Dr., Kazuko
; TITLE OF INVENTION: Modification of xylanase to improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,370
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/709,312
; FILING DATE: 09-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Schizopyllum commune
; STRAIN: xylanase A
; PUBLICATION INFORMATION:
; AUTHORS: Oku, T
; AUTHORS: Yaguchi, M
; AUTHORS: Parse, M
; AUTHORS: Uraeek, L
; JOURNAL: Canadian Fed. Biol. Soc. annual meeting

```

AUTHORS: Oku, T
 AUTHORS: Yaguchi, M
 AUTHORS: Parse, M
 AUTHORS: Jurasek, L
 JOURNAL: Canadian Fed. Biol. Soc. annual meeting

PAGES: Abstract #676
DATE: 1988
US-09-047-370-9

Query Match 60.9%; Score 663; DB 1; Length 197;
Best Local Similarity 61.3%; Pred. No. 3,46-56;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 3 TPNSGHHDDYYYSWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGNPGLNAPAIH 61
DB 3 TPSTGTGGGYYYSWMTDGAADATYQNNGGSYLTWNGNNGLVGGKGNPGLNAPAIH 62
QY 62 FEGVYQPNNGSYLAVYGMTRNPLVEYYIVENFGTYDSSGATDLGTYECDGSIYRLGKT 121
DB 63 YSGTYQPNNGSYLAVYGMTRNPLVEYYIVESYGSYDSSAASHKGSYTCNGATYDILSTW 122
QY 122 RVNAPSIDGTQTFEQFWSVNRPKAPGSGISGTYDVQCHFDAMKGLGMLNLSGHNQYIVA 176
DB 123 RVNAPSIDGTQTFEQFWSVNRPKAPGSGISGTYDVQCHFDAMKGLGMLNLSGHNQYIVA 182
QY 177 TEGYSSGATITV 190
DB 183 TEGYSSGATITV 196

RESULT 9

US-09-570-856B-18
Sequence 18, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Benzie, Joerg M
APPLICANT: Dahivac, Basell I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
PRIOR FILING DATE: 2002-04-15
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patent version 3.1
SEQ ID NO 18
LENGTH: 197
TYPE: PRT
ORGANISM: Schizophyllum commune
US-09-570-856B-18

Query Match 60.9%; Score 663; DB 2; Length 197;
Best Local Similarity 61.3%; Pred. No. 3,46-56;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 3 TPNSGHHDDYYYSWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGNPGLNAPAIH 61
DB 3 TPSTGTGGGYYYSWMTDGAADATYQNNGGSYLTWNGNNGLVGGKGNPGLNAPAIH 62
QY 62 FEGVYQPNNGSYLAVYGMTRNPLVEYYIVENFGTYDSSGATDLGTYECDGSIYRLGKT 121
DB 63 YSGTYQPNNGSYLAVYGMTRNPLVEYYIVESYGSYDSSAASHKGSYTCNGATYDILSTW 122
QY 122 RVNAPSIDGTQTFEQFWSVNRPKAPGSGISGTYDVQCHFDAMKGLGMLNLSGHNQYIVA 176
DB 123 RVNAPSIDGTQTFEQFWSVNRPKAPGSGISGTYDVQCHFDAMKGLGMLNLSGHNQYIVA 182
QY 177 TEGYSSGATITV 190
DB 183 TEGYSSGATITV 196

RESULT 10
US-08-458-023B-4
Sequence 4, Application US/08458023B
Patent No. 5667990
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.

APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boomdian, Karuppan C
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 5667990 No. 5667990disk of No. 5667990th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowmyer Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-023B-4

Query Match 59.3%; Score 645; DB 1; Length 227;
Best Local Similarity 59.5%; Pred. No. 2,36-54;
Matches 113; Conservative 26; Mismatches 49; Indels 2; Gaps 2;

QY 1 QTPNSGHHDDYYYSWSDGGAQATYTNLEGGTYEISW-GDGGNLVGGKGNPGLNAPAIH 60
DB 37 QVTPNGBGHHNGYFYWSWSDGGQVQVYTNLEGGTYEISW-GDGGNLVGGKGNPGLNAPAIH 95
QY 61 HFBGVYQPNNGSYLAVYGMTRNPLVEYYIVENFGTYDSSGATDLGTYECDGSIYRLGKT 120
DB 96 NYGTYQPNNGSYLAVYGMTRNPLVEYYIVESYGSYDSSAASHKGSYTCNGATYDILSTW 155
QY 121 TRVAPSIDGTQTFEQFWSVNRPKAPGSGISGTYDVQCHFDAMKGLGMLNLSGHNQYIVA 180
DB 156 TRVAPSIDGTQTFEQFWSVNRPKAPGSGISGTYDVQCHFDAMKGLGMLNLSGHNQYIVA 214
QY 181 FSSGATITV 190
DB 215 QSSGATITV 224

RESULT 11
US-09-254-733-7
Sequence 7, Application US/09254733
Patent No. 6277596
GENERAL INFORMATION:
APPLICANT: WATANABE, MANABU
APPLICANT: MORIYA, TATSUKI
APPLICANT: AOYAGI, KAORI
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING
TITLE OF INVENTION: IN TRICHOBERA VIRIDE AND SYSTEM FOR MASS-PRODUCING
FILE REFERENCE: 99-0266*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07

NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 223
TYPE: PRT
ORGANISM: TRICHODERMA VIRIDE MC300-1
US-09-254-733-7

Query Match 58.7%; Score 638.5; DB 2; Length 223;
Best Local Similarity 60.2%; Pred. No. 9,4e-54;
Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;

QY 1 QTTPNSGMDGYXXYXWMSDGAQATYTNLEGTYSISWGDGNLVGGKGNPGLNARAI 60
DB 34 QTIQPGYVNNYGYYSWINDGHGVTYTNPGQGFVWMSNSGNFVGKGMQPGTKAKVI 93
QY 61 HFEQVQPNNGNSYLAVGMTRNPLVEYYIVENFGTYDPSSGATDLGTYECDGSIYRLGKT 120
DB 94 NFGSTYPNGNSYLSYVGSWSRNPLEYIYVENFGTYDPSTGATDLGTYSDGSVYDIYRT 153
QY 121 TRVNPASIDGTQTPDOYVSVRQDKRTSGTYQVGCFFDAMARAGLVNNGDHYQIYATEGY 180
DB 154 QRVNPSTEGTSTYQYVSWARTRSQSVNTAHNFNASHGLTL-CTMDYQIYAVEGY 212
QY 181 FSSGVARITYA 191
DB 213 FSSGSASITVS 223

RESULT 12

US-08-768-373-2

Sequence 2, Application US/08768373

Patent No. 6228629

GENERAL INFORMATION:

APPLICANT: PALOHEIMO, MARJA

APPLICANT: HAKOLA, SATU

APPLICANT: M NTYL, ARJA

APPLICANT: VEHMAANPER, JARI

APPLICANT: LANTTO, RAUJA

APPLICANT: LAHTINEN, TARJA

APPLICANT: FAGERSTR M, RICHARD

APPLICANT: SUOMINEN, PIRKKO

TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: US

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/768,373

FILING DATE: 17-DEC-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/008,746

FILING DATE: 18-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/020,839

FILING DATE: 28-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: CIMBALA, MICHELE A.

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 1050.0540003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Chaetomium thermophilum

STRAIN: CB5730.95

FEATURE:

NAME/KEY: Protein

LOCATION: 1..261

OTHER INFORMATION: /label=XLNA

US-08-768-373-2

Query Match 58.6%; Score 637.5; DB 2; Length 261;
Best Local Similarity 60.1%; Pred. No. 1,4e-53;
Matches 113; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

QY 3 TPNSGMDGYXXYXWMSDGAQATYTNLEGTYSISWGDGNLVGGKGNPGLNARAIHF 62
DB 30 TSSATGHNGYYSFMTDGGNIRFNLESQGYSVTWSGNGVGGKGNPGLNARAIYV 89
QY 63 EGYVQPNNGNSYLAVGMTRNPLVEYYIVENFGTYDPSSGATDLGTYECDGSIYRLGKTR 122
DB 90 TADYRPNNGNSYLAVGMTRNPLVEYYIVENFGTYDPSTGATDMGSAVTTDGTNYIYRTQR 149
QY 123 VNAPSIDGTQTPDOYVSVRQDKRTSGTYQVGCFFDAMARAGLVNNGDHYQIYATEGYFS 182
DB 150 VNAPSIDGTQTPDOYVSVRQDKRTSGTYQVGCFFDAMARAGLVNNGDHYQIYATEGYFS 208
QY 183 SGYARITYV 190
DB 209 SSGATYVAV 216

RESULT 13

US-09-849-242A-2

Sequence 2, Application US/09849242A

Patent No. 6635464

GENERAL INFORMATION:

APPLICANT: PALOHEIMO, MARJA

APPLICANT: HAKOLA, SATU

APPLICANT: MONTYLO, ARJA

APPLICANT: VEHMAANPERO, JARI

APPLICANT: LANTTO, RAUJA

APPLICANT: LAHTINEN, TARJA

APPLICANT: FAGERSTRIM, RICHARD

APPLICANT: SUOMINEN, PIRKKO

TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: US

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/849,242A

FILING DATE: 07-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/768,373

FILING DATE: 17-DEC-1996

APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716, 0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: Protein
LOCATION: 1..261
OTHER INFORMATION: /label= XLNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-849-242A-2

Query Match 58.6%; Score 637.5; DB 2; Length 261;
Best Local Similarity 60.1%; Pred. No. 1,4e-53;
Matches 113; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

QY 3 TPNSGHHDDYYYSWMSDGAQATYTNLEGGTYEISMGDGNLVGKGNPGLNARAIHF 62
DB 30 TSSATGHNHYYYSFWTDGQGNIRFNLSSGQSVTSNGMNGWGKGNPGLDNRYINY 89
QY 63 EGYQPNNGNSYLAAYGWTNRNPLVEYYIYENFGTYDPSSGATDLGTVBCDSIYRLGKTR 122
DB 90 TADYRPNNGNSYLAAYGWTNRNPLVEYYIYENFGTYDPSSGATDLGTVBCDSIYRLGKTR 149
QY 123 VNAPSIDGTQTPQYWSVRQDKRTSGTVQTCHEPDANARAGLVNNGDHYQIVATGEGYS 162
DB 150 VNAPSIETGTFYQYWSVRSKRTGTVTMANHNARQAGLQ- GSHDYQIVATGEGYS 208
QY 183 SGYARITV 190
DB 209 SSGASATVY 216

RESULT 14
US-08-044-621D-28
; Sequence 28; Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Makarchuk
; APPLICANT: Ming L. Sung
; APPLICANT: Makoto Yaguchi
; APPLICANT: Robert L. Campbell
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gowling, Strachy & Henderson
; STREET: Suite 2600, 160 Elgin Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1P 1C3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
; OPERATING SYSTEM: PC-DOS

SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
STRAIN: Trichoderma harzianum, 20KD
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
AUTHORS: F., Tan L.U., Senior D.J., & Saddler
AUTHORS: J.N.
TITLE:
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 435-438
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-28

Query Match 58.5%; Score 636.5; DB 1; Length 190;
Best Local Similarity 60.7%; Pred. No. 1.2e-53;
Matches 116; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

QY 1 QTPNSGHHDDYYYSWMSDGAQATYTNLEGGTYEISMGDGNLVGKGNPGLNARAI 60
DB 1 QTIQPGTGYSNGYIYVNDGHGVTYTNNGGGGSPVNMNSNGNPFVGGKMGQGTNKKVI 60
QY 61 HFEQYQPNNGNSYLAAYGWTNRNPLVEYYIYENFGTYDPSSGATDLGTVBCDSIYRLGKT 120
DB 61 NFGSYNPNNGNSYLAAYGWTNRNPLVEYYIYENFGTYDPSSGATDLGTVBCDSIYRLGKT 120
QY 121 TRYNAPSIDGTQTPQYWSVRQDKRTSGTVQTCHEPDANARAGLVNNGDHYQIVATGEGY 180
DB 121 QRVNPSIITGATFFYQYWSVRNRRSSGVNTANHNARASHGLTL-GTMDYQIVAVEGY 179
QY 181 FSSGYARITVA 191
DB 180 FSSGASATVYS 190

RESULT 15
US-08-709-912-14
; Sequence 14; Application US/08709912

Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr., Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Thrichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Sadler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992

| | |
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| QY | 181 FSSGYARITVA 191 |
| | : |
| Db | 180 FSSGSASITVS 190 |

Search completed: February 10, 2006, 15:03:37
Job time : 33.8735 secs

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| | Best Local Similarity | 60.7% | Pred.No.1.2e-53; | | |
| | Matches 116; | Conservative 27; | Mismatches 47; | Indels 1; | Gaps 1. |
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| Dd | 1 | QTIGGTCTSYNSGYYSVYNNDHGAGTLYTNCGGGSTVAWMSGNVTGGKMGPGTKNNKYI | 60 | | |
| | | ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | | | |
| Cy | 61 | HFEGYIQENGNSYLAVYGKTRNPLEYIIVENFGTYDPSSGATDGTVECDGSITRLKGI | 120 | | |
| | | ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | | | |
| Dd | 61 | NFSGSYNPNNGNSYLSIYGWSRNPYLEEYIVENFGTNPBTGATKLGEVTSDSVDYIRKT | 120 | | |
| | | ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | | | |
| Cy | 121 | TRYNAPSIDGQTPOFYQSVSRDKRTSGVQVQCPEPDMARGLVNVDGHYYQIYAATGY | 180 | | |
| | | ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | | | |
| Dd | 121 | QRWDNPSTIIIGTAFFQYQWSVRNRNHSSGVGVANFNPAASHGLTL-GTMDQVIYAALVGXY | 179 | | |

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 15:17:55 ; Search time 113.437 Seconds
(without alignments)
714.573 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225
Perfect score: 1088
Sequence: 1 QTPNSEGMDHYGYSWMSD.....VATEGYSSGARITVADVG 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptcdaca/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptcdaca/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptcdaca/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptcdaca/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptcdaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1088 | 100.0 | 194 | US-10-307-441-20 | Sequence 20, Appl |
| 2 | 1088 | 100.0 | 194 | US-11-088-725A-46 | Sequence 46, Appl |
| 3 | 1088 | 100.0 | 225 | US-09-467-368-2 | Sequence 2, Appl |
| 4 | 1088 | 100.0 | 225 | US-10-237-386-24 | Sequence 24, Appl |
| 5 | 758 | 69.7 | 227 | US-10-237-386-21 | Sequence 21, Appl |
| 6 | 742 | 68.2 | 221 | US-10-237-386-20 | Sequence 20, Appl |
| 7 | 737 | 67.7 | 227 | US-10-425-115-221836 | Sequence 221836, |
| 8 | 725 | 66.6 | 221 | US-10-425-115-267585 | Sequence 267585, |
| 9 | 721 | 66.3 | 227 | US-10-237-386-22 | Sequence 22, Appl |
| 10 | 712 | 65.4 | 224 | US-10-425-115-361946 | Sequence 361946, |
| 11 | 663 | 60.9 | 197 | US-10-307-441-9 | Sequence 9, Appl |
| 12 | 663 | 60.9 | 197 | US-11-088-725A-36 | Sequence 36, Appl |
| 13 | 663 | 60.9 | 201 | US-10-237-386-23 | Sequence 23, Appl |
| 14 | 656 | 60.3 | 219 | US-10-237-386-29 | Sequence 29, Appl |
| 15 | 656 | 60.3 | 231 | US-10-237-386-26 | Sequence 26, Appl |
| 16 | 648 | 59.6 | 231 | US-10-237-386-25 | Sequence 25, Appl |
| 17 | 646 | 59.4 | 227 | US-10-237-386-27 | Sequence 27, Appl |
| 18 | 642.5 | 59.1 | 241 | US-10-237-386-35 | Sequence 35, Appl |
| 19 | 641 | 58.9 | 234 | US-10-213-990-69 | Sequence 69, Appl |
| 20 | 636.5 | 58.5 | 190 | US-10-307-441-14 | Sequence 14, Appl |
| 21 | 636.5 | 58.5 | 190 | US-11-088-725A-41 | Sequence 41, Appl |
| 22 | 635.5 | 58.4 | 222 | US-10-237-386-32 | Sequence 32, Appl |
| 23 | 635.5 | 58.4 | 222 | US-10-237-386-31 | Sequence 31, Appl |
| 24 | 633 | 58.2 | 189 | US-10-307-441-19 | Sequence 19, Appl |
| 25 | 633 | 58.2 | 189 | US-11-088-725A-28 | Sequence 28, Appl |
| 26 | 632.5 | 58.1 | 190 | US-10-307-441-17 | Sequence 17, Appl |
| 27 | 632.5 | 58.1 | 190 | US-10-307-441-17 | Sequence 17, Appl |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 632.5 | 58.1 | 190 | 6 | US-11-088-725A-42 | Sequence 42, Appl |
| 29 | 630.5 | 58.0 | 190 | 4 | US-10-237-386-33 | Sequence 33, Appl |
| 30 | 630 | 57.9 | 221 | 4 | US-10-213-990-66 | Sequence 66, Appl |
| 31 | 624.5 | 57.4 | 190 | 6 | US-11-088-725A-1 | Sequence 1, Appl |
| 32 | 623.5 | 57.3 | 223 | 4 | US-10-237-386-30 | Sequence 30, Appl |
| 33 | 616 | 56.6 | 225 | 4 | US-10-237-386-36 | Sequence 36, Appl |
| 34 | 609 | 56.0 | 233 | 4 | US-10-237-386-28 | Sequence 28, Appl |
| 35 | 604 | 55.5 | 221 | 4 | US-10-237-386-44 | Sequence 44, Appl |
| 36 | 585.5 | 53.8 | 223 | 4 | US-10-237-386-34 | Sequence 34, Appl |
| 37 | 576 | 52.9 | 223 | 4 | US-10-239-393-2 | Sequence 2, Appl |
| 38 | 576 | 52.9 | 223 | 6 | US-11-154-793-2 | Sequence 2, Appl |
| 39 | 573 | 52.7 | 313 | 4 | US-10-213-990-72 | Sequence 72, Appl |
| 40 | 571 | 52.5 | 240 | 4 | US-10-237-386-42 | Sequence 42, Appl |
| 41 | 568 | 52.2 | 189 | 4 | US-10-307-441-13 | Sequence 13, Appl |
| 42 | 568 | 52.2 | 189 | 6 | US-11-088-725A-40 | Sequence 40, Appl |
| 43 | 562.5 | 51.7 | 191 | 4 | US-10-307-441-10 | Sequence 10, Appl |
| 44 | 562.5 | 51.7 | 191 | 6 | US-11-088-725A-38 | Sequence 38, Appl |
| 45 | 562.5 | 51.7 | 228 | 4 | US-10-237-386-39 | Sequence 39, Appl |

ALIGNMENTS

```
RESULT 1
US-10-307-441-20
; Sequence 20, Application US/10307441
; Publication No. US2003016236A1
; GENERAL INFORMATION:
; APPLICANT: SING, Ming L.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307, 441
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213, 803
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
US-10-307-441-20

Query Match      100.0%; Score 1088; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QTPNSEGMDHYGYSWMSDGAQATYTNLEGCTYEISWDCGNLVGKGMNGLNARAI 60
Db      1 QTPNSEGMDHYGYSWMSDGAQATYTNLEGCTYEISWDCGNLVGKGMNGLNARAI 60

QY      61 HFEQVQPNNSLAVYGMTRNPLVEYIYENGTDPSSGATDLGVECDGSIYRIGKT 120
Db      61 HFEQVQPNNSLAVYGMTRNPLVEYIYENGTDPSSGATDLGVECDGSIYRIGKT 120

QY      121 TRNAPSIDGTQTFPDQYSVRQDKRTSGTVQTSCHFDAMARAGLNVGDHYOIVATEGY 180
Db      121 TRNAPSIDGTQTFPDQYSVRQDKRTSGTVQTSCHFDAMARAGLNVGDHYOIVATEGY 180

QY      181 FSSGYARITVADVG 194
Db      181 FSSGYARITVADVG 194

RESULT 2
US-11-088-725A-46
; Sequence 46, Application US/11088725A
; Publication No. US20050214410A1
; GENERAL INFORMATION:
```

APPLICANT: Iogen Bio-Products Corporation
APPLICANT: White, Theresa C
APPLICANT: Giroux, Genevieve R
APPLICANT: Wallace, Katie E.A.
TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
FILE REFERENCE: Q80712
CURRENT APPLICATION NUMBER: US/11/088,725A
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/556,061
PRIOR FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.2
SEQ ID NO 46
LENGTH: 194
TYPE: PRT
ORGANISM: Thermomyces lanuginosus
US-11-088-725A-46

Query Match 100.0%; Score 1088; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 1,7e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSRGMDGYYSWSDGGAQATYTNLEGTYEISWGDGNTLVGKGNPGLNRAI 60
DB 1 QTPNSRGMDGYYSWSDGGAQATYTNLEGTYEISWGDGNTLVGKGNPGLNRAI 60
QY HFEGVOPNGNSYLAAYGWTNPLVEYYIENFGTYDPSGATDLGTVCDGSIYRLGKT 120
DB 61 HFEGVOPNGNSYLAAYGWTNPLVEYYIENFGTYDPSGATDLGTVCDGSIYRLGKT 120
QY 121 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVGDHYQIVATEGY 180
DB 121 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVGDHYQIVATEGY 180
QY 181 FSSGARITVADV 194
DB 181 FSSGARITVADV 194

RESULT 3
US-09-467-368-2
Sequence 2, Application US/09467368
Patent No. US20020160080A1
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
Mullertz, Anette
Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: No. US20020160080A1o No. US20020160080A1disk of No. US200201600
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,368
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-467-368-2

Query Match 100.0%; Score 1088; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSRGMDGYYSWSDGGAQATYTNLEGTYEISWGDGNTLVGKGNPGLNRAI 60
DB 32 QTPNSRGMDGYYSWSDGGAQATYTNLEGTYEISWGDGNTLVGKGNPGLNRAI 91
QY 61 HFEGVOPNGNSYLAAYGWTNPLVEYYIENFGTYDPSGATDLGTVCDGSIYRLGKT 120
DB 92 HFEGVOPNGNSYLAAYGWTNPLVEYYIENFGTYDPSGATDLGTVCDGSIYRLGKT 151
QY 121 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVGDHYQIVATEGY 180
DB 152 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVGDHYQIVATEGY 211
QY 181 FSSGARITVADV 194
DB 212 FSSGARITVADV 225

RESULT 4
US-10-237-386-24
Sequence 24, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 225
TYPE: PRT
ORGANISM: T. lanuginosus
US-10-237-386-24

Query Match 100.0%; Score 1088; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSRGMDGYYSWSDGGAQATYTNLEGTYEISWGDGNTLVGKGNPGLNRAI 60
DB 32 QTPNSRGMDGYYSWSDGGAQATYTNLEGTYEISWGDGNTLVGKGNPGLNRAI 91
QY 61 HFEGVOPNGNSYLAAYGWTNPLVEYYIENFGTYDPSGATDLGTVCDGSIYRLGKT 120
DB 92 HFEGVOPNGNSYLAAYGWTNPLVEYYIENFGTYDPSGATDLGTVCDGSIYRLGKT 151
QY 121 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVGDHYQIVATEGY 180

Db 152 TRVNAPEIDGTQFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 211
Qy 181 FSSGYARITVADVG 194
Db 212 FSSGYARITVADVG 225

RESULT 5

US-10-237-386-21
Sequence 21, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanae Variants Having Altered Sensitivity to Xylanae Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 227
TYPE: PRT
ORGANISM: H. turcicum
US-10-237-386-21

Query Match 69.7%; Score 758; DB 4; Length 227;
Best Local Similarity 71.6%; Pred. No. 2.5e-65;
Matches 136; Conservative 20; Mismatches 32; Indels 2; Gaps 2;

Qy 1 QTPNBSGMDGYGYSWMSDGAQATYTNLEGGTYEISWMDGGLVGGKGMNPGLNARAI 60
Db 37 QSTPNBEGTNGGCFYSWMTDGGSKVYTNAGAGSYSVWGTGGTLVGGKGMNPG-TARTI 95
Qy 61 HPEGVYQPNNGNSYLAIVGWRNPLVEYYIENFGTYDPSSGATDLGVECDGSIYRLGKT 120
Db 96 TYSGVYNPNNGNSYLAIVGWRNPLVEYYIENFGTYDPSSGATDLGVECDGSIYRLGKT 155
Qy 121 TRVNAPEIDGTQFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 180
Db 156 TRTNQPSIDGTRTFQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 214
Qy 181 FSSGYARITV 190
Db 215 FSSGSASITV 224

RESULT 6

US-10-237-386-20
Sequence 20, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanae Variants Having Altered Sensitivity to Xylanae Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 221
TYPE: PRT
ORGANISM: C. carbonum
US-10-237-386-20

Query Match 68.2%; Score 742; DB 4; Length 221;
Best Local Similarity 70.0%; Pred. No. 8.5e-64;
Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

Qy 1 QTPNBSGMDGYGYSWMSDGAQATYTNLEGGTYEISWMDGGLVGGKGMNPGLNARAI 60
Db 31 QSTPNBEGTNGGCFYSWMTDGGSKVYTNAGAGSYSVWGTGGTLVGGKGMNPG-TARTI 89
Qy 61 HPEGVYQPNNGNSYLAIVGWRNPLVEYYIENFGTYDPSSGATDLGVECDGSIYRLGKT 120
Db 90 TYSGVYNPNNGNSYLAIVGWRNPLVEYYIENFGTYDPSSGATDLGVECDGSIYRLGKT 149
Qy 121 TRVNAPEIDGTQFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 180
Db 150 TRTNQPSIDGTRTFQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 208
Qy 181 FSSGYARITV 190
Db 209 FSTGNAGITV 218

RESULT 7

US-10-425-115-221836
Sequence 221836, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
PRIOR FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 221836
LENGTH: 227
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_133906C.1.pep
US-10-425-115-221836

Query Match 67.7%; Score 737; DB 4; Length 227;
Best Local Similarity 67.4%; Pred. No. 2.7e-63;
Matches 128; Conservative 28; Mismatches 32; Indels 2; Gaps 2;

Qy 1 QTPNBSGMDGYGYSWMSDGAQATYTNLEGGTYEISWMDGGLVGGKGMNPGLNARAI 60
Db 37 QSTPNBEGTNGGCFYSWMTDGGSKVYTNAGAGSYSVWGTGGTLVGGKGMNPG-SARTV 95
Qy 61 HPEGVYQPNNGNSYLAIVGWRNPLVEYYIENFGTYDPSSGATDLGVECDGSIYRLGKT 120
Db 96 TYSGVYNPNNGNSYLAIVGWRNPLVEYYIENFGTYDPSSGATDLGVECDGSIYRLGKT 155
Qy 121 TRVNAPEIDGTQFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 180
Db 156 TRTNQPSIDGTRTFQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 214
Qy 181 FSSGYARITV 190
Db 215 FSTGSASITV 224

RESULT 8

US-10-425-115-267585
; Sequence 267585, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 267585
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(221)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_175642C.1.pep
US-10-425-115-267585

Query Match 66.6%; Score 725; DB 4; Length 221;
Best Local Similarity 68.4%; Pred. No. 3.8e-62;
Matches 130; Conservative 22; Mismatches 36; Indels 2; Gaps 2;

QY 1 QTTPNSBGMHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNIYVGKGNPGLNARAI 60
DB 31 QNTNGEGTHNGCFWMSWSDGAAATYTNAGAGSYVWSGGNLYVGKGNPG-TARTI 89
QY 61 HPEGYOPNGNSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECGSIYRLGKT 120
DB 90 TYSGTYYNNGNSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECGSIYRLGKT 149
QY 121 TRVAPSIDGTQTPDOQYVSRQDKRTSGTGTGCFDAMARAGLVNNGDHYQIVATEGY 180
DB 150 TRNOPSIDGTRITQOQYVSRQDKRTSGTGTGCFDAMARAGLVNNGDHYQIVATEGY 208
QY 181 FSGYARITV 190
DB 209 FSTGNGQITV 218

RESULT 9
US-10-237-386-22
; Sequence 22, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent version 3.0
; SEQ ID NO 22
; LENGTH: 227
; TYPE: PRT
; ORGANISM: A. pisi
US-10-237-386-22

Query Match 66.3%; Score 721; DB 4; Length 227;
Best Local Similarity 69.1%; Pred. No. 9.7e-62;
Matches 130; Conservative 22; Mismatches 34; Indels 2; Gaps 2;

QY 3 TPNSBGMHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNIYVGKGNPGLNARAIHF 62
DB 39 TPSSQGTTHNGCFWMSWSDGAAATYTNAGAGSYVWSGGNLYVGKGNPG-AKITTY 97
QY 63 EGYVOPNGNSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECGSIYRLGKTTR 122
DB 98 SGTYSPGNSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECGSIYRLGKTTR 157
QY 123 VNAPSIDGTQTPDOQYVSRQDKRTSGTGTGCFDAMARAGLVNNGDHYQIVATEGYFS 182
DB 158 TNQPSIDGTITFQOQYVSRQDKRTSGTGTGCFDAMARAGLVNNGDHYQIVATEGYFS 216
QY 183 SGYARITV 190
DB 217 SSGSITV 224

RESULT 10
US-10-425-115-361946
; Sequence 361946, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 361946
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_93271C.1.pep
US-10-425-115-361946

Query Match 65.4%; Score 712; DB 4; Length 234;
Best Local Similarity 67.6%; Pred. No. 7.5e-61;
Matches 127; Conservative 24; Mismatches 35; Indels 2; Gaps 2;

QY 3 TPNSBGMHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNIYVGKGNPGLNARAIHF 62
DB 43 TPSSQGTTHNGCFWMSWSDGAAATYTNAGAGSYVWSGGNLYVGKGNPG-AKITTY 101
QY 63 EGYVOPNGNSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECGSIYRLGKTTR 122
DB 102 SGTYSPGNSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECGSIYRLGKTTR 161
QY 123 VNAPSIDGTQTPDOQYVSRQDKRTSGTGTGCFDAMARAGLVNNGDHYQIVATEGYFS 182
DB 162 VNQPSIDGTITFQOQYVSRQDKRTSGTGTGCFDAMARAGLVNNGDHYQIVATEGYFS 220
QY 183 SGYARITV 190
DB 221 SSGSITV 228

RESULT 11
US-10-307-441-9
; Sequence 9, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity

TITLE OF INVENTION: and Alkalophilicity
FILE REFERENCE: 027367-5006US
CURRENT APPLICATION NUMBER: US/10/307,441
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: PCT/CA01/00769
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/213,803
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 197
TYPE: PRT
ORGANISM: Schizopyllum commune
US-10-307-441-9

Query Match 60.9%; Score 663; DB 4; Length 197;
Best Local Similarity 61.3%; Pred. No. 3.5e-56;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 3 TPNSGMDGYYSWMSDGAQATYTNLEGGTYEISW-GDGGNLVGGKGNPGLNARAH 61
DB 3 TPSTGTGGYYSWMTDAGADATYQNNGGSYTLTWSGNNGNLVGGKGNPGLNARAH 62
QY 62 FEGVYQPNNGSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECDSIYRLGKT 121
DB 63 YSGTYQPNNGSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECDSIYRLGKT 122
QY 122 RVNAPSIDGTQTFEQFWSVNPVKAPGSGISGTVDVQCHFDAMKGLGMLGSEHNYQIVA 176
DB 123 RVNAPSIDGTQTFEQFWSVNPVKAPGSGISGTVDVQCHFDAMKGLGMLGSEHNYQIVA 182
QY 177 TEGYQSSGATITV 190
DB 183 TEGYQSSGATITV 196

RESULT 12

US-11-088-725A-36
Sequence 36, Application US/11088725A
Publication No. US20050214410A1
GENERAL INFORMATION:
APPLICANT: Iogen Bio-Products Corporation
APPLICANT: White, Theresa C
APPLICANT: Gloux, Genevieve R
APPLICANT: Wallace, Katie E.A.
TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
FILE REFERENCE: 080712
CURRENT APPLICATION NUMBER: US/11/088,725A
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/556,061
PRIOR FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36
LENGTH: 197
TYPE: PRT
ORGANISM: Schizopyllum commune
US-11-088-725A-36

Query Match 60.9%; Score 663; DB 6; Length 197;
Best Local Similarity 61.3%; Pred. No. 3.5e-56;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 3 TPNSGMDGYYSWMSDGAQATYTNLEGGTYEISW-GDGGNLVGGKGNPGLNARAH 61
DB 3 TPSTGTGGYYSWMTDAGADATYQNNGGSYTLTWSGNNGNLVGGKGNPGLNARAH 62
QY 62 FEGVYQPNNGSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECDSIYRLGKT 121
DB 63 YSGTYQPNNGSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECDSIYRLGKT 122
QY 122 RVNAPSIDGTQTFEQFWSVNPVKAPGSGISGTVDVQCHFDAMKGLGMLGSEHNYQIVA 176

DB 123 RVNAPSIDGTQTFEQFWSVNPVKAPGSGISGTVDVQCHFDAMKGLGMLGSEHNYQIVA 182
QY 177 TEGYQSSGATITV 190
DB 183 TEGYQSSGATITV 196

RESULT 13

US-10-237-386-23
Sequence 23, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibiessen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 201
TYPE: PRT
ORGANISM: S. commune
US-10-237-386-23

Query Match 60.9%; Score 663; DB 4; Length 201;
Best Local Similarity 61.3%; Pred. No. 3.6e-56;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 3 TPNSGMDGYYSWMSDGAQATYTNLEGGTYEISW-GDGGNLVGGKGNPGLNARAH 61
DB 5 TPSTGTGGYYSWMTDAGADATYQNNGGSYTLTWSGNNGNLVGGKGNPGLNARAH 64
QY 62 FEGVYQPNNGSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECDSIYRLGKT 121
DB 65 YSGTYQPNNGSYLAIVGWTNPLVEYYIVENFGTYDPSSGATDLGTYECDSIYRLGKT 124
QY 122 RVNAPSIDGTQTFEQFWSVNPVKAPGSGISGTVDVQCHFDAMKGLGMLGSEHNYQIVA 176
DB 125 RVNAPSIDGTQTFEQFWSVNPVKAPGSGISGTVDVQCHFDAMKGLGMLGSEHNYQIVA 184
QY 177 TEGYQSSGATITV 190
DB 185 TEGYQSSGATITV 198

RESULT 14

US-10-237-386-29
Sequence 29, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibiessen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27

```

; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 29
; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
US-10-237-386-29

```

```

Query Match 60.3%; Score 656; DB 4; Length 219;
Best Local Similarity 61.9%; Pred. No. 1.9e-55;
Matches 117; Conservative 28; Mismatches 42; Indels 2; Gaps 2;

```

```

QY 3 TPNSGMDGYYSWSDGQAQATYTNLEGGTYEISWDDGNLVGKGNPGLNARAIHF 62
DB 33 TPSTGTNGYFYSFMTDGGGTNYONGAGGSYSQWQNCNFGVGGKWNPGA-ARTINF 91
QY 63 EGVQPNNGSLAYVGMTNPLVEYIVENFGTYDPSSGATDLGTVPCDGSIVRLGKTR 122
DB 92 SGTSPQNGYLAIVGWTQNPVLEIVESFTYDPSSQASKFTIQDGSITYIAKTR 151
QY 123 VNAPSIDGTOTPDQWYSVRQDKRTSGTVQTCGHPDAMARAGLANVNGDHYIQIVATEGYFS 182
DB 152 VNQPSIDGTSTFPDQWYSVRQDKRTSGTVQTCGHPDAMARAGLANVNGDHYIQIVATEGYFS 210
QY 183 SGYARITVA 191
DB 211 SGSSSITVS 219

```

```

RESULT 15
US-10-237-386-26
; Sequence 26, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 26
; LENGTH: 231
; TYPE: PRT
; ORGANISM: C. sativus
US-10-237-386-26

```

```

Query Match 60.3%; Score 656; DB 4; Length 211;
Best Local Similarity 61.1%; Pred. No. 2.1e-55;
Matches 116; Conservative 27; Mismatches 45; Indels 2; Gaps 2;

```

```

QY 1 QTPNSGMDGYYSWSDGQAQATYTNLEGGTYEISWDDGNLVGKGNPGLNARAI 60
DB 41 QSTPSESGYHNGYFYSFMTDGGGSAQYTMGSGRSYVTWRNTGNFVGGKWNPGA-TGRVI 99
QY 61 HPEGVYQPNNGSLAYVGMTNPLVEYIVENFGTYDPSSGATDLGTVPCDGSIVRLGKT 120
DB 100 NYGAFNPQNGYLAIVGWTNPLVEIVISYGTNPSSGAQYKGSFOTDGGTYINAVS 159
QY 121 TRVAPSIDGTOTPDQWYSVRQDKRTSGTVQTCGHPDAMARAGLANVNGDHYIQIVATEGY 180
DB 160 TRVNPISIDGTTRTPQYQWYSVRQDKRTSGTVQTCGHPDAMARAGLANVNGDHYIQIVATEGY 218
QY 181 FSSGYARITV 190

```

DB 219 QSSGSSDIYV 228

Search completed: February 10, 2006, 15:22:35
Job time : 113.437 sec

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: February 10, 2006, 15:18:39 ; Search time 9.72315 Seconds
(without alignments)
261.826 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225
Perfect score: 1088
Sequence: 1 QTPNSEGMDGYYSWMSD.....VATEGYSSGARITVADVG 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/prodata/1/pubppa/US08 NEW PUB.pep:*
2: /cgn2_6/prodata/1/pubppa/US06 NEW PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US07 NEW PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubppa/US09 NEW PUB.pep:*
6: /cgn2_6/prodata/1/pubppa/US10 NEW PUB.pep:*
7: /cgn2_6/prodata/1/pubppa/US11 NEW PUB.pep:*
8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------------------------|
| 1 | 1088 | 100.0 | 225 | 7 | US-11-170-653-24 Sequence 24, Appl |
| 2 | 758 | 69.7 | 227 | 7 | US-11-170-653-21 Sequence 21, Appl |
| 3 | 742 | 68.2 | 221 | 7 | US-11-170-653-20 Sequence 20, Appl |
| 4 | 721 | 66.3 | 227 | 7 | US-11-170-653-22 Sequence 22, Appl |
| 5 | 663 | 60.9 | 201 | 7 | US-11-170-653-23 Sequence 23, Appl |
| 6 | 656 | 60.3 | 219 | 7 | US-11-170-653-29 Sequence 29, Appl |
| 7 | 656 | 60.3 | 231 | 7 | US-11-170-653-26 Sequence 26, Appl |
| 8 | 648 | 59.6 | 231 | 7 | US-11-170-653-25 Sequence 25, Appl |
| 9 | 646 | 59.4 | 227 | 7 | US-11-170-653-27 Sequence 27, Appl |
| 10 | 642.5 | 59.1 | 241 | 7 | US-11-170-653-35 Sequence 35, Appl |
| 11 | 635.5 | 58.4 | 222 | 7 | US-11-170-653-32 Sequence 32, Appl |
| 12 | 635.5 | 58.0 | 223 | 7 | US-11-170-653-31 Sequence 31, Appl |
| 13 | 630.5 | 58.0 | 190 | 7 | US-11-170-653-33 Sequence 33, Appl |
| 14 | 623.5 | 57.3 | 223 | 7 | US-11-170-653-30 Sequence 30, Appl |
| 15 | 616 | 56.6 | 225 | 7 | US-11-170-653-36 Sequence 36, Appl |
| 16 | 609 | 56.0 | 223 | 7 | US-11-170-653-28 Sequence 28, Appl |
| 17 | 604 | 55.5 | 221 | 7 | US-11-170-653-44 Sequence 44, Appl |
| 18 | 598 | 55.0 | 432 | 6 | US-10-517-939-178 Sequence 178, Appl |
| 19 | 585.5 | 53.8 | 223 | 7 | US-11-170-653-34 Sequence 34, Appl |
| 20 | 571 | 52.5 | 240 | 7 | US-11-170-653-42 Sequence 42, Appl |
| 21 | 569.5 | 52.3 | 335 | 6 | US-10-517-939-232 Sequence 232, Appl |
| 22 | 564 | 51.8 | 348 | 6 | US-10-517-939-166 Sequence 166, Appl |
| 23 | 562.5 | 51.7 | 228 | 7 | US-11-170-653-39 Sequence 39, Appl |
| 24 | 560 | 51.5 | 193 | 7 | US-11-108-163B-14 Sequence 14, Appl |
| 25 | 560 | 51.5 | 217 | 7 | US-11-108-163B-13 Sequence 13, Appl |

| | | | | | |
|----|-------|------|-----|---|--------------------------------------|
| 26 | 560 | 51.5 | 220 | 7 | US-11-108-163B-12 Sequence 12, Appl |
| 27 | 560 | 51.5 | 301 | 7 | US-11-108-163B-11 Sequence 11, Appl |
| 28 | 560 | 51.5 | 344 | 7 | US-11-108-163B-10 Sequence 10, Appl |
| 29 | 555.5 | 51.1 | 221 | 7 | US-11-170-653-37 Sequence 37, Appl |
| 30 | 554 | 50.9 | 239 | 7 | US-11-170-653-40 Sequence 40, Appl |
| 31 | 554 | 50.9 | 242 | 7 | US-11-170-653-41 Sequence 41, Appl |
| 32 | 544 | 50.0 | 241 | 7 | US-11-170-653-43 Sequence 43, Appl |
| 33 | 543.5 | 50.0 | 240 | 7 | US-11-170-653-38 Sequence 38, Appl |
| 34 | 541 | 49.7 | 354 | 6 | US-10-517-939-216 Sequence 216, Appl |
| 35 | 537 | 49.4 | 358 | 6 | US-10-517-939-182 Sequence 182, Appl |
| 36 | 535 | 49.2 | 352 | 6 | US-10-517-939-226 Sequence 226, Appl |
| 37 | 533.5 | 49.0 | 542 | 6 | US-10-517-939-262 Sequence 262, Appl |
| 38 | 532.5 | 48.9 | 216 | 7 | US-11-170-653-45 Sequence 45, Appl |
| 39 | 531 | 48.8 | 303 | 6 | US-10-517-939-214 Sequence 214, Appl |
| 40 | 526.5 | 48.4 | 347 | 6 | US-10-517-939-196 Sequence 196, Appl |
| 41 | 524 | 48.2 | 445 | 6 | US-10-517-939-368 Sequence 368, Appl |
| 42 | 524 | 48.2 | 237 | 7 | US-11-170-653-47 Sequence 47, Appl |
| 43 | 522.5 | 48.0 | 225 | 6 | US-10-517-939-172 Sequence 172, Appl |
| 44 | 520.5 | 47.8 | 358 | 6 | US-10-517-939-370 Sequence 370, Appl |
| 45 | 512.5 | 47.1 | 346 | 6 | US-10-517-939-160 Sequence 160, Appl |

ALIGNMENTS

RESULT 1
US-11-170-653-24
Sequence 24, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 225
TYPE: PRT
ORGANISM: T. lanuginosus
US-11-170-653-24

Query Match 100.0%; Score 1088; DB 7; length 225;
Best Local Similarity 100.0%; Pred. No. 1.7e-93;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSEGMDGYYSWMSDGAQATYTNLEGGTYIISWGGNLYGKGMNGLNARAI 60
DB 32 QTPNSEGMDGYYSWMSDGAQATYTNLEGGTYIISWGGNLYGKGMNGLNARAI 91
QY 61 HFEQGVOPNGNSLAVYGTWRNPLVEYIVENGTDPSSGATDLGTVECDGSYRLGKT 120
DB 92 HFEQGVOPNGNSLAVYGTWRNPLVEYIVENGTDPSSGATDLGTVECDGSYRLGKT 151
QY 121 TRVNASIDGTQTFPDQYMSVRQDKRTSGTVQSGCHFDANARAGLNNGHYOIVATEGY 180
DB 152 TRVNASIDGTQTFPDQYMSVRQDKRTSGTVQSGCHFDANARAGLNNGHYOIVATEGY 211
QY 181 FSSGYARITVADVG 194
DB 212 FSSGYARITVADVG 225

```

RESULT 2
US-11-170-653-21
; Sequence 21, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 227
; TYPE: prt
; ORGANISM: H. turcicum
US-11-170-653-21

```

| | | | | |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 69.7%; | Score 758; | DB 7; | Length 227; |
| Best Local Similarity | 71.6%; | Pred. No. 4.7e-63; | | |
| Matches 136; | Conservative 20; | Mismatches 32; | Indels 2; | Gaps 24 |

```
QY 1 OTTPNSEGHHDCYYYSWMSDGGQAQAYTNLEGGTYELSMWDDGNLVGKKMNNGLNARAI 60
Db 37 OSTEPGEGBHCNCFYSWMSDGGARATYTGAGGSISVSMCTGNNLVGKKMNNFG-TARTI 95
QY 61 HBEGVQPPNGNSYLAVYGWTRNPLVEYYIIVENGTDPSSGATDLGVECDGSIYRLGKT 120
Db 96 TYSQGYNPPNGNSYLAIYGMTRNPLVEYYVENGTDPSSQAQNNKTVYSDGSYKAAQS 155
QY 121 TRVNAPSIDGTOTFDQYMSVVRQDKRTSGYQTCGHPDAMARAGLNVNGDHYIQIVATEGY 180
Db 156 TRTNQPSIDGTRTFQCYMSVVRQDKRSSGSVNMKTHFDAMASKMNNL-GSHYQIVATEGY 214
QY 181 FSSGYSARTIV 190
Db 215 FSSGSASITV 224
```

```

/ RESULT 3
/ US-11-170-653-20
/ Sequence 20, Application US/11170653
/ Publication No. US20050271769A1
/ GENERAL INFORMATION:
/ APPLICANT: Danisco A/S
/ APPLICANT: Sildesen, Ole
/ APPLICANT: Sorensen, Jens
/ TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
/ FILE REFERENCE: 674509-2046
/ CURRENT APPLICATION NUMBER: US/11/170,653
/ CURRENT FILING DATE: 2005-06-23
/ PRIOR APPLICATION NUMBER: US/10/237,386
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: PCT/IB01/00426
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: GB 0005585.5
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: GB 0015751.1
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 20

```

```

; LENGTH: 221
; TYPE: PRT
; ORGANISM: C. carbonum
US-11-170-653-20

```

| | | | | |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 68.2%; | Score 742; | DB 7; | Length 221; |
| Best Local Similarity | 70.0%; | Pred. No. 1.4e-61; | | |
| Matches 133; | Conservative 22; | Mismatches 33; | Indels 2; | Gaps 2; |

QY 1 QTPNPECEMHQGYYSWMSDGAQKTYTNLEGATYEISMGDGNLVGGKGNPGLNARAI 60
 Db 31 QNTNGEBETHNGCFRSMWSDGARITYTNAGAGSISVSMGSGNLVGGKGNPFG-TARTI 89
 QY 61 HFEGYOENGSYLAIVGWTNPLVEYYIVENFGTYDPSGATDLGYECDGSIYRLGKT 120
 Db 90 TYSGTNNNGNSYLAIVGWTNPLVEYYIVENFGTYDPSGQGNKGTATSDSSYKLAOS 149
 QY 121 TRVNAAPSIDGQTPDQYWSVRQDKTSGTVQTGCFPDANARGLNVNNGHYIYQIVATGEY 180
 Db 150 TRINQPSIDGTRTFQOQYWSVRQNKRSRSGSVNNKTHFDMAASKMNL-GQHYIYQIVATGEY 208
 QY 181 FSSGVARITV 190
 Db 209 FSTGNAQILT 218

RESULT 4
US-11-170-653-22

```

1  APPLICANT: Danisco A/S
2  APPLICANT: Sildesen, Ole
3  APPLICANT: Sorensen, Jens
4  TITLE OF INVENTION: Xylanae Variants Having Altered Sensitivity to Xylanae Inhibitors
5  FILE REFERENCE: 674509-2046
6  CURRENT APPLICATION NUMBER: US/11/170,653
7  CURRENT FILING DATE: 2005-06-23
8  PRIOR APPLICATION NUMBER: US/10/237,386
9  PRIOR FILING DATE: 2002-09-09
10 PRIOR APPLICATION NUMBER: PCT/IB01/00426
11 PRIOR FILING DATE: 2001-03-08
12 PRIOR APPLICATION NUMBER: GB 0005585.5
13 PRIOR FILING DATE: 2000-03-08
14 PRIOR APPLICATION NUMBER: GB 0015751.1
15 PRIOR FILING DATE: 2000-06-27
16 NUMBER OF SEQ ID NOS: 66
17 SOFTWARE: PatentIn version 3.0
18 SEQ ID NO 22
19 LENGTH: 227
20 TYPE: PRT
21 ORGANISM: A. pisi
22 US-11-170-653-22

```

| | | | | |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 66.3% | Score 721; | DB 7; | Length 227; |
| Best Local Similarity | 69.1%; | Pred. No. 1.2e-59; | | |
| Matches 130; | Conservative 22; | Mismatches 34; | Indels 2; | Gaps 2; |

[illegible]

```

RESULT 5
US-11-170-653-23
: Sequence 23, Application US/11170653
: Publication No. US20050271769A1
: GENERAL INFORMATION:
:   APPLICANT: Danisco A/S
:   APPLICANT: Sidsesen, Ole
:   APPLICANT: Sorensen, Jens
:   TITLE OR INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
:   FILE REFERENCE: 674509-2046
:   CURRENT APPLICATION NUMBER: US/11/170, 653
:   CURRENT FILING DATE: 2005-06-23
:   PRIOR APPLICATION NUMBER: US/10/237,386
:   PRIOR FILING DATE: 2002-09-09
:   PRIOR APPLICATION NUMBER: PCT/IB01/00426
:   PRIOR FILING DATE: 2001-03-08
:   PRIOR APPLICATION NUMBER: GB 0005585.5
:   PRIOR FILING DATE: 2000-03-08
:   PRIOR APPLICATION NUMBER: GB 0015751.1
:   PRIOR FILING DATE: 2000-06-27
:   NUMBER OF SEQ ID NOS: 66
:   SOFTWARE: PatentIn version 3.0
:   SEQ ID NO 23
:   LENGTH: 201
:   TYPE: PRF
:   ORGANISM: S. commune
US-11-170-653-23

```

| | | | | |
|---------------------------|-------|-------------------|----------|------------|
| Query Match | 60.9% | Score 663 | DB 7 | Length 201 |
| Best Local Similarity | 61.3% | Pred. NO. 2.3e-54 | | |
| Matches 119, Conservative | 26 | Mismatches 43 | Indels 6 | Gaps 2 |

[illegible]

```

1      RESULT 6
2      US-11-170-653-29
3      ; Sequence 29, Application US/11170653
4      ; Publication NO. US20050271769A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Danisco A/S
7      ; APPLICANT: Stibbeeen, Ole
8      ; APPLICANT: Sorensen, Jens
9      ; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
10     ; FILE REFERENCE: 674509-2046
11     ; CURRENT APPLICATION NUMBER: US/11/170,653
12     ; CURRENT FILING DATE: 2005-06-23
13     ; PRIOR APPLICATION NUMBER: US/10/237,386
14     ; PRIOR FILING DATE: 2002-09-09
15     ; PRIOR APPLICATION NUMBER: PCT/IB01/00426
16     ; PRIOR FILING DATE: 2001-03-08
17     ; PRIOR APPLICATION NUMBER: GB 0005585.5
18     ; PRIOR FILING DATE: 2000-03-08
19     ; PRIOR APPLICATION NUMBER: GB 0015751.1
20     ; PRIOR FILING DATE: 2000-06-27
21     ; NUMBER OF SEQ ID NOS: 66
22     ; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 29
; LENGTH: 219
; TYPE: prt
; ORGANISM: C. gracile
US-11-170-653-29

```

| | | | | |
|-----------------------|-----------------|-------------------|----------|------------|
| Query Match | 60.3% | Score 656 | DB 7 | length 219 |
| Best Local Similarity | 61.9% | Pred. No. 1.1e-53 | | |
| Matches 117 | Conservative 28 | Mismatches 42 | Indels 2 | Gaps 2 |

[illegible]

RESULT 7
US-11-170-653-26

; Sequence 26, Application US/11170653
; Publication No. US20050271769A1

```

; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26

```

ORGANISM: C. sativus
US-11-170-653-26

| | | | | |
|-----------------------|-----------------|-------------------|----------|------------|
| Query Match | 60.3% | Score 656 | DB 7 | Length 231 |
| Best Local Similarity | 61.1% | Pred. No. 1.2e-53 | | |
| Matches 116 | Conservative 27 | Mismatches 45 | Indels 2 | Gaps 2 |

```

0Y      1 OTTPBSECMHOGYXXYSMSDDGAQATNTNLBEGTBEISWDDGDNVLVGKGMNGLNARAI 60
      2 |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      41 OSTPBSEGYHNGYFISWMTDGGGSAQYTMGBESRSVYWRATGNFVGKGMNPG -GRVY 99

0Y      61 HPEGYOQNGNSYLAIVGCMTRNPLVEYYIVENFGTYDPSSGATDUGTBCDSIYRLGKT 120
      62 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      100 NYGGAFFNQGNGYLAIVGCMTRNPLVEYYIIBSYBGYENPSSGQVKGSSFOITDGGTVNAVAS 159

0Y      121 TRVNAPSIDGOTPDQYMSVRODKRTSGTVQTCGHPDAARAGLANNNGHYQIVATEGY 180
      122 |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      160 TRYNOPSIDGRTTRFOQYMSVROQKQVKGSSVMNQNHFNAMSRGLNL -GHHYQIVATEGY 218

0Y      181 FSSGYARITV 190
      182 |||::|::|

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Db 219 QSSGSSDIYV 228

RESULT 8

Sequence 25, Application US/11170653
Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sbbeen, Ole

APPLICANT: Sbbeen, Jens

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170, 653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 25

LENGTH: 231

TYPE: PRT

ORGANISM: C. carbonum

US-11-170-653-25

Query Match 59.6%; Score 648; DB 7; Length 231;

Best Local Similarity 60.0%; Pred. No. 6,7e-53;

Matches 114; Conservative 29; Mismatches 45; Indels 2; Gaps 2;

QY 1 QTPNBSGMDHYYSWSDGQAQATYTNLEGGTYEISWGDGGLVGGKGNPGLNARA 60

Db 41 QSTPSAGYHNGFYYSWTDGSGSAQYMGESRYSVTWRNTGNFVGKGNPG-SGRVI 99

QY 61 HFEGVYQPNNGSYLAAYGWTNPLVEYYIVENFGTYDPSSGATDGLGTVBCDGSYRLGKT 120

Db 100 NYGAFNPQNGSYLAAYGWTNPLVEYYIVENFGTYDPSSGATDGLGTVBCDGSYRLGKT 159

QY 121 TRVAPSIDGTOTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLVNNGDHYQIVATEGY 180

Db 160 TRVNPISIDGTRTFQYWSVRQDKRTSGTVQTCGHPDAMARAGLVNNGDHYQIVATEGY 218

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

Db 219 QSSGSSDIYV 228

QY 181 FSSGYARITV 190

SOFTWARE: PatentIn version 3.0

SEQ ID NO 27

LENGTH: 227

TYPE: PRT

ORGANISM: H. insolens

US-11-170-653-27

Query Match 59.4%; Score 646; DB 7; Length 227;

Best Local Similarity 59.5%; Pred. No. 1e-52;

Matches 113; Conservative 27; Mismatches 48; Indels 2; Gaps 2;

QY 1 QTPNBSGMDHYYSWSDGQAQATYTNLEGGTYEISWGDGGLVGGKGNPGLNARA 60

Db 37 QTPNBSGMDHYYSWSDGQAQATYTNLEGGTYEISWGDGGLVGGKGNPGLNARA 95

QY 61 HFEGVYQPNNGSYLAAYGWTNPLVEYYIVENFGTYDPSSGATDGLGTVBCDGSYRLGKT 120

Db 96 HFEGVYQPNNGSYLAAYGWTNPLVEYYIVENFGTYDPSSGATDGLGTVBCDGSYRLGKT 155

QY 121 TRVAPSIDGTOTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLVNNGDHYQIVATEGY 180

Db 156 TRVNPISIDGTRTFQYWSVRQDKRTSGTVQTCGHPDAMARAGLVNNGDHYQIVATEGY 214

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

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Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 215 QSSGSSDIYV 224

QY 181 FSSGYARITV 190

Db 209 YSSGSATVAV 219

RESULT 11

US-11-170-653-32
Sequence 32, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibielsen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 32
LENGTH: 222
TYPE: PRT
ORGANISM: T. reesei
US-11-170-653-32

Query Match 58.4%; Score 635.5; DB 7; Length 222;

Best Local Similarity 60.2%; Pred. No. 9e-52; Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 1 QTPNBSGMDGVYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGMNPGLNARAI 60
DB 33 QTIQPGGVNNGYFYISWMDHGGVYTTNPGQGFYSWMSNSGNFVGKGMQGTAKKVI 92
QY 61 HFEGVYQPNNSYLAIVGWTNPLVEYYIYENFGTYDPSGATDLGVECDGSYIRLGKT 120
DB 93 NFGSYNPNNSYLSYVGMGRNPLIEYYIYENFGTYDPSGATDLGVECDGSYIRLT 152
QY 121 TRNAPSIDGTQTFDQYWSVRQDKRTSGYQTCGHPAMARAGLVNNGDHYQIVATEGY 180
DB 153 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQGLTL-GTMDYQIVAVEGY 211
QY 181 FSSGYARITVA 191
DB 212 FSSGSASITVS 222

RESULT 12

US-11-170-653-31
Sequence 31, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibielsen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENGTH: 223
TYPE: PRT
ORGANISM: T. reesei
US-11-170-653-31

Query Match 58.4%; Score 635.5; DB 7; Length 223;
Best Local Similarity 60.2%; Pred. No. 9.1e-52; Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 1 QTPNBSGMDGVYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGMNPGLNARAI 60
DB 34 QTIQPGGVNNGYFYISWMDHGGVYTTNPGQGFYSWMSNSGNFVGKGMQGTAKKVI 93
QY 61 HFEGVYQPNNSYLAIVGWTNPLVEYYIYENFGTYDPSGATDLGVECDGSYIRLGKT 120
DB 94 NFGSYNPNNSYLSYVGMGRNPLIEYYIYENFGTYDPSGATDLGVECDGSYIRLT 153
QY 121 TRNAPSIDGTQTFDQYWSVRQDKRTSGYQTCGHPAMARAGLVNNGDHYQIVATEGY 180
DB 154 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQGLTL-GTMDYQIVAVEGY 212
QY 181 FSSGYARITVA 191
DB 213 FSSGSASITVS 223

RESULT 13

US-11-170-653-33
Sequence 33, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibielsen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 33
LENGTH: 190
TYPE: PRT
ORGANISM: T. harzianum
US-11-170-653-33

Query Match 58.0%; Score 630.5; DB 7; Length 190;
Best Local Similarity 60.2%; Pred. No. 2.2e-51; Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;

QY 1 QTPNBSGMDGVYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGMNPGLNARAI 60
DB 1 QTIQPGGVNNGYFYISWMDHGGVYTTNPGQGFYSWMSNSGNFVGKGMQGTAKKVI 60
QY 61 HFEGVYQPNNSYLAIVGWTNPLVEYYIYENFGTYDPSGATDLGVECDGSYIRLGKT 120
DB 61 NFGSYNPNNSYLSYVGMGRNPLIEYYIYENFGTYDPSGATDLGVECDGSYIRLT 120
QY 121 TRNAPSIDGTQTFDQYWSVRQDKRTSGYQTCGHPAMARAGLVNNGDHYQIVATEGY 180
DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQGLTL-GTMDYQIVAVEGY 179

Qy 181 FSSGVARITVA 191
Db 180 FSSGSASITVS 190

RESULT 14

US-11-170-653-30
; Sequence 30, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-11-170-653-30

Query Match 57.3%; Score 623.5; DB 7; Length 223;
Best Local Similarity 59.2%; Pred. No. 1.2e-50;
Matches 113; Conservative 29; Mismatches 48; Indels 1; Gaps 1;

Qy 1 QTPNSGEMHDGYYSWSDGAAQATYTNLEGTYEISWGDGNLVGKGMNPGANARAI 60
Db 34 QTLOPGGYNNNGYHSYNDHGHGVTYTNNGPGQPSVWMSNSGNFVGKGMQPGTKNKVI 93
Qy 61 HFEGVYQPNNGSYLAVYGWTRNPLVEYYIVENFGTYDPSGATDLGTVBCDGSYIRLQKT 120
Db 94 NFSGSYNPNNGNSYLSYVGWMSRNPILIEYYIVGNFGTYNPSTGATKLGVTSDGSYYDIYRT 153
Qy 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTYQTGCHFDAMARAGLVNNGDHYOIVATEGY 180
Db 154 QRVNQPSLIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTL-GTMDYQIVAVEGY 212
Qy 181 FSSGVARITVA 191
Db 213 FSSGSASITVS 223

RESULT 15

US-11-170-653-36
; Sequence 36, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 225
; TYPE: PRT
; ORGANISM: A. niger
US-11-170-653-36

Query Match 56.6%; Score 616; DB 7; Length 225;
Best Local Similarity 58.4%; Pred. No. 5.8e-50;
Matches 111; Conservative 30; Mismatches 47; Indels 2; Gaps 2;

Qy 1 QTPNSGEMHDGYYSWSDGAAQATYTNLEGTYEISWGDGNLVGKGMNPGANARAI 60
Db 37 RSTPSTGENNGFYISFMTDGGDDVTYTNDAQATYVEMSNVGNFVGKGMNPG-SAQDI 95
Qy 61 HFEGVYQPNNGSYLAVYGWTRNPLVEYYIVENFGTYDPSGATDLGTVBCDGSYIRLQKT 120
Db 96 TYSGETPSSGNGYLSYGWTTDPLIEYYIVESYGDYNPGSGGTYKGTVTSDGSYYDIYTA 155
Qy 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTYQTGCHFDAMARAGLVNNGDHYOIVATEGY 180
Db 156 TRTNASISQGTATFTQYWSVRQNKRVGGIVTTSNHFNAKLGML-GTANYQIVATEGY 214
Qy 181 FSSGVARITV 190
Db 215 QSSGSSSITV 224

Search completed: February 10, 2006, 15:23:01
Job time : 9.72315 secs